

- Alignment No. 8372
- gi No. 1666232
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8373
- gi No. 1666234
- % Identity 89.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8374
- gi No. 1669387
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8375
- gi No. 1669389
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8376
- gi No. 167589
- % Identity 88
- Alignment Length 83
- Location of Alignment in SEQ ID NO 923: from 25 to 107
  
- Alignment No. 8377
- gi No. 167600
- % Identity 90.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 923: from 47 to 107
  
- Alignment No. 8378
- gi No. 167605
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 923: from 43 to 107
  
- Alignment No. 8379
- gi No. 167612
- % Identity 88.5
- Alignment Length 87
- Location of Alignment in SEQ ID NO 923: from 21 to 107
  
- Alignment No. 8380
- gi No. 167642
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 923: from 20 to 107
  
- Alignment No. 8381
- gi No. 167652
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 923: from 54 to 107
  
- Alignment No. 8382

- gi No. 168404
- % Identity 84.8
- Alignment Length 138
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8383
- gi No. 1703100
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8384
- gi No. 1703101
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8385
- gi No. 1703102
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8386
- gi No. 1703103
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8387
- gi No. 1703106
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8388
- gi No. 1703107
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8389
- gi No. 1703108
- % Identity 98.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8390
- gi No. 1703109
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8391
- gi No. 1703110
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8392
- gi No. 1703111



- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8393
- gi No. 1703112
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8394
- gi No. 1703114
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8395
- gi No. 1703115
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8396
- gi No. 1703116
- % Identity 85.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8397
- gi No. 1703117
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8398
- gi No. 1703118
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8399
- gi No. 1703119
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8400
- gi No. 1703120
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8401
- gi No. 1703121
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8402
- gi No. 1703122
- % Identity 86.1

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8403
- gi No. 1703123
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8404
- gi No. 1703124
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8405
- gi No. 1703125
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8406
- gi No. 1703127
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8407
- gi No. 1703128
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8408
- gi No. 1703129
- % Identity 93.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8409
- gi No. 1703130
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8410
- gi No. 1703131
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8411
- gi No. 1703132
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8412
- gi No. 1703133
- % Identity 86.1
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8413
- gi No. 1703134
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8414
- gi No. 1703135
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8415
- gi No. 1703136
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8416
- gi No. 1703137
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8417
- gi No. 1703138
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8418
- gi No. 1703139
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8419
- gi No. 1703140
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8420
- gi No. 1703141
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8421
- gi No. 1703142
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8422
- gi No. 1703147
- % Identity 78.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8423
- gi No. 1703148
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8424
- gi No. 1703149
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8425
- gi No. 1703151
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8426
- gi No. 1703152
- % Identity 74.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8427
- gi No. 1703153
- % Identity 81.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8428
- gi No. 1703154
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8429
- gi No. 1703156
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8430
- gi No. 1703157
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8431
- gi No. 1703158
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8432
- gi No. 1703160
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8433
- gi No. 1703161
- % Identity 70.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8434
- gi No. 178067
- % Identity 82.2
- Alignment Length 90
- Location of Alignment in SEQ ID NO 923: from 1 to 60
  
- Alignment No. 8435
- gi No. 1813478
- % Identity 72.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8436
- gi No. 1871174
- % Identity 86.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8437
- gi No. 1882997
- % Identity 79.6
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8438
- gi No. 1883024
- % Identity 83.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8439
- gi No. 1883032
- % Identity 78.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8440
- gi No. 1906607
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8441
- gi No. 20322
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8442
- gi No. 2072156
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8443

- gi No. 2119321
- % Identity 83.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 923: from 1 to 13
  
- Alignment No. 8444
- gi No. 2119323
- % Identity 80.3
- Alignment Length 71
- Location of Alignment in SEQ ID NO 923: from 1 to 64
  
- Alignment No. 8445
- gi No. 2119324
- % Identity 89.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 923: from 41 to 107
  
- Alignment No. 8446
- gi No. 2119325
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 923: from 34 to 87
  
- Alignment No. 8447
- gi No. 2119327
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 923: from 1 to 12
  
- Alignment No. 8448
- gi No. 2119330
- % Identity 91.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 923: from 61 to 107
  
- Alignment No. 8449
- gi No. 2129524
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8450
- gi No. 2129529
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8451
- gi No. 2136927
- % Identity 84.1
- Alignment Length 44
- Location of Alignment in SEQ ID NO 923: from 1 to 14
  
- Alignment No. 8452
- gi No. 2136927
- % Identity 84.7
- Alignment Length 72
- Location of Alignment in SEQ ID NO 923: from 36 to 107
  
- Alignment No. 8453
- gi No. 223071

- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8454
- gi No. 2231555
- % Identity 73.9
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63
  
- Alignment No. 8455
- gi No. 2231557
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63
  
- Alignment No. 8456
- gi No. 2231561
- % Identity 72.8
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63
  
- Alignment No. 8457
- gi No. 223597
- % Identity 73
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8458
- gi No. 223855
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8459
- gi No. 224304
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8460
- gi No. 224305
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8461
- gi No. 224306
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8462
- gi No. 2244734
- % Identity 96.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8463
- gi No. 225100
- % Identity 78.8

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8464
- gi No. 2253214
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8465
- gi No. 2253217
- % Identity 84.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8466
- gi No. 2253219
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8467
- gi No. 2253221
- % Identity 84.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8468
- gi No. 2253223
- % Identity 76.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8469
- gi No. 2289966
- % Identity 84.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8470
- gi No. 2289971
- % Identity 81.9
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8471
- gi No. 2289975
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8472
- gi No. 229690
- % Identity 84.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 923: from 1 to 104
  
- Alignment No. 8473
- gi No. 2304965
- % Identity 85.4
- Alignment Length 137



- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8474
- gi No. 2304969
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8475
- gi No. 231494
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8476
- gi No. 231495
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8477
- gi No. 231496
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8478
- gi No. 231498
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8479
- gi No. 231499
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8480
- gi No. 231501
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8481
- gi No. 231503
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8482
- gi No. 231504
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8483
- gi No. 231505
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8484
- gi No. 231506
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8485
- gi No. 2315847
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8486
- gi No. 2315849
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8487
- gi No. 2318133
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8488
- gi No. 2318135
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8489
- gi No. 2492664
- % Identity 84.7
- Alignment Length 118
- Location of Alignment in SEQ ID NO 923: from 1 to 88
  
- Alignment No. 8490
- gi No. 2492666
- % Identity 82
- Alignment Length 111
- Location of Alignment in SEQ ID NO 923: from 1 to 81
  
- Alignment No. 8491
- gi No. 2492667
- % Identity 96.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 923: from 76 to 107
  
- Alignment No. 8492
- gi No. 2492668
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8493
- gi No. 2492669
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8494
- gi No. 2492670
- % Identity 82.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8495
- gi No. 2492671
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8496
- gi No. 2492672
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8497
- gi No. 2492674
- % Identity 76.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8498
- gi No. 2588914
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8499
- gi No. 2624850
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8500
- gi No. 2641233
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 923: from 1 to 82
  
- Alignment No. 8501
- gi No. 2641235
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 923: from 1 to 82
  
- Alignment No. 8502
- gi No. 2665740
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 923: from 1 to 93
  
- Alignment No. 8503
- gi No. 2673902
- % Identity 86.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8504

- gi No. 2706871
- % Identity 91.1
- Alignment Length 56
- Location of Alignment in SEQ ID NO 923: from 52 to 107
  
- Alignment No. 8505
- gi No. 2724046
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8506
- gi No. 2738264
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 923: from 1 to 26
  
- Alignment No. 8507
- gi No. 2829750
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8508
- gi No. 2829754
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8509
- gi No. 2829755
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8510
- gi No. 2833326
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8511
- gi No. 2944389
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8512
- gi No. 294850
- % Identity 88
- Alignment Length 100
- Location of Alignment in SEQ ID NO 923: from 8 to 107
  
- Alignment No. 8513
- gi No. 294852
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8514
- gi No. 2967678

- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8515
- gi No. 2982279
- % Identity 96.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 923: from 55 to 107
  
- Alignment No. 8516
- gi No. 2996154
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 923: from 85 to 107
  
- Alignment No. 8517
- gi No. 3036959
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8518
- gi No. 3044210
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8519
- gi No. 3046986
- % Identity 77.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8520
- gi No. 309090
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8521
- gi No. 3107919
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8522
- gi No. 311755
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8523
- gi No. 3121741
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8524
- gi No. 3121742
- % Identity 85.4

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8525
- gi No. 3123181
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8526
- gi No. 3127131
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8527
- gi No. 3127133
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8528
- gi No. 3127135
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8529
- gi No. 3127137
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106
  
- Alignment No. 8530
- gi No. 3182886
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8531
- gi No. 3182891
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8532
- gi No. 3182892
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8533
- gi No. 3182893
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8534
- gi No. 3182894
- % Identity 86.1
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8535
- gi No. 3182895
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8536
- gi No. 3182896
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8537
- gi No. 3182897
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8538
- gi No. 3182898
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8539
- gi No. 3182899
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8540
- gi No. 3182902
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8541
- gi No. 3182903
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8542
- gi No. 3182904
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8543
- gi No. 3182905
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8544
- gi No. 3182906
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8545
- gi No. 321010
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 923: from 22 to 35
  
- Alignment No. 8546
- gi No. 3219758
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8547
- gi No. 3219759
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8548
- gi No. 3219760
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8549
- gi No. 3219761
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8550
- gi No. 3219762
- % Identity 94
- Alignment Length 117
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8551
- gi No. 3219763
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8552
- gi No. 3219764
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8553
- gi No. 3219765
- % Identity 96.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8554
- gi No. 3219766
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86



- Alignment No. 8555
- gi No. 3219767
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 923: from 1 to 85
  
- Alignment No. 8556
- gi No. 3219768
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8557
- gi No. 3219769
- % Identity 94.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8558
- gi No. 3219770
- % Identity 89.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8559
- gi No. 3219771
- % Identity 93.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8560
- gi No. 3219772
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8561
- gi No. 3219773
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8562
- gi No. 3249717
- % Identity 79.6
- Alignment Length 98
- Location of Alignment in SEQ ID NO 923: from 1 to 68
  
- Alignment No. 8563
- gi No. 3287956
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8564
- gi No. 3319951
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8565

- gi No. 3328
- % Identity 80.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8566
- gi No. 3336984
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8567
- gi No. 3348131
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8568
- gi No. 3386376
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8569
- gi No. 3386380
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8570
- gi No. 3386382
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8571
- gi No. 3396073
- % Identity 83.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 85
  
- Alignment No. 8572
- gi No. 3420239
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8573
- gi No. 3421457
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8574
- gi No. 3550350
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8575
- gi No. 3642631

- % Identity 80.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 923: from 1 to 59
  
- Alignment No. 8576
- gi No. 3746936
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8577
- gi No. 3746938
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8578
- gi No. 3746940
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8579
- gi No. 3746942
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8580
- gi No. 3860317
- % Identity 96.1
- Alignment Length 103
- Location of Alignment in SEQ ID NO 923: from 5 to 107
  
- Alignment No. 8581
- gi No. 3860544
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8582
- gi No. 387082
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8583
- gi No. 3879474
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8584
- gi No. 3880219
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8585
- gi No. 3907620
- % Identity 81

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8586
- gi No. 3907622
- % Identity 76.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8587
- gi No. 3912969
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8588
- gi No. 3924630
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8589
- gi No. 399003
- % Identity 82.3
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8590
- gi No. 4009328
- % Identity 83.7
- Alignment Length 49
- Location of Alignment in SEQ ID NO 923: from 1 to 19
  
- Alignment No. 8591
- gi No. 409694
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8592
- gi No. 4105262
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8593
- gi No. 4139264
- % Identity 97.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8594
- gi No. 4204812
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8595
- gi No. 4220623
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 923: from 1 to 90
- Alignment No. 8596
- gi No. 4235277
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8597
- gi No. 4249564
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8598
- gi No. 4376057
- % Identity 83.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 923: from 1 to 75
- Alignment No. 8599
- gi No. 4490385
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8600
- gi No. 4501881
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8601
- gi No. 4501883
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8602
- gi No. 4501885
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8603
- gi No. 4501887
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8604
- gi No. 4501889
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8605
- gi No. 4574288
- % Identity 86.3
- Alignment Length 131
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8606
- gi No. 4587217
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8607
- gi No. 461465
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8608
- gi No. 467215
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8609
- gi No. 4691448
- % Identity 93.6
- Alignment Length 94
- Location of Alignment in SEQ ID NO 923: from 1 to 71
  
- Alignment No. 8610
- gi No. 476332
- % Identity 84.9
- Alignment Length 119
- Location of Alignment in SEQ ID NO 923: from 1 to 89
  
- Alignment No. 8611
- gi No. 476768
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8612
- gi No. 477248
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8613
- gi No. 481515
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8614
- gi No. 482262
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 923: from 48 to 65
  
- Alignment No. 8615
- gi No. 482696
- % Identity 81.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8616
- gi No. 4837604
- % Identity 75.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8617
- gi No. 4837606
- % Identity 77.5
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8618
- gi No. 4837610
- % Identity 72.1
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8619
- gi No. 4850238
- % Identity 75.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8620
- gi No. 4850240
- % Identity 77.5
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8621
- gi No. 4885049
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8622
- gi No. 4887630
- % Identity 81
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8623
- gi No. 4902905
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8624
- gi No. 49864
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8625
- gi No. 49868
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8626

- gi No. 5031514
- % Identity 80
- Alignment Length 135
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8627
- gi No. 5031524
- % Identity 73.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106
  
- Alignment No. 8628
- gi No. 5053109
- % Identity 79.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8629
- gi No. 5114428
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8630
- gi No. 5230839
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8631
- gi No. 5230841
- % Identity 97.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8632
- gi No. 543484
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8633
- gi No. 543766
- % Identity 82.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8634
- gi No. 543767
- % Identity 77.1
- Alignment Length 144
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8635
- gi No. 543768
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8636
- gi No. 544861



- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8637
- gi No. 55675
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 923: from 83 to 107
  
- Alignment No. 8638
- gi No. 5578749
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 923: from 1 to 16
  
- Alignment No. 8639
- gi No. 5597005
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8640
- gi No. 567192
- % Identity 84.9
- Alignment Length 119
- Location of Alignment in SEQ ID NO 923: from 1 to 89
  
- Alignment No. 8641
- gi No. 5702223
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8642
- gi No. 5702225
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8643
- gi No. 5702227
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8644
- gi No. 5702229
- % Identity 86.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 923: from 19 to 107
  
- Alignment No. 8645
- gi No. 5714394
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 923: from 71 to 107
  
- Alignment No. 8646
- gi No. 5726016
- % Identity 94.1

- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8647
- gi No. 5726018
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8648
- gi No. 5726020
- % Identity 87.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8649
- gi No. 5751
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8650
- gi No. 576368
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8651
- gi No. 602958
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 923: from 1 to 20
  
- Alignment No. 8652
- gi No. 627304
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8653
- gi No. 627834
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8654
- gi No. 63018
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8655
- gi No. 630802
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8656
- gi No. 631529
- % Identity 76.3
- Alignment Length 97

- Location of Alignment in SEQ ID NO 923: from 9 to 105
- Alignment No. 8657
- gi No. 64509
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8658
- gi No. 6628
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8659
- gi No. 693709
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8660
- gi No. 71611
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8661
- gi No. 71614
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8662
- gi No. 71616
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8663
- gi No. 71620
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8664
- gi No. 71621
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8665
- gi No. 71622
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8666
- gi No. 71625
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8667
- gi No. 71627
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8668
- gi No. 71629
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8669
- gi No. 71634
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8670
- gi No. 71638
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8671
- gi No. 71639
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8672
- gi No. 728791
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8673
- gi No. 728792
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8674
- gi No. 728793
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8675
- gi No. 728796
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8676
- gi No. 728798
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8677
- gi No. 797290
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8678
- gi No. 809561
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8679
- gi No. 818016
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 923: from 15 to 107
  
- Alignment No. 8680
- gi No. 825616
- % Identity 86.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8681
- gi No. 83999
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8682
- gi No. 84000
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8683
- gi No. 84082
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8684
- gi No. 84344
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8685
- gi No. 84751
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8686
- gi No. 84879
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8687

- gi No. 84880
- % Identity 92.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 923: from 55 to 107
  
- Alignment No. 8688
- gi No. 85358
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8689
- gi No. 85495
- % Identity 81.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 923: from 1 to 60
  
- Alignment No. 8690
- gi No. 86169
- % Identity 80.6
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8691
- gi No. 86742
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8692
- gi No. 871546
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8693
- gi No. 90263
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8694
- gi No. 91918
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 923: from 66 to 107
  
- Alignment No. 8695
- gi No. 950002
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 923: from 1 to 57

Maximum Length Sequence corresponding to clone ID 159438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 924
- Ceres seq\_id 1499214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 925
- Ceres seq\_id 1499215
- Location of start within SEQ ID NO 924: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8696
- EF hand
- Location within SEQ ID NO 925: from 40 to 68 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 926
- Ceres seq\_id 1499216
- Location of start within SEQ ID NO 924: at 437 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8697
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 926: from 15 to 66 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8698
- gi No. 2129684
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 926: from 15 to 48
- Alignment No. 8699
- gi No. 2827715
- % Identity 82.6
- Alignment Length 163
- Location of Alignment in SEQ ID NO 926: from 15 to 175

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 927
- Ceres seq\_id 1499217
- Location of start within SEQ ID NO 924: at 446 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8700
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 927: from 12 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8701
- gi No. 2129684
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 927: from 12 to 45
- Alignment No. 8702
- gi No. 2827715
- % Identity 82.6
- Alignment Length 163
- Location of Alignment in SEQ ID NO 927: from 12 to 172

Maximum Length Sequence corresponding to clone ID 159568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 928
- Ceres seq\_id 1499218

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 929
- Ceres seq\_id 1499219
- Location of start within SEQ ID NO 928: at 305 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8703
- Tetrapyrrole (Corrin/Porphyrin) Methylases.
- Location within SEQ ID NO 929: from 116 to 329 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8704
- gi No. 1146165
- % Identity 100
- Alignment Length 369
- Location of Alignment in SEQ ID NO 929: from 1 to 369
- Alignment No. 8705
- gi No. 1490606
- % Identity 99.2
- Alignment Length 369
- Location of Alignment in SEQ ID NO 929: from 1 to 369
- Alignment No. 8706
- gi No. 1531541
- % Identity 73.1
- Alignment Length 334
- Location of Alignment in SEQ ID NO 929: from 35 to 368

Maximum Length Sequence corresponding to clone ID 159614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 930
- Ceres seq\_id 1499220

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 931
- Ceres seq\_id 1499221
- Location of start within SEQ ID NO 930: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8707
- SRP54-type protein
- Location within SEQ ID NO 931: from 146 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8708
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 931: from 296 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 932
- Ceres seq\_id 1499222
- Location of start within SEQ ID NO 930: at 270 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8709
- SRP54-type protein



- Location within SEQ ID NO 932: from 57 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8710
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 932: from 207 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 933
- Ceres seq\_id 1499223
- Location of start within SEQ ID NO 930: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8711
- SRP54-type protein
- Location within SEQ ID NO 933: from 56 to 337 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8712
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 933: from 206 to 337

Maximum Length Sequence corresponding to clone ID 205489

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 934
- Ceres seq\_id 1499224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 935
- Ceres seq\_id 1499225
- Location of start within SEQ ID NO 934: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8713
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 935: from 18 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8714
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 935: from 1 to 124
- Alignment No. 8715
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 935: from 1 to 124

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 936
- Ceres seq\_id 1499226
- Location of start within SEQ ID NO 934: at 302 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8716
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 936: from 1 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8717
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 936: from 1 to 72
- Alignment No. 8718
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 936: from 1 to 72

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 937
- Ceres seq\_id 1499227
- Location of start within SEQ ID NO 934: at 314 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8719
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 937: from 1 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8720
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 937: from 1 to 68
- Alignment No. 8721
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 937: from 1 to 68

Maximum Length Sequence corresponding to clone ID 205976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 938
- Ceres seq\_id 1499228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 939
- Ceres seq\_id 1499229
- Location of start within SEQ ID NO 938: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8722
- gi No. 4836868
- % Identity 98.8
- Alignment Length 509
- Location of Alignment in SEQ ID NO 939: from 20 to 528

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 940
  - Ceres seq\_id 1499230
  - Location of start within SEQ ID NO 938: at 59 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 8723
  - gi No. 4836868
  - % Identity 98.8
  - Alignment Length 509
  - Location of Alignment in SEQ ID NO 940: from 1 to 509

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 941
  - Ceres seq\_id 1499231
  - Location of start within SEQ ID NO 938: at 374 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 8724
  - gi No. 4836868
  - % Identity 98.8
  - Alignment Length 509
  - Location of Alignment in SEQ ID NO 941: from 1 to 404

Maximum Length Sequence corresponding to clone ID 206045

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 942
  - Ceres seq\_id 1499232
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 943
  - Ceres seq\_id 1499233
  - Location of start within SEQ ID NO 942: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8725
- Mucin-like glycoprotein
- Location within SEQ ID NO 943: from 8 to 89 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 206237

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 944
  - Ceres seq\_id 1499242
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 945
  - Ceres seq\_id 1499243
  - Location of start within SEQ ID NO 944: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8726
- Pectinesterase
- Location within SEQ ID NO 945: from 70 to 123 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 946
- Ceres seq\_id 1499244
- Location of start within SEQ ID NO 944: at 872 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 947
- Ceres seq\_id 1499245
- Location of start within SEQ ID NO 944: at 995 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 206518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 948
- Ceres seq\_id 1499250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 949
- Ceres seq\_id 1499251
- Location of start within SEQ ID NO 948: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8727
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 949: from 102 to 404 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8728
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 949: from 377 to 387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 950
- Ceres seq\_id 1499252
- Location of start within SEQ ID NO 948: at 287 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8729
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 950: from 48 to 350 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8730
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 950: from 323 to 333

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 951

- Ceres seq\_id 1499253
- Location of start within SEQ ID NO 948: at 356 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8731
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 951: from 25 to 327 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8732
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 951: from 300 to 310

Maximum Length Sequence corresponding to clone ID 207043

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 952
- Ceres seq\_id 1499254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 953
- Ceres seq\_id 1499255
- Location of start within SEQ ID NO 952: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8733
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 953: from 83 to 529

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 954
- Ceres seq\_id 1499256
- Location of start within SEQ ID NO 952: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8734
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 954: from 1 to 447

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 955
- Ceres seq\_id 1499257
- Location of start within SEQ ID NO 952: at 374 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8735
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 955: from 1 to 412

Maximum Length Sequence corresponding to clone ID 207137

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 956
- Ceres seq\_id 1499258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 957
- Ceres seq\_id 1499259
- Location of start within SEQ ID NO 956: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8736
- L1P family of ribosomal proteins
- Location within SEQ ID NO 957: from 124 to 329 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8737
- gi No. 1350625
- % Identity 79.5
- Alignment Length 176
- Location of Alignment in SEQ ID NO 957: from 89 to 264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 958
- Ceres seq\_id 1499260
- Location of start within SEQ ID NO 956: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8738
- L1P family of ribosomal proteins
- Location within SEQ ID NO 958: from 114 to 319 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8739
- gi No. 1350625
- % Identity 79.5
- Alignment Length 176
- Location of Alignment in SEQ ID NO 958: from 79 to 254

Maximum Length Sequence corresponding to clone ID 207419

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 959
- Ceres seq\_id 1499261

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 960
- Ceres seq\_id 1499262
- Location of start within SEQ ID NO 959: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8740
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 960: from 235 to 262 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 961
- Ceres seq\_id 1499263

- Location of start within SEQ ID NO 959: at 395 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8741
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 961: from 128 to 155 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 207558

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 962
- Ceres seq\_id 1499264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 963
- Ceres seq\_id 1499265
- Location of start within SEQ ID NO 962: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8742
- Adhesion lipoprotein
- Location within SEQ ID NO 963: from 182 to 232 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8743
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 963: from 184 to 210
- Alignment No. 8744
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 963: from 210 to 220
- Alignment No. 8745
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 963: from 1 to 398
- Alignment No. 8746
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 963: from 181 to 198
- Alignment No. 8747
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 963: from 1 to 398
- Alignment No. 8748
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 963: from 181 to 195

- Alignment No. 8749
- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 963: from 181 to 196

- Alignment No. 8750
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 963: from 182 to 198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 964
- Ceres seq\_id 1499266
- Location of start within SEQ ID NO 962: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8751
- Adhesion lipoprotein
- Location within SEQ ID NO 964: from 128 to 178 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8752
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 964: from 130 to 156
- Alignment No. 8753
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 964: from 156 to 166
- Alignment No. 8754
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 964: from 1 to 344
- Alignment No. 8755
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 964: from 127 to 144
- Alignment No. 8756
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 964: from 1 to 344
- Alignment No. 8757
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 964: from 127 to 141



- Alignment No. 8758
- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 964: from 127 to 142

- Alignment No. 8759
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 964: from 128 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 965
- Ceres seq\_id 1499267
- Location of start within SEQ ID NO 962: at 300 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8760
- Adhesion lipoprotein
- Location within SEQ ID NO 965: from 114 to 164 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8761
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 965: from 116 to 142
- Alignment No. 8762
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 965: from 142 to 152
- Alignment No. 8763
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 965: from 1 to 330
- Alignment No. 8764
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 965: from 113 to 130
- Alignment No. 8765
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 965: from 1 to 330
- Alignment No. 8766
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 965: from 113 to 127
- Alignment No. 8767

- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 965: from 113 to 128
- Alignment No. 8768
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 965: from 114 to 130

Maximum Length Sequence corresponding to clone ID 218944

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 966
- Ceres seq\_id 1499310

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 967
- Ceres seq\_id 1499311
- Location of start within SEQ ID NO 966: at 202 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8769
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 967: from 40 to 109 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 968
- Ceres seq\_id 1499312
- Location of start within SEQ ID NO 966: at 232 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8770
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 968: from 30 to 99 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 969
- Ceres seq\_id 1499313
- Location of start within SEQ ID NO 966: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8771
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 969: from 22 to 91 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 219286

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 970
- Ceres seq\_id 1499314

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 971
- Ceres seq\_id 1499315

- Location of start within SEQ ID NO 970: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8772
  - 60s Acidic ribosomal protein
  - Location within SEQ ID NO 971: from 73 to 129 aa.
- Alignment No. 8773
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 971: from 64 to 167 aa.
- Alignment No. 8774
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 971: from 75 to 171 aa.
- Alignment No. 8775
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 971: from 99 to 171 aa.
- Alignment No. 8776
  - Syndecan domain
  - Location within SEQ ID NO 971: from 1 to 142 aa.
- Alignment No. 8777
  - 11-S plant seed storage protein
  - Location within SEQ ID NO 971: from 76 to 170 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8778
  - gi No. 482700
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 971: from 151 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 972
- Ceres seq\_id 1499316
- Location of start within SEQ ID NO 970: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8779
  - 60s Acidic ribosomal protein
  - Location within SEQ ID NO 972: from 36 to 92 aa.
- Alignment No. 8780
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 972: from 27 to 130 aa.
- Alignment No. 8781
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 972: from 38 to 134 aa.
- Alignment No. 8782
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 972: from 62 to 134 aa.
- Alignment No. 8783
  - Syndecan domain
  - Location within SEQ ID NO 972: from 1 to 105 aa.

- Alignment No. 8784
- 11-S plant seed storage protein
- Location within SEQ ID NO 972: from 39 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8785
- gi No. 482700
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 972: from 114 to 124

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 973
- Ceres seq\_id 1499317
- Location of start within SEQ ID NO 970: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 219894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 974
- Ceres seq\_id 1499344

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 975
- Ceres seq\_id 1499345
- Location of start within SEQ ID NO 974: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 976
- Ceres seq\_id 1499346
- Location of start within SEQ ID NO 974: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8786
- gi No. 3108209
- % Identity 78.8
- Alignment Length 179
- Location of Alignment in SEQ ID NO 976: from 35 to 213

Maximum Length Sequence corresponding to clone ID 220920

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 977
- Ceres seq\_id 1499353

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 978
- Ceres seq\_id 1499354
- Location of start within SEQ ID NO 977: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8787

- gi No. 129805
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 978: from 28 to 56
  
- Alignment No. 8788
- gi No. 1491776
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 978: from 28 to 56
  
- Alignment No. 8789
- gi No. 1633130
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 978: from 31 to 56
  
- Alignment No. 8790
- gi No. 520570
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 978: from 24 to 55

Maximum Length Sequence corresponding to clone ID 221164

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 979
- Ceres seq\_id 1499362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 980
- Ceres seq\_id 1499363
- Location of start within SEQ ID NO 979: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 981
- Ceres seq\_id 1499364
- Location of start within SEQ ID NO 979: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8791
- EF hand
- Location within SEQ ID NO 981: from 45 to 73 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8792
- gi No. 115480
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
  
- Alignment No. 8793
- gi No. 115500
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
  
- Alignment No. 8794

- gi No. 115534
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
  
- Alignment No. 8795
- gi No. 16225
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
  
- Alignment No. 8796
- gi No. 167676
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
  
- Alignment No. 8797
- gi No. 189020
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 981: from 70 to 80
  
- Alignment No. 8798
- gi No. 189022
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 981: from 70 to 80
  
- Alignment No. 8799
- gi No. 2119353
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80
  
- Alignment No. 8800
- gi No. 2129557
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 981: from 38 to 61
  
- Alignment No. 8801
- gi No. 2267084
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
  
- Alignment No. 8802
- gi No. 228408
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 981: from 46 to 80
  
- Alignment No. 8803
- gi No. 4379369
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80
  
- Alignment No. 8804
- gi No. 71673

- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 982
- Ceres seq\_id 1499365
- Location of start within SEQ ID NO 979: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8805
- EF hand
- Location within SEQ ID NO 982: from 13 to 41 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8806
- gi No. 115480
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
  
- Alignment No. 8807
- gi No. 115500
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
  
- Alignment No. 8808
- gi No. 115534
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
  
- Alignment No. 8809
- gi No. 16225
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
  
- Alignment No. 8810
- gi No. 167676
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
  
- Alignment No. 8811
- gi No. 189020
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 982: from 38 to 48
  
- Alignment No. 8812
- gi No. 189022
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 982: from 38 to 48
  
- Alignment No. 8813
- gi No. 2119353
- % Identity 70.5

- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48
  
- Alignment No. 8814
- gi No. 2129557
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 982: from 6 to 29
  
- Alignment No. 8815
- gi No. 2267084
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
  
- Alignment No. 8816
- gi No. 228408
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 982: from 14 to 48
  
- Alignment No. 8817
- gi No. 4379369
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48
  
- Alignment No. 8818
- gi No. 71673
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48

Maximum Length Sequence corresponding to clone ID 221169

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 983
- Ceres seq\_id 1499370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 984
- Ceres seq\_id 1499371
- Location of start within SEQ ID NO 983: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8819
- gi No. 1070652
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 984: from 68 to 81
  
- Alignment No. 8820
- gi No. 131007
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 984: from 68 to 81
  
- Alignment No. 8821
- gi No. 350218
- % Identity 71.4
- Alignment Length 14



- Location of Alignment in SEQ ID NO 984: from 68 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 985
- Ceres seq\_id 1499372
- Location of start within SEQ ID NO 983: at 455 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 986
- Ceres seq\_id 1499373
- Location of start within SEQ ID NO 983: at 473 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 221212

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 987
- Ceres seq\_id 1499380

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 988
- Ceres seq\_id 1499381
- Location of start within SEQ ID NO 987: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8822
- ADP-ribosylation factor family
- Location within SEQ ID NO 988: from 54 to 230 aa.
- Alignment No. 8823
- Ras family
- Location within SEQ ID NO 988: from 70 to 219 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 989
- Ceres seq\_id 1499382
- Location of start within SEQ ID NO 987: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8824
- ADP-ribosylation factor family
- Location within SEQ ID NO 989: from 5 to 181 aa.
- Alignment No. 8825
- Ras family
- Location within SEQ ID NO 989: from 21 to 170 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 990
- Ceres seq\_id 1499383

- Location of start within SEQ ID NO 987: at 207 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8826
- ADP-ribosylation factor family
- Location within SEQ ID NO 990: from 1 to 162 aa.
- Alignment No. 8827
- Ras family
- Location within SEQ ID NO 990: from 2 to 151 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 221234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 991
- Ceres seq\_id 1499384

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 992
- Ceres seq\_id 1499385
- Location of start within SEQ ID NO 991: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8828
- Papain family cysteine protease
- Location within SEQ ID NO 992: from 123 to 158 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8829
- gi No. 108585
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 992: from 122 to 141
- Alignment No. 8830
- gi No. 1093503
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8831
- gi No. 115738
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8832
- gi No. 1340178
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8833
- gi No. 1498185
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8834

- gi No. 162042
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159
  
- Alignment No. 8835
- gi No. 162044
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 992: from 141 to 161
  
- Alignment No. 8836
- gi No. 1705639
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8837
- gi No. 1911708
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159
  
- Alignment No. 8838
- gi No. 2144502
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8839
- gi No. 2146900
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8840
- gi No. 2665820
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 992: from 141 to 158
  
- Alignment No. 8841
- gi No. 2706547
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8842
- gi No. 2914174
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 992: from 127 to 162
  
- Alignment No. 8843
- gi No. 3929737
- % Identity 78.6
- Alignment Length 28
- Location of Alignment in SEQ ID NO 992: from 135 to 162
  
- Alignment No. 8844
- gi No. 3929819

- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 992: from 144 to 157
  
- Alignment No. 8845
- gi No. 419920
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159
  
- Alignment No. 8846
- gi No. 452254
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 992: from 141 to 162
  
- Alignment No. 8847
- gi No. 541900
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 992: from 128 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 993
- Ceres seq\_id 1499386
- Location of start within SEQ ID NO 991: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8848
- Papain family cysteine protease
- Location within SEQ ID NO 993: from 115 to 150 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8849
- gi No. 108585
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 993: from 114 to 133
  
- Alignment No. 8850
- gi No. 1093503
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8851
- gi No. 115738
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8852
- gi No. 1340178
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8853
- gi No. 1498185
- % Identity 71.1

- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8854
- gi No. 162042
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
  
- Alignment No. 8855
- gi No. 162044
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 993: from 133 to 153
  
- Alignment No. 8856
- gi No. 1705639
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8857
- gi No. 1911708
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
  
- Alignment No. 8858
- gi No. 2144502
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8859
- gi No. 2146900
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8860
- gi No. 2665820
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 993: from 133 to 150
  
- Alignment No. 8861
- gi No. 2706547
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8862
- gi No. 2914174
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 993: from 119 to 154
  
- Alignment No. 8863
- gi No. 3929737
- % Identity 78.6
- Alignment Length 28

- Location of Alignment in SEQ ID NO 993: from 127 to 154
- Alignment No. 8864
- gi No. 3929819
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 993: from 136 to 149
- Alignment No. 8865
- gi No. 419920
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
- Alignment No. 8866
- gi No. 452254
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 993: from 133 to 154
- Alignment No. 8867
- gi No. 541900
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 993: from 120 to 149

Maximum Length Sequence corresponding to clone ID 222003

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 994
- Ceres seq\_id 1499389

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 995
- Ceres seq\_id 1499390
- Location of start within SEQ ID NO 994: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8868
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 995: from 86 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 996
- Ceres seq\_id 1499391
- Location of start within SEQ ID NO 994: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8869
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 996: from 34 to 93 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 222544

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 997
- Ceres seq\_id 1499402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 998
- Ceres seq\_id 1499403
- Location of start within SEQ ID NO 997: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 8870
  - gi No. 400249
  - % Identity 94.4
  - Alignment Length 36
  - Location of Alignment in SEQ ID NO 998: from 17 to 52

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 999
  - Ceres seq\_id 1499404
  - Location of start within SEQ ID NO 997: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1000
  - Ceres seq\_id 1499405
  - Location of start within SEQ ID NO 997: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 8871
  - gi No. 400249
  - % Identity 94.4
  - Alignment Length 36
  - Location of Alignment in SEQ ID NO 1000: from 1 to 36

Maximum Length Sequence corresponding to clone ID 222547

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1001
  - Ceres seq\_id 1499406
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1002
  - Ceres seq\_id 1499407
  - Location of start within SEQ ID NO 1001: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 8872
  - gi No. 4204294
  - % Identity 75.1
  - Alignment Length 198
  - Location of Alignment in SEQ ID NO 1002: from 54 to 247

Maximum Length Sequence corresponding to clone ID 223028

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1003
  - Ceres seq\_id 1499408
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1004
  - Ceres seq\_id 1499409

- Location of start within SEQ ID NO 1003: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1005
- Ceres seq\_id 1499410
- Location of start within SEQ ID NO 1003: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8873
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1005: from 15 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1006
- Ceres seq\_id 1499411
- Location of start within SEQ ID NO 1003: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8874
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1006: from 1 to 66

Maximum Length Sequence corresponding to clone ID 225428

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1007
- Ceres seq\_id 1499412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1008
- Ceres seq\_id 1499413
- Location of start within SEQ ID NO 1007: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1009
- Ceres seq\_id 1499414
- Location of start within SEQ ID NO 1007: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8875
- gi No. 113003
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41



- Alignment No. 8876
- gi No. 168397
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41
  
- Alignment No. 8877
- gi No. 168422
- % Identity 100
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1010
- Ceres seq\_id 1499415
- Location of start within SEQ ID NO 1007: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8878
- gi No. 113003
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24
  
- Alignment No. 8879
- gi No. 168397
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24
  
- Alignment No. 8880
- gi No. 168422
- % Identity 100
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24

Maximum Length Sequence corresponding to clone ID 225429

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1011
- Ceres seq\_id 1499416

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1012
- Ceres seq\_id 1499417
- Location of start within SEQ ID NO 1011: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1013
- Ceres seq\_id 1499418
- Location of start within SEQ ID NO 1011: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8881
- S-adenosylmethionine synthetase
- Location within SEQ ID NO 1013: from 5 to 95 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8882
- gi No. 1076485
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1013: from 3 to 84
  
- Alignment No. 8883
- gi No. 1170936
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8884
- gi No. 1170937
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8885
- gi No. 1170938
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8886
- gi No. 1170939
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8887
- gi No. 127041
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8888
- gi No. 127045
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8889
- gi No. 127046
- % Identity 87.6
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8890
- gi No. 1346520
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8891
- gi No. 1346523
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8892
- gi No. 1346524
- % Identity 93.6
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95
  
- Alignment No. 8893
- gi No. 1346525
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95
  
- Alignment No. 8894
- gi No. 1346526
- % Identity 90.6
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8895
- gi No. 147855
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1013: from 7 to 52
  
- Alignment No. 8896
- gi No. 1708995
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8897
- gi No. 1709000
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8898
- gi No. 1709001
- % Identity 85.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1013: from 30 to 95
  
- Alignment No. 8899
- gi No. 1709002
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8900
- gi No. 1709004
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8901
- gi No. 1709006
- % Identity 90.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1013: from 36 to 95

- Alignment No. 8902
  - gi No. 172534
  - % Identity 70.2
  - Alignment Length 94
  - Location of Alignment in SEQ ID NO 1013: from 3 to 95
- Alignment No. 8903
  - gi No. 2129889
  - % Identity 90.6
  - Alignment Length 96
  - Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8904
  - gi No. 2315140
  - % Identity 91.4
  - Alignment Length 93
  - Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8905
  - gi No. 2665652
  - % Identity 72.9
  - Alignment Length 96
  - Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8906
  - gi No. 3024121
  - % Identity 88.2
  - Alignment Length 93
  - Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8907
  - gi No. 3024122
  - % Identity 95.8
  - Alignment Length 96
  - Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8908
  - gi No. 3024126
  - % Identity 92.5
  - Alignment Length 93
  - Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8909
  - gi No. 3024127
  - % Identity 92.5
  - Alignment Length 93
  - Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8910
  - gi No. 3024148
  - % Identity 90.3
  - Alignment Length 93
  - Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8911
  - gi No. 3914019
  - % Identity 89.2
  - Alignment Length 93
  - Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8912

- gi No. 4883604
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8913
- gi No. 4894592
- % Identity 72.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8914
- gi No. 4927188
- % Identity 71.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8915
- gi No. 5726594
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8916
- gi No. 609557
- % Identity 85.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1013: from 30 to 95

Maximum Length Sequence corresponding to clone ID 225478

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1014
- Ceres seq\_id 1499422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1015
- Ceres seq\_id 1499423
- Location of start within SEQ ID NO 1014: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1016
- Ceres seq\_id 1499424
- Location of start within SEQ ID NO 1014: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8917
- 3' exoribonuclease family
- Location within SEQ ID NO 1016: from 40 to 134 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1017
- Ceres seq\_id 1499425
- Location of start within SEQ ID NO 1014: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8918
- 3' exoribonuclease family
- Location within SEQ ID NO 1017: from 24 to 118 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 230791

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1018
- Ceres seq\_id 1499446

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1019
- Ceres seq\_id 1499447
- Location of start within SEQ ID NO 1018: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8919
- Mur ligase family
- Location within SEQ ID NO 1019: from 60 to 127 aa.
- Alignment No. 8920
- Mur ligase family
- Location within SEQ ID NO 1019: from 121 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8921
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468
- Alignment No. 8922
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468
- Alignment No. 8923
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1020
- Ceres seq\_id 1499448
- Location of start within SEQ ID NO 1018: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8924
- Mur ligase family
- Location within SEQ ID NO 1020: from 3 to 70 aa.
- Alignment No. 8925
- Mur ligase family
- Location within SEQ ID NO 1020: from 64 to 248 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8926
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411
  
- Alignment No. 8927
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411
  
- Alignment No. 8928
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1021
- Ceres seq\_id 1499449
- Location of start within SEQ ID NO 1018: at 612 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8929
- Mur ligase family
- Location within SEQ ID NO 1021: from 1 to 138 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8930
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301
  
- Alignment No. 8931
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301
  
- Alignment No. 8932
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301

Maximum Length Sequence corresponding to clone ID 230831

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1022
- Ceres seq\_id 1499450

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1023
- Ceres seq\_id 1499451
- Location of start within SEQ ID NO 1022: at 501 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8933
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1023: from 282 to 356
  
- Alignment No. 8934
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1023: from 3 to 250
  
- Alignment No. 8935
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357
  
- Alignment No. 8936
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357
  
- Alignment No. 8937
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1024
- Ceres seq\_id 1499452
- Location of start within SEQ ID NO 1022: at 552 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8938
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1024: from 265 to 339
  
- Alignment No. 8939
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1024: from 1 to 233
  
- Alignment No. 8940
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340
  
- Alignment No. 8941
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340



- Alignment No. 8942
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1025
- Ceres seq\_id 1499453
- Location of start within SEQ ID NO 1022: at 639 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8943
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1025: from 236 to 310
  
- Alignment No. 8944
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1025: from 1 to 204
  
- Alignment No. 8945
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1025: from 1 to 311
  
- Alignment No. 8946
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1025: from 1 to 311
  
- Alignment No. 8947
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1025: from 1 to 311

Maximum Length Sequence corresponding to clone ID 230894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1026
- Ceres seq\_id 1499458

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1027
- Ceres seq\_id 1499459
- Location of start within SEQ ID NO 1026: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8948
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177

- Location of Alignment in SEQ ID NO 1027: from 227 to 403
- Alignment No. 8949
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1027: from 1 to 201

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1028
- Ceres seq\_id 1499460
- Location of start within SEQ ID NO 1026: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8950
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177
- Location of Alignment in SEQ ID NO 1028: from 209 to 385
- Alignment No. 8951
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1028: from 1 to 183

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1029
- Ceres seq\_id 1499461
- Location of start within SEQ ID NO 1026: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8952
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177
- Location of Alignment in SEQ ID NO 1029: from 199 to 375
- Alignment No. 8953
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1029: from 1 to 173

Maximum Length Sequence corresponding to clone ID 230897

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1030
- Ceres seq\_id 1499462

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1031
- Ceres seq\_id 1499463
- Location of start within SEQ ID NO 1030: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1032
- Ceres seq\_id 1499464
- Location of start within SEQ ID NO 1030: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8954
- gi No. 2651297
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1032: from 1 to 39

Maximum Length Sequence corresponding to clone ID 230925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1033
- Ceres seq\_id 1499465

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1034
- Ceres seq\_id 1499466
- Location of start within SEQ ID NO 1033: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8955
- gi No. 3834313
- % Identity 99
- Alignment Length 195
- Location of Alignment in SEQ ID NO 1034: from 1 to 195

Maximum Length Sequence corresponding to clone ID 231096

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1035
- Ceres seq\_id 1499467

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1036
- Ceres seq\_id 1499468
- Location of start within SEQ ID NO 1035: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1037
- Ceres seq\_id 1499469
- Location of start within SEQ ID NO 1035: at 591 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8956
- gi No. 4835243
- % Identity 77.7
- Alignment Length 175
- Location of Alignment in SEQ ID NO 1037: from 1 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1038

- Ceres seq\_id 1499470
- Location of start within SEQ ID NO 1035: at 651 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8957
- gi No. 4835243
- % Identity 77.7
- Alignment Length 175
- Location of Alignment in SEQ ID NO 1038: from 1 to 99

Maximum Length Sequence corresponding to clone ID 231239

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1039
- Ceres seq\_id 1499474

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1040
- Ceres seq\_id 1499475
- Location of start within SEQ ID NO 1039: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1041
- Ceres seq\_id 1499476
- Location of start within SEQ ID NO 1039: at 573 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8958
- Syntaxin
- Location within SEQ ID NO 1041: from 1 to 140 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1042
- Ceres seq\_id 1499477
- Location of start within SEQ ID NO 1039: at 756 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8959
- Syntaxin
- Location within SEQ ID NO 1042: from 1 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231303

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1043
- Ceres seq\_id 1499486

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1044
- Ceres seq\_id 1499487
- Location of start within SEQ ID NO 1043: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8960
- gi No. 2129778
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1044: from 22 to 85
  
- Alignment No. 8961
- gi No. 3236241
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1044: from 13 to 25
  
- Alignment No. 8962
- gi No. 4581965
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1044: from 22 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1045
- Ceres seq\_id 1499488
- Location of start within SEQ ID NO 1043: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8963
- gi No. 2129778
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1045: from 17 to 80
  
- Alignment No. 8964
- gi No. 3236241
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1045: from 8 to 20
  
- Alignment No. 8965
- gi No. 4581965
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1045: from 17 to 80

Maximum Length Sequence corresponding to clone ID 231598

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1046
- Ceres seq\_id 1499501

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1047
- Ceres seq\_id 1499502
- Location of start within SEQ ID NO 1046: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 8966
- ParA family ATPase
- Location within SEQ ID NO 1047: from 278 to 364 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1048
- Ceres seq\_id 1499503
- Location of start within SEQ ID NO 1046: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8967
- ParA family ATPase
- Location within SEQ ID NO 1048: from 262 to 348 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1049
- Ceres seq\_id 1499504
- Location of start within SEQ ID NO 1046: at 445 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8968
- ParA family ATPase
- Location within SEQ ID NO 1049: from 130 to 216 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231731

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1050
- Ceres seq\_id 1499509

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1051
- Ceres seq\_id 1499510
- Location of start within SEQ ID NO 1050: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8969
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1051: from 92 to 159 aa.
- Alignment No. 8970
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1051: from 259 to 322 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1052
- Ceres seq\_id 1499511
- Location of start within SEQ ID NO 1050: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8971
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1052: from 91 to 158 aa.

- Alignment No. 8972
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1052: from 258 to 321 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1053
- Ceres seq\_id 1499512
- Location of start within SEQ ID NO 1050: at 535 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8973
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1053: from 98 to 161 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231750

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1054
- Ceres seq\_id 1499513

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1055
- Ceres seq\_id 1499514
- Location of start within SEQ ID NO 1054: at 318 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8974
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1055: from 134 to 182 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8975
- gi No. 2244797
- % Identity 97.8
- Alignment Length 274
- Location of Alignment in SEQ ID NO 1055: from 12 to 283

Maximum Length Sequence corresponding to clone ID 231906

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1056
- Ceres seq\_id 1499519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1057
- Ceres seq\_id 1499520
- Location of start within SEQ ID NO 1056: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8976
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1057: from 99 to 169 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1058
- Ceres seq\_id 1499521

- Location of start within SEQ ID NO 1056: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8977
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1058: from 76 to 146 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1059
- Ceres seq\_id 1499522
- Location of start within SEQ ID NO 1056: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8978
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1059: from 54 to 124 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231948

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1060
- Ceres seq\_id 1499523

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1061
- Ceres seq\_id 1499524
- Location of start within SEQ ID NO 1060: at 187 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8979
- Zinc finger, CCHC class
- Location within SEQ ID NO 1061: from 196 to 213 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8980
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287
- Location of Alignment in SEQ ID NO 1061: from 116 to 402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1062
- Ceres seq\_id 1499525
- Location of start within SEQ ID NO 1060: at 244 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8981
- Zinc finger, CCHC class
- Location within SEQ ID NO 1062: from 177 to 194 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8982
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287



- Location of Alignment in SEQ ID NO 1062: from 97 to 383

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1063
- Ceres seq\_id 1499526
- Location of start within SEQ ID NO 1060: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8983
- Zinc finger, CCHC class
- Location within SEQ ID NO 1063: from 173 to 190 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8984
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287
- Location of Alignment in SEQ ID NO 1063: from 93 to 379

Maximum Length Sequence corresponding to clone ID 231976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1064
- Ceres seq\_id 1499527

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1065
- Ceres seq\_id 1499528
- Location of start within SEQ ID NO 1064: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8985
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1065: from 1 to 95

- Alignment No. 8986
- gi No. 4586255
- % Identity 79.3
- Alignment Length 213
- Location of Alignment in SEQ ID NO 1065: from 59 to 271

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1066
- Ceres seq\_id 1499529
- Location of start within SEQ ID NO 1064: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8987
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1066: from 1 to 63
- Alignment No. 8988
- gi No. 4586255
- % Identity 79.3

- Alignment Length 213
- Location of Alignment in SEQ ID NO 1066: from 27 to 239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1067
- Ceres seq\_id 1499530
- Location of start within SEQ ID NO 1064: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8989
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1067: from 1 to 45
- Alignment No. 8990
- gi No. 4586255
- % Identity 79.3
- Alignment Length 213
- Location of Alignment in SEQ ID NO 1067: from 9 to 221

Maximum Length Sequence corresponding to clone ID 232208

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1068
- Ceres seq\_id 1499538

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1069
- Ceres seq\_id 1499539
- Location of start within SEQ ID NO 1068: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8991
- gi No. 1168470
- % Identity 72.5
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1069: from 1 to 90
- Alignment No. 8992
- gi No. 3461835
- % Identity 92.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1069: from 1 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1070
- Ceres seq\_id 1499540
- Location of start within SEQ ID NO 1068: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8993
- gi No. 1168470
- % Identity 72.5
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1070: from 1 to 67

- Alignment No. 8994
- gi No. 3461835
- % Identity 92.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1070: from 1 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1071
- Ceres seq\_id 1499541
- Location of start within SEQ ID NO 1068: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1072
- Ceres seq\_id 1499542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1073
- Ceres seq\_id 1499543
- Location of start within SEQ ID NO 1072: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8995
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1073: from 190 to 432
  
- Alignment No. 8996
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1073: from 14 to 433

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1074
- Ceres seq\_id 1499544
- Location of start within SEQ ID NO 1072: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8997
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1074: from 177 to 419
  
- Alignment No. 8998
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1074: from 1 to 420

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1075

- Ceres seq\_id 1499545
- Location of start within SEQ ID NO 1072: at 397 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8999
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1075: from 58 to 300
  
- Alignment No. 9000
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1075: from 1 to 301

Maximum Length Sequence corresponding to clone ID 232986

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1076
- Ceres seq\_id 1499547

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1077
- Ceres seq\_id 1499548
- Location of start within SEQ ID NO 1076: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9001
- gi No. 1076641
- % Identity 72.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9002
- gi No. 1170711
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9003
- gi No. 1431622
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1077: from 68 to 101
  
- Alignment No. 9004
- gi No. 1480078
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1077: from 32 to 101
  
- Alignment No. 9005
- gi No. 1709129
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9006

- gi No. 2129738
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1077: from 33 to 101
  
- Alignment No. 9007
- gi No. 2129739
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1077: from 35 to 101
  
- Alignment No. 9008
- gi No. 2182029
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1077: from 42 to 101
  
- Alignment No. 9009
- gi No. 2398519
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9010
- gi No. 3201623
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1077: from 33 to 101
  
- Alignment No. 9011
- gi No. 4539390
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1077: from 35 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1078
- Ceres seq\_id 1499549
- Location of start within SEQ ID NO 1076: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9012
- gi No. 1076641
- % Identity 72.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9013
- gi No. 1170711
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9014
- gi No. 1431622
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1078: from 41 to 74

- Alignment No. 9015
- gi No. 1480078
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1078: from 5 to 74
  
- Alignment No. 9016
- gi No. 1709129
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9017
- gi No. 2129738
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1078: from 6 to 74
  
- Alignment No. 9018
- gi No. 2129739
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1078: from 8 to 74
  
- Alignment No. 9019
- gi No. 2182029
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1078: from 15 to 74
  
- Alignment No. 9020
- gi No. 2398519
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9021
- gi No. 3201623
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1078: from 6 to 74
  
- Alignment No. 9022
- gi No. 4539390
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1078: from 8 to 74

Maximum Length Sequence corresponding to clone ID 246205

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1079
- Ceres seq\_id 1499558

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1080
- Ceres seq\_id 1499559
- Location of start within SEQ ID NO 1079: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9023

- gi No. 1172663
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1080: from 100 to 122
  
- Alignment No. 9024
- gi No. 131185
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1080: from 101 to 119
  
- Alignment No. 9025
- gi No. 131186
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1080: from 101 to 118
  
- Alignment No. 9026
- gi No. 3885892
- % Identity 73.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1080: from 27 to 131
  
- Alignment No. 9027
- gi No. 478522
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1080: from 100 to 123
  
- Alignment No. 9028
- gi No. 548604
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1080: from 27 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1081
- Ceres seq\_id 1499560
- Location of start within SEQ ID NO 1079: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9029
- gi No. 1172663
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1081: from 74 to 96
  
- Alignment No. 9030
- gi No. 131185
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1081: from 75 to 93
  
- Alignment No. 9031
- gi No. 131186
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1081: from 75 to 92

- Alignment No. 9032
- gi No. 3885892
- % Identity 73.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1081: from 1 to 105
  
- Alignment No. 9033
- gi No. 478522
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1081: from 74 to 97
  
- Alignment No. 9034
- gi No. 548604
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1081: from 1 to 105

Maximum Length Sequence corresponding to clone ID 246509

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1082
- Ceres seq\_id 1499567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1083
- Ceres seq\_id 1499568
- Location of start within SEQ ID NO 1082: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9035
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1083: from 11 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9036
- gi No. 3386565
- % Identity 95
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1083: from 1 to 78

Maximum Length Sequence corresponding to clone ID 246543

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1084
- Ceres seq\_id 1499576

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1085
- Ceres seq\_id 1499577
- Location of start within SEQ ID NO 1084: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9037
- gi No. 100448
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9038
- gi No. 100449
- % Identity 76.9



- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9039
- gi No. 1076665
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9040
- gi No. 1086103
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9041
- gi No. 129640
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9042
- gi No. 129641
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9043
- gi No. 129642
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9044
- gi No. 129643
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9045
- gi No. 129644
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9046
- gi No. 169497
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1085: from 27 to 46
  
- Alignment No. 9047
- gi No. 169520
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9048
- gi No. 21415
- % Identity 76.9
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9049
- gi No. 261222
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9050
- gi No. 320598
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9051
- gi No. 695756
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9052
- gi No. 82272
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1086
- Ceres seq\_id 1499578
- Location of start within SEQ ID NO 1084: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9053
- gi No. 100448
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9054
- gi No. 100449
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9055
- gi No. 1076665
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9056
- gi No. 1086103
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9057
- gi No. 129640
- % Identity 76.9

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9058
- gi No. 129641
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9059
- gi No. 129642
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9060
- gi No. 129643
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9061
- gi No. 129644
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9062
- gi No. 169497
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1086: from 20 to 39
  
- Alignment No. 9063
- gi No. 169520
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9064
- gi No. 21415
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9065
- gi No. 261222
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9066
- gi No. 320598
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
  
- Alignment No. 9067
- gi No. 695756
- % Identity 76.9
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9068
- gi No. 82272
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1087
- Ceres seq\_id 1499579
- Location of start within SEQ ID NO 1084: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246728

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1088
- Ceres seq\_id 1499591

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1089
- Ceres seq\_id 1499592
- Location of start within SEQ ID NO 1088: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9069
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1089: from 43 to 127 aa.
- Alignment No. 9070
- Adhesion lipoprotein
- Location within SEQ ID NO 1089: from 24 to 113 aa.
- Alignment No. 9071
- Adhesion lipoprotein
- Location within SEQ ID NO 1089: from 74 to 125 aa.
- Alignment No. 9072
- Osteopontin
- Location within SEQ ID NO 1089: from 6 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9073
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1089: from 106 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1090
- Ceres seq\_id 1499593
- Location of start within SEQ ID NO 1088: at 187 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9074
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1090: from 12 to 96 aa.

- Alignment No. 9075
- Adhesion lipoprotein
- Location within SEQ ID NO 1090: from 1 to 82 aa.
  
- Alignment No. 9076
- Adhesion lipoprotein
- Location within SEQ ID NO 1090: from 43 to 94 aa.
  
- Alignment No. 9077
- Osteopontin
- Location within SEQ ID NO 1090: from 1 to 93 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9078
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1090: from 75 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1091
- Ceres seq\_id 1499594
- Location of start within SEQ ID NO 1088: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9079
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1091: from 3 to 87 aa.
  
- Alignment No. 9080
- Adhesion lipoprotein
- Location within SEQ ID NO 1091: from 1 to 73 aa.
  
- Alignment No. 9081
- Adhesion lipoprotein
- Location within SEQ ID NO 1091: from 34 to 85 aa.
  
- Alignment No. 9082
- Osteopontin
- Location within SEQ ID NO 1091: from 1 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9083
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1091: from 66 to 83

Maximum Length Sequence corresponding to clone ID 246776

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1092
- Ceres seq\_id 1499605

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1093
- Ceres seq\_id 1499606
- Location of start within SEQ ID NO 1092: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9084
- gi No. 1172977
- % Identity 88.5
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1093: from 23 to 48
  
- Alignment No. 9085
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84
  
- Alignment No. 9086
- gi No. 2501188
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84
  
- Alignment No. 9087
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84
  
- Alignment No. 9088
- gi No. 2529670
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1093: from 24 to 48
  
- Alignment No. 9089
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1093: from 48 to 86
  
- Alignment No. 9090
- gi No. 3021348
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1093: from 26 to 48
  
- Alignment No. 9091
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1093: from 50 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1094
- Ceres seq\_id 1499607
- Location of start within SEQ ID NO 1092: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9092
- gi No. 1172977
- % Identity 88.5
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1094: from 1 to 26
- Alignment No. 9093
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9094
- gi No. 2501188
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9095
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9096
- gi No. 2529670
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1094: from 2 to 26
- Alignment No. 9097
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1094: from 26 to 64
- Alignment No. 9098
- gi No. 3021348
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1094: from 4 to 26
- Alignment No. 9099
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1094: from 28 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1095
- Ceres seq\_id 1499608
- Location of start within SEQ ID NO 1092: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9100
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9101
- gi No. 2501188
- % Identity 91.9

- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9102
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9103
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1095: from 1 to 36
- Alignment No. 9104
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1095: from 1 to 31

Maximum Length Sequence corresponding to clone ID 246878

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1096
- Ceres seq\_id 1499627

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1097
- Ceres seq\_id 1499628
- Location of start within SEQ ID NO 1096: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9105
- gi No. 4006881
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1097: from 8 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1098
- Ceres seq\_id 1499629
- Location of start within SEQ ID NO 1096: at 331 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1099
- Ceres seq\_id 1499630
- Location of start within SEQ ID NO 1096: at 337 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247172

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1100
- Ceres seq\_id 1499649



(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1101
- Ceres seq\_id 1499650
- Location of start within SEQ ID NO 1100: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9106
- 11-S plant seed storage protein
- Location within SEQ ID NO 1101: from 18 to 105 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1102
- Ceres seq\_id 1499651
- Location of start within SEQ ID NO 1100: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1103
- Ceres seq\_id 1499652
- Location of start within SEQ ID NO 1100: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247194

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1104
- Ceres seq\_id 1499655

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1105
- Ceres seq\_id 1499656
- Location of start within SEQ ID NO 1104: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9107
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
- Alignment No. 9108
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
- Alignment No. 9109
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9110
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9111
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9112
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9113
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9114
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9115
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9116
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9117
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9118
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1105: from 22 to 65
  
- Alignment No. 9119
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1105: from 26 to 63
  
- Alignment No. 9120

- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9121
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9122
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
  
- Alignment No. 9123
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1106
- Ceres seq\_id 1499657
- Location of start within SEQ ID NO 1104: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9124
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9125
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9126
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9127
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9128
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9129
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9130
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9131
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9132
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9133
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9134
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9135
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9136
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1106: from 1 to 38
  
- Alignment No. 9137
- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9138
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9139

- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
  
- Alignment No. 9140
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1107
- Ceres seq\_id 1499658
- Location of start within SEQ ID NO 1104: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9141
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9142
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9143
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9144
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9145
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9146
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9147
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9148
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9149
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9150
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9151
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9152
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9153
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1107: from 1 to 25
  
- Alignment No. 9154
- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9155
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9156
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
  
- Alignment No. 9157
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

Maximum Length Sequence corresponding to clone ID 247264

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1108
  - Ceres seq\_id 1499667
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1109
  - Ceres seq\_id 1499668
  - Location of start within SEQ ID NO 1108: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1110
  - Ceres seq\_id 1499669
  - Location of start within SEQ ID NO 1108: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9158
  - Uncharacterized protein family
  - Location within SEQ ID NO 1110: from 81 to 166 aa.
- (D) Related Amino Acid Sequences
  - Alignment No. 9159
  - gi No. 4886288
  - % Identity 86.1
  - Alignment Length 79
  - Location of Alignment in SEQ ID NO 1110: from 82 to 160
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1111
  - Ceres seq\_id 1499670
  - Location of start within SEQ ID NO 1108: at 21 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9160
  - Uncharacterized protein family
  - Location within SEQ ID NO 1111: from 75 to 160 aa.
- (D) Related Amino Acid Sequences
  - Alignment No. 9161
  - gi No. 4886288
  - % Identity 86.1
  - Alignment Length 79
  - Location of Alignment in SEQ ID NO 1111: from 76 to 154

Maximum Length Sequence corresponding to clone ID 247265

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1112
  - Ceres seq\_id 1499671
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1113
  - Ceres seq\_id 1499672
  - Location of start within SEQ ID NO 1112: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1114
  - Ceres seq\_id 1499673
  - Location of start within SEQ ID NO 1112: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9162
  - gi No. 1523800
  - % Identity 71.4
  - Alignment Length 15
  - Location of Alignment in SEQ ID NO 1114: from 16 to 29
- Alignment No. 9163
  - gi No. 3219273
  - % Identity 71.4
  - Alignment Length 15
  - Location of Alignment in SEQ ID NO 1114: from 16 to 29

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1115
  - Ceres seq\_id 1499674
  - Location of start within SEQ ID NO 1112: at 193 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9164
  - Eukaryotic protein kinase domain
  - Location within SEQ ID NO 1115: from 21 to 115 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247273

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1116
  - Ceres seq\_id 1499675
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1117
  - Ceres seq\_id 1499676
  - Location of start within SEQ ID NO 1116: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9165
  - gi No. 123704
  - % Identity 70
  - Alignment Length 20
  - Location of Alignment in SEQ ID NO 1117: from 52 to 70

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1118
  - Ceres seq\_id 1499677
  - Location of start within SEQ ID NO 1116: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence



- Pat. Appln. SEQ ID NO 1119
- Ceres seq\_id 1499678
- Location of start within SEQ ID NO 1116: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247522

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1120
- Ceres seq\_id 1499686

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1121
- Ceres seq\_id 1499687
- Location of start within SEQ ID NO 1120: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9166
- Sugar (and other) transporter
- Location within SEQ ID NO 1121: from 24 to 142 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1122
- Ceres seq\_id 1499688
- Location of start within SEQ ID NO 1120: at 148 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9167
- Sugar (and other) transporter
- Location within SEQ ID NO 1122: from 1 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1123
- Ceres seq\_id 1499689
- Location of start within SEQ ID NO 1120: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9168
- Sugar (and other) transporter
- Location within SEQ ID NO 1123: from 1 to 101 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247534

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1124
- Ceres seq\_id 1499690

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1125
- Ceres seq\_id 1499691
- Location of start within SEQ ID NO 1124: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9169
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1125: from 78 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1126
- Ceres seq\_id 1499692
- Location of start within SEQ ID NO 1124: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9170
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1126: from 53 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1127
- Ceres seq\_id 1499693
- Location of start within SEQ ID NO 1124: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9171
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1127: from 41 to 94 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247548

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1128
- Ceres seq\_id 1499694

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1129
- Ceres seq\_id 1499695
- Location of start within SEQ ID NO 1128: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9172
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1129: from 70 to 93

- Alignment No. 9173
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1129: from 71 to 92

- Alignment No. 9174
- gi No. 2459430
- % Identity 73.1

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1129: from 70 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1130
- Ceres seq\_id 1499696
- Location of start within SEQ ID NO 1128: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9175
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1130: from 10 to 33

- Alignment No. 9176
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1130: from 11 to 32

- Alignment No. 9177
- gi No. 2459430
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1130: from 10 to 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1131
- Ceres seq\_id 1499697
- Location of start within SEQ ID NO 1128: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9178
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1131: from 5 to 28

- Alignment No. 9179
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1131: from 6 to 27

- Alignment No. 9180
- gi No. 2459430
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1131: from 5 to 30

Maximum Length Sequence corresponding to clone ID 247645

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1132
- Ceres seq\_id 1499720

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1133

- Ceres seq\_id 1499721
- Location of start within SEQ ID NO 1132: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9181
  - gi No. 4883616
  - % Identity 73.3
  - Alignment Length 60
  - Location of Alignment in SEQ ID NO 1133: from 57 to 116

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1134
- Ceres seq\_id 1499722
- Location of start within SEQ ID NO 1132: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9182
  - gi No. 4883616
  - % Identity 73.3
  - Alignment Length 60
  - Location of Alignment in SEQ ID NO 1134: from 39 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1135
- Ceres seq\_id 1499723
- Location of start within SEQ ID NO 1132: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9183
  - gi No. 4883616
  - % Identity 73.3
  - Alignment Length 60
  - Location of Alignment in SEQ ID NO 1135: from 25 to 84

Maximum Length Sequence corresponding to clone ID 247783

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1136
- Ceres seq\_id 1499728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1137
- Ceres seq\_id 1499729
- Location of start within SEQ ID NO 1136: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9184
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1137: from 46 to 146 aa.
  
- Alignment No. 9185
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1137: from 256 to 355 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1138
- Ceres seq\_id 1499730
- Location of start within SEQ ID NO 1136: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9186
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1138: from 9 to 109 aa.
- Alignment No. 9187
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1138: from 219 to 318 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1139
- Ceres seq\_id 1499731
- Location of start within SEQ ID NO 1136: at 617 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9188
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1139: from 99 to 198 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247881

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1140
- Ceres seq\_id 1499732

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1141
- Ceres seq\_id 1499733
- Location of start within SEQ ID NO 1140: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9189
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1141: from 134 to 181 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1142
- Ceres seq\_id 1499734
- Location of start within SEQ ID NO 1140: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9190
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1142: from 131 to 178 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1143
- Ceres seq\_id 1499735
- Location of start within SEQ ID NO 1140: at 332 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9191
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1143: from 50 to 97 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248288

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1144
- Ceres seq\_id 1499740

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1145
- Ceres seq\_id 1499741
- Location of start within SEQ ID NO 1144: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1146
- Ceres seq\_id 1499742
- Location of start within SEQ ID NO 1144: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1147
- Ceres seq\_id 1499743
- Location of start within SEQ ID NO 1144: at 744 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9192
- Integral membrane protein
- Location within SEQ ID NO 1147: from 1 to 122 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248560

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1148
- Ceres seq\_id 1499748

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1149
- Ceres seq\_id 1499749
- Location of start within SEQ ID NO 1148: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9193
- gi No. 3004561

- % Identity 100
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1149: from 1 to 125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1150
- Ceres seq\_id 1499750
- Location of start within SEQ ID NO 1148: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9194
- gi No. 3004561
- % Identity 100
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1150: from 1 to 92

Maximum Length Sequence corresponding to clone ID 248721

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1151
- Ceres seq\_id 1499751

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1152
- Ceres seq\_id 1499752
- Location of start within SEQ ID NO 1151: at 31 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9195
- gi No. 5262162
- % Identity 97.5
- Alignment Length 197
- Location of Alignment in SEQ ID NO 1152: from 1 to 197

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1153
- Ceres seq\_id 1499753
- Location of start within SEQ ID NO 1151: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9196
- gi No. 5262162
- % Identity 97.5
- Alignment Length 197
- Location of Alignment in SEQ ID NO 1153: from 1 to 170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1154
- Ceres seq\_id 1499754
- Location of start within SEQ ID NO 1151: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9197
- gi No. 5262162
- % Identity 97.5

- Alignment Length 197
- Location of Alignment in SEQ ID NO 1154: from 1 to 161

Maximum Length Sequence corresponding to clone ID 248969

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1155
- Ceres seq\_id 1499755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1156
- Ceres seq\_id 1499756
- Location of start within SEQ ID NO 1155: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1157
- Ceres seq\_id 1499757
- Location of start within SEQ ID NO 1155: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9198
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1157: from 63 to 115 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248974

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1158
- Ceres seq\_id 1499758

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1159
- Ceres seq\_id 1499759
- Location of start within SEQ ID NO 1158: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9199
- Ribosomal L10
- Location within SEQ ID NO 1159: from 19 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9200
- gi No. 1172806
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
  
- Alignment No. 9201
- gi No. 1172807
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9202
- gi No. 1172808
- % Identity 75.6
- Alignment Length 41



- Location of Alignment in SEQ ID NO 1159: from 25 to 65
- Alignment No. 9203
- gi No. 1172809
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9204
- gi No. 1172810
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9205
- gi No. 1172811
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9206
- gi No. 1172812
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9207
- gi No. 1172813
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1159: from 19 to 64
- Alignment No. 9208
- gi No. 2317762
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9209
- gi No. 2500351
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9210
- gi No. 2500352
- % Identity 70.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9211
- gi No. 2500353
- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1159: from 19 to 64
- Alignment No. 9212
- gi No. 2500354
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70

- Alignment No. 9213
- gi No. 2500356
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9214
- gi No. 3123840
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9215
- gi No. 4063389
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9216
- gi No. 4107323
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9217
- gi No. 4262180
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
  
- Alignment No. 9218
- gi No. 4493745
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9219
- gi No. 4929242
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9220
- gi No. 5174431
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9221
- gi No. 88079
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1159: from 18 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1160
- Ceres seq\_id 1499760
- Location of start within SEQ ID NO 1158: at 56 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9222
- Ribosomal L10
- Location within SEQ ID NO 1160: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9223
- gi No. 1172806
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9224
- gi No. 1172807
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9225
- gi No. 1172808
- % Identity 75.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1160: from 7 to 47
- Alignment No. 9226
- gi No. 1172809
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9227
- gi No. 1172810
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9228
- gi No. 1172811
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9229
- gi No. 1172812
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9230
- gi No. 1172813
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1160: from 1 to 46
- Alignment No. 9231
- gi No. 2317762
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9232
- gi No. 2500351
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9233
- gi No. 2500352
- % Identity 70.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9234
- gi No. 2500353
- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1160: from 1 to 46
  
- Alignment No. 9235
- gi No. 2500354
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
  
- Alignment No. 9236
- gi No. 2500356
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9237
- gi No. 3123840
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9238
- gi No. 4063389
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9239
- gi No. 4107323
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9240
- gi No. 4262180
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
  
- Alignment No. 9241
- gi No. 4493745
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9242

- gi No. 4929242
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9243
- gi No. 5174431
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
  
- Alignment No. 9244
- gi No. 88079
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

Maximum Length Sequence corresponding to clone ID 249321

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1161
- Ceres seq\_id 1499765

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1162
- Ceres seq\_id 1499766
- Location of start within SEQ ID NO 1161: at 608 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9245
- gi No. 123530
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1162: from 29 to 39
  
- Alignment No. 9246
- gi No. 3875708
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1162: from 4 to 14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1163
- Ceres seq\_id 1499767
- Location of start within SEQ ID NO 1161: at 773 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1164
- Ceres seq\_id 1499768
- Location of start within SEQ ID NO 1161: at 777 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249331

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1165
- Ceres seq\_id 1499769
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1166
  - Ceres seq\_id 1499770
  - Location of start within SEQ ID NO 1165: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9247
  - gi No. 4972053
  - % Identity 90.4
  - Alignment Length 115
  - Location of Alignment in SEQ ID NO 1166: from 1 to 102

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1167
  - Ceres seq\_id 1499771
  - Location of start within SEQ ID NO 1165: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9248
  - gi No. 4972053
  - % Identity 90.4
  - Alignment Length 115
  - Location of Alignment in SEQ ID NO 1167: from 1 to 81

Maximum Length Sequence corresponding to clone ID 249334

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1168
  - Ceres seq\_id 1499772
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1169
  - Ceres seq\_id 1499773
  - Location of start within SEQ ID NO 1168: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9249
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1169: from 180 to 249 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249340

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1170
  - Ceres seq\_id 1499777
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1171
  - Ceres seq\_id 1499778
  - Location of start within SEQ ID NO 1170: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9250
  - gi No. 1531760

- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
  
- Alignment No. 9251
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
  
- Alignment No. 9252
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
  
- Alignment No. 9253
- gi No. 4164139
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1171: from 40 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1172
- Ceres seq\_id 1499779
- Location of start within SEQ ID NO 1170: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9254
- gi No. 1531760
- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
  
- Alignment No. 9255
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
  
- Alignment No. 9256
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
  
- Alignment No. 9257
- gi No. 4164139
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1172: from 1 to 19

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1173
- Ceres seq\_id 1499780
- Location of start within SEQ ID NO 1170: at 402 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9258
  - gi No. 1531760
  - % Identity 99.3
  - Alignment Length 273
  - Location of Alignment in SEQ ID NO 1173: from 1 to 179
- Alignment No. 9259
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179
- Alignment No. 9260
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179

Maximum Length Sequence corresponding to clone ID 249370

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1174
  - Ceres seq\_id 1499785
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1175
  - Ceres seq\_id 1499786
  - Location of start within SEQ ID NO 1174: at 50 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9261
  - Zinc-binding dehydrogenases
  - Location within SEQ ID NO 1175: from 73 to 167 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1176
  - Ceres seq\_id 1499787
  - Location of start within SEQ ID NO 1174: at 62 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9262
  - Zinc-binding dehydrogenases
  - Location within SEQ ID NO 1176: from 69 to 163 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1177
  - Ceres seq\_id 1499788
  - Location of start within SEQ ID NO 1174: at 170 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9263
  - Zinc-binding dehydrogenases
  - Location within SEQ ID NO 1177: from 33 to 127 aa.
- (D) Related Amino Acid Sequences



Maximum Length Sequence corresponding to clone ID 249388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1178
- Ceres seq\_id 1499789

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1179
- Ceres seq\_id 1499790
- Location of start within SEQ ID NO 1178: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9264
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 1179: from 110 to 240 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1180
- Ceres seq\_id 1499791
- Location of start within SEQ ID NO 1178: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9265
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 1180: from 71 to 201 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249485

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1181
- Ceres seq\_id 1499792

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1182
- Ceres seq\_id 1499793
- Location of start within SEQ ID NO 1181: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9266
- Dehydrogenase E1 component
- Location within SEQ ID NO 1182: from 73 to 377 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9267
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1182: from 47 to 412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1183
- Ceres seq\_id 1499794
- Location of start within SEQ ID NO 1181: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9268

- Dehydrogenase E1 component
- Location within SEQ ID NO 1183: from 70 to 374 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9269
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1183: from 44 to 409

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1184
- Ceres seq\_id 1499795
- Location of start within SEQ ID NO 1181: at 376 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9270
- Dehydrogenase E1 component
- Location within SEQ ID NO 1184: from 1 to 303 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9271
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1184: from 1 to 338

Maximum Length Sequence corresponding to clone ID 249591

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1185
- Ceres seq\_id 1499800

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1186
- Ceres seq\_id 1499801
- Location of start within SEQ ID NO 1185: at 335 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9272
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1186: from 32 to 292

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1187
- Ceres seq\_id 1499802
- Location of start within SEQ ID NO 1185: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9273
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1187: from 31 to 291

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1188
- Ceres seq\_id 1499803
- Location of start within SEQ ID NO 1185: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9274
  - gi No. 2708751
  - % Identity 83.1
  - Alignment Length 267
  - Location of Alignment in SEQ ID NO 1188: from 23 to 283

Maximum Length Sequence corresponding to clone ID 249631

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1189
- Ceres seq\_id 1499811

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1190
- Ceres seq\_id 1499812
- Location of start within SEQ ID NO 1189: at 381 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9275
- Phosphoglycerate mutase family
- Location within SEQ ID NO 1190: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9276
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1190: from 1 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1191
- Ceres seq\_id 1499813
- Location of start within SEQ ID NO 1189: at 384 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9277
- Phosphoglycerate mutase family
- Location within SEQ ID NO 1191: from 1 to 77 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9278
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1191: from 1 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1192
- Ceres seq\_id 1499814
- Location of start within SEQ ID NO 1189: at 483 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9279
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1192: from 1 to 89

Maximum Length Sequence corresponding to clone ID 249747

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1193
- Ceres seq\_id 1499823

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1194
- Ceres seq\_id 1499824
- Location of start within SEQ ID NO 1193: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9280
- Tropomyosins
- Location within SEQ ID NO 1194: from 126 to 244 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9281
- gi No. 2832682
- % Identity 96.3
- Alignment Length 244
- Location of Alignment in SEQ ID NO 1194: from 1 to 244

Maximum Length Sequence corresponding to clone ID 249756

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1195
- Ceres seq\_id 1499825

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1196
- Ceres seq\_id 1499826
- Location of start within SEQ ID NO 1195: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9282
- Protein phosphatase 2C
- Location within SEQ ID NO 1196: from 243 to 317 aa.

- Alignment No. 9283
- Protein phosphatase 2C
- Location within SEQ ID NO 1196: from 309 to 452 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1197
- Ceres seq\_id 1499827
- Location of start within SEQ ID NO 1195: at 535 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9284
- Protein phosphatase 2C
- Location within SEQ ID NO 1197: from 134 to 208 aa.
- Alignment No. 9285

- Protein phosphatase 2C
- Location within SEQ ID NO 1197: from 200 to 343 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1198
- Ceres seq\_id 1499828
- Location of start within SEQ ID NO 1195: at 607 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9286
- Protein phosphatase 2C
- Location within SEQ ID NO 1198: from 110 to 184 aa.
  
- Alignment No. 9287
- Protein phosphatase 2C
- Location within SEQ ID NO 1198: from 176 to 319 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249769

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1199
- Ceres seq\_id 1499829

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1200
- Ceres seq\_id 1499830
- Location of start within SEQ ID NO 1199: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9288
- gi No. 4914402
- % Identity 99.6
- Alignment Length 515
- Location of Alignment in SEQ ID NO 1200: from 17 to 531

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1201
- Ceres seq\_id 1499831
- Location of start within SEQ ID NO 1199: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9289
- gi No. 4914402
- % Identity 99.6
- Alignment Length 515
- Location of Alignment in SEQ ID NO 1201: from 1 to 515

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1202
- Ceres seq\_id 1499832
- Location of start within SEQ ID NO 1199: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9290
  - gi No. 4914402
  - % Identity 99.6
  - Alignment Length 515
  - Location of Alignment in SEQ ID NO 1202: from 1 to 419

Maximum Length Sequence corresponding to clone ID 249772

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1203
  - Ceres seq\_id 1499833
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1204
  - Ceres seq\_id 1499834
  - Location of start within SEQ ID NO 1203: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9291
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1204: from 121 to 388 aa.

- (D) Related Amino Acid Sequences
  - Alignment No. 9292
  - gi No. 3068714
  - % Identity 75.5
  - Alignment Length 343
  - Location of Alignment in SEQ ID NO 1204: from 64 to 405

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1205
  - Ceres seq\_id 1499835
  - Location of start within SEQ ID NO 1203: at 496 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9293
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1205: from 1 to 246 aa.

- (D) Related Amino Acid Sequences
  - Alignment No. 9294
  - gi No. 3068714
  - % Identity 75.5
  - Alignment Length 343
  - Location of Alignment in SEQ ID NO 1205: from 1 to 263

Maximum Length Sequence corresponding to clone ID 249844

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1206
  - Ceres seq\_id 1499844
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1207
  - Ceres seq\_id 1499845
  - Location of start within SEQ ID NO 1206: at 174 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9295
- Tropomyosins
- Location within SEQ ID NO 1207: from 122 to 242 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9296
- gi No. 2832682
- % Identity 96.7
- Alignment Length 242
- Location of Alignment in SEQ ID NO 1207: from 1 to 242

Maximum Length Sequence corresponding to clone ID 250092

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1208
- Ceres seq\_id 1499850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1209
- Ceres seq\_id 1499851
- Location of start within SEQ ID NO 1208: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1210
- Ceres seq\_id 1499852
- Location of start within SEQ ID NO 1208: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9297
- gi No. 4097571
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1210: from 91 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1211
- Ceres seq\_id 1499853
- Location of start within SEQ ID NO 1208: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250127

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1212
- Ceres seq\_id 1499854

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1213
- Ceres seq\_id 1499855
- Location of start within SEQ ID NO 1212: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9298
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1213: from 113 to 153 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1214
  - Ceres seq\_id 1499856
  - Location of start within SEQ ID NO 1212: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9299
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1214: from 48 to 88 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1215
  - Ceres seq\_id 1499857
  - Location of start within SEQ ID NO 1212: at 357 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9300
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1215: from 39 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250751

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1216
  - Ceres seq\_id 1499875
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1217
  - Ceres seq\_id 1499876
  - Location of start within SEQ ID NO 1216: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9301
  - gi No. 1698582
  - % Identity 74.2
  - Alignment Length 376
  - Location of Alignment in SEQ ID NO 1217: from 62 to 435

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1218
  - Ceres seq\_id 1499877
  - Location of start within SEQ ID NO 1216: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9302
  - gi No. 1698582
  - % Identity 74.2
  - Alignment Length 376
  - Location of Alignment in SEQ ID NO 1218: from 51 to 424

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1219
  - Ceres seq\_id 1499878



- Location of start within SEQ ID NO 1216: at 404 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9303
- gi No. 1698582
- % Identity 74.2
- Alignment Length 376
- Location of Alignment in SEQ ID NO 1219: from 1 to 301

Maximum Length Sequence corresponding to clone ID 251247

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1220
- Ceres seq\_id 1499899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1221
- Ceres seq\_id 1499900
- Location of start within SEQ ID NO 1220: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9304
- Response regulator receiver domain
- Location within SEQ ID NO 1221: from 22 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9305
- gi No. 3687688
- % Identity 78.9
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1221: from 1 to 142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1222
- Ceres seq\_id 1499901
- Location of start within SEQ ID NO 1220: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9306
- Response regulator receiver domain
- Location within SEQ ID NO 1222: from 1 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9307
- gi No. 3687688
- % Identity 78.9
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1222: from 1 to 104

Maximum Length Sequence corresponding to clone ID 251438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1223
- Ceres seq\_id 1499902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1224
- Ceres seq\_id 1499903
- Location of start within SEQ ID NO 1223: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9308
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1224: from 73 to 136 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1225
- Ceres seq\_id 1499904
- Location of start within SEQ ID NO 1223: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9309
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1225: from 50 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1226
- Ceres seq\_id 1499905
- Location of start within SEQ ID NO 1223: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9310
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1226: from 19 to 82 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251466

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1227
- Ceres seq\_id 1499906

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1228
- Ceres seq\_id 1499907
- Location of start within SEQ ID NO 1227: at 53 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9311
- AP2 domain
- Location within SEQ ID NO 1228: from 62 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9312
- gi No. 1246403
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1228: from 59 to 112

- Alignment No. 9313
- gi No. 3643601
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1228: from 64 to 112

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1229
  - Ceres seq\_id 1499908
  - Location of start within SEQ ID NO 1227: at 490 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251549

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1230
  - Ceres seq\_id 1499909

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1231
  - Ceres seq\_id 1499910
  - Location of start within SEQ ID NO 1230: at 430 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9314
  - gi No. 4982498
  - % Identity 100
  - Alignment Length 154
  - Location of Alignment in SEQ ID NO 1231: from 6 to 159

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1232
  - Ceres seq\_id 1499911
  - Location of start within SEQ ID NO 1230: at 439 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9315
  - gi No. 4982498
  - % Identity 100
  - Alignment Length 154
  - Location of Alignment in SEQ ID NO 1232: from 3 to 156

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1233
  - Ceres seq\_id 1499912
  - Location of start within SEQ ID NO 1230: at 466 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9316
  - gi No. 4982498
  - % Identity 100
  - Alignment Length 154
  - Location of Alignment in SEQ ID NO 1233: from 1 to 147

Maximum Length Sequence corresponding to clone ID 251841

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1234
  - Ceres seq\_id 1499924
- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1235
- Ceres seq\_id 1499925
- Location of start within SEQ ID NO 1234: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9317
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1235: from 46 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9318
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1235: from 46 to 152

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1236
- Ceres seq\_id 1499926
- Location of start within SEQ ID NO 1234: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9319
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1236: from 4 to 71 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9320
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1236: from 4 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1237
- Ceres seq\_id 1499927
- Location of start within SEQ ID NO 1234: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9321
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1237: from 1 to 76

Maximum Length Sequence corresponding to clone ID 251906

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1238
- Ceres seq\_id 1499928

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1239
- Ceres seq\_id 1499929
- Location of start within SEQ ID NO 1238: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9322

- Pollen proteins Ole e I family
- Location within SEQ ID NO 1239: from 48 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1240
- Ceres seq\_id 1499930
- Location of start within SEQ ID NO 1238: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9323
- Pollen proteins Ole e I family
- Location within SEQ ID NO 1240: from 32 to 92 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1241
- Ceres seq\_id 1499931
- Location of start within SEQ ID NO 1238: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9324
- Pollen proteins Ole e I family
- Location within SEQ ID NO 1241: from 27 to 87 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 252299

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1242
- Ceres seq\_id 1499935

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1243
- Ceres seq\_id 1499936
- Location of start within SEQ ID NO 1242: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9325
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1243: from 62 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9326
- gi No. 100607
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113

- Alignment No. 9327
- gi No. 1084336
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1243: from 20 to 114

- Alignment No. 9328
- gi No. 115764

- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
  
- Alignment No. 9329
- gi No. 115833
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113
  
- Alignment No. 9330
- gi No. 115834
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113
  
- Alignment No. 9331
- gi No. 2326947
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1243: from 83 to 113
  
- Alignment No. 9332
- gi No. 2498362
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1243: from 98 to 112
  
- Alignment No. 9333
- gi No. 282865
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
  
- Alignment No. 9334
- gi No. 322377
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1243: from 96 to 112
  
- Alignment No. 9335
- gi No. 322380
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 84 to 110
  
- Alignment No. 9336
- gi No. 322392
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1243: from 87 to 112
  
- Alignment No. 9337
- gi No. 322393
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1243: from 87 to 112
  
- Alignment No. 9338
- gi No. 543939
- % Identity 100

- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113
  
- Alignment No. 9339
- gi No. 625547
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
  
- Alignment No. 9340
- gi No. 82078
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
  
- Alignment No. 9341
- gi No. 82079
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
  
- Alignment No. 9342
- gi No. 99485
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
  
- Alignment No. 9343
- gi No. 99488
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1244
- Ceres seq\_id 1499937
- Location of start within SEQ ID NO 1242: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9344
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1244: from 59 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9345
- gi No. 100607
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110
  
- Alignment No. 9346
- gi No. 1084336
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1244: from 17 to 111
  
- Alignment No. 9347
- gi No. 115764
- % Identity 70.4
- Alignment Length 27

- Location of Alignment in SEQ ID NO 1244: from 84 to 110
- Alignment No. 9348
- gi No. 115833
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9349
- gi No. 115834
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9350
- gi No. 2326947
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1244: from 80 to 110
- Alignment No. 9351
- gi No. 2498362
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1244: from 95 to 109
- Alignment No. 9352
- gi No. 282865
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
- Alignment No. 9353
- gi No. 322377
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1244: from 93 to 109
- Alignment No. 9354
- gi No. 322380
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 81 to 107
- Alignment No. 9355
- gi No. 322392
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1244: from 84 to 109
- Alignment No. 9356
- gi No. 322393
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1244: from 84 to 109
- Alignment No. 9357
- gi No. 543939
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110



- Alignment No. 9358
- gi No. 625547
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
  
- Alignment No. 9359
- gi No. 82078
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
  
- Alignment No. 9360
- gi No. 82079
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
  
- Alignment No. 9361
- gi No. 99485
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
  
- Alignment No. 9362
- gi No. 99488
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1245
- Ceres seq\_id 1499938
- Location of start within SEQ ID NO 1242: at 532 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9363
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1245: from 1 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9364
- gi No. 1084336
- % Identity 97.2
- Alignment Length 143
- Location of Alignment in SEQ ID NO 1245: from 1 to 113

Maximum Length Sequence corresponding to clone ID 252372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1246
- Ceres seq\_id 1499939

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1247
- Ceres seq\_id 1499940
- Location of start within SEQ ID NO 1246: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9365
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1247: from 46 to 122
  
- Alignment No. 9366
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1247: from 46 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1248
- Ceres seq\_id 1499941
- Location of start within SEQ ID NO 1246: at 138 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9367
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1248: from 1 to 77
  
- Alignment No. 9368
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1248: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1249
- Ceres seq\_id 1499942
- Location of start within SEQ ID NO 1246: at 168 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9369
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1249: from 1 to 67
  
- Alignment No. 9370
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1249: from 1 to 67

Maximum Length Sequence corresponding to clone ID 252497

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1250
- Ceres seq\_id 1499943

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1251
- Ceres seq\_id 1499944
- Location of start within SEQ ID NO 1250: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9371
- Core histone H2A/H2B/H3/H4
- Location within SEQ ID NO 1251: from 17 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9372
- gi No. 10253
- % Identity 88.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9373
- gi No. 103198
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9374
- gi No. 104698
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1251: from 2 to 26
- Alignment No. 9375
- gi No. 1053045
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9376
- gi No. 1053047
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9377
- gi No. 1053053
- % Identity 89.8
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9378
- gi No. 1053055
- % Identity 82.8
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1251: from 1 to 29
- Alignment No. 9379
- gi No. 1053057
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9380
- gi No. 1053059
- % Identity 92.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9381
- gi No. 1076583
- % Identity 95
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1251: from 1 to 60
  
- Alignment No. 9382
- gi No. 1079199
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9383
- gi No. 1085857
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 34 to 116
  
- Alignment No. 9384
- gi No. 1085858
- % Identity 92.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 34 to 116
  
- Alignment No. 9385
- gi No. 108593
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1251: from 112 to 128
  
- Alignment No. 9386
- gi No. 109977
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1251: from 2 to 36
  
- Alignment No. 9387
- gi No. 1166436
- % Identity 81.4
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1251: from 36 to 94
  
- Alignment No. 9388
- gi No. 1197519
- % Identity 82.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
  
- Alignment No. 9389
- gi No. 1208642
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9390
- gi No. 1208644
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9391

- gi No. 1208646
- % Identity 98.2
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9392
- gi No. 1208656
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9393
- gi No. 1208658
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9394
- gi No. 1208664
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9395
- gi No. 1208668
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9396
- gi No. 1208699
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9397
- gi No. 1208701
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9398
- gi No. 1208707
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9399
- gi No. 1208715
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9400
- gi No. 1208725
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9401
- gi No. 1208727

- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9402
- gi No. 1213291
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9403
- gi No. 1213307
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9404
- gi No. 1213313
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9405
- gi No. 1213315
- % Identity 89.3
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
  
- Alignment No. 9406
- gi No. 122065
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9407
- gi No. 122066
- % Identity 83.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9408
- gi No. 122068
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9409
- gi No. 122070
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9410
- gi No. 122071
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41
  
- Alignment No. 9411
- gi No. 122072
- % Identity 78

- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41
  
- Alignment No. 9412
- gi No. 122074
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9413
- gi No. 122076
- % Identity 86.7
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9414
- gi No. 122077
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
  
- Alignment No. 9415
- gi No. 122078
- % Identity 77.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 1 to 132
  
- Alignment No. 9416
- gi No. 122079
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9417
- gi No. 122080
- % Identity 85.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9418
- gi No. 122081
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9419
- gi No. 122082
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9420
- gi No. 122083
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
  
- Alignment No. 9421
- gi No. 122084
- % Identity 95.8
- Alignment Length 72

- Location of Alignment in SEQ ID NO 1251: from 57 to 128
- Alignment No. 9422
- gi No. 122085
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9423
- gi No. 122086
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9424
- gi No. 122087
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9425
- gi No. 122088
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9426
- gi No. 122089
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9427
- gi No. 122090
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9428
- gi No. 122091
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9429
- gi No. 1360625
- % Identity 78.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 1 to 129
- Alignment No. 9430
- gi No. 1360627
- % Identity 76.5
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1251: from 1 to 96
- Alignment No. 9431
- gi No. 1362108
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127



- Alignment No. 9432
- gi No. 1362171
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1251: from 105 to 128
  
- Alignment No. 9433
- gi No. 159967
- % Identity 89.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9434
- gi No. 161319
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9435
- gi No. 166384
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9436
- gi No. 1708108
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9437
- gi No. 1708109
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9438
- gi No. 171637
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1251: from 3 to 35
  
- Alignment No. 9439
- gi No. 1723293
- % Identity 90.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 46 to 128
  
- Alignment No. 9440
- gi No. 1731925
- % Identity 90.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 3 to 117
  
- Alignment No. 9441
- gi No. 1762791
- % Identity 71.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 4 to 128

- Alignment No. 9442
- gi No. 1763308
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9443
- gi No. 1870700
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 1 to 111
  
- Alignment No. 9444
- gi No. 1881589
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1251: from 89 to 128
  
- Alignment No. 9445
- gi No. 1881594
- % Identity 91
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1251: from 1 to 87
  
- Alignment No. 9446
- gi No. 1881601
- % Identity 93.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1251: from 1 to 87
  
- Alignment No. 9447
- gi No. 19611
- % Identity 92.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 14 to 128
  
- Alignment No. 9448
- gi No. 19614
- % Identity 90
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1251: from 79 to 128
  
- Alignment No. 9449
- gi No. 208463
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1251: from 3 to 35
  
- Alignment No. 9450
- gi No. 2116601
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9451
- gi No. 211855
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9452

- gi No. 2119011
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9453
- gi No. 2119012
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9454
- gi No. 2119013
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
  
- Alignment No. 9455
- gi No. 2119014
- % Identity 91.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1251: from 61 to 128
  
- Alignment No. 9456
- gi No. 2119018
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9457
- gi No. 2135356
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1251: from 1 to 27
  
- Alignment No. 9458
- gi No. 2136686
- % Identity 89.7
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1251: from 2 to 30
  
- Alignment No. 9459
- gi No. 2147399
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1251: from 1 to 39
  
- Alignment No. 9460
- gi No. 2252516
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1251: from 1 to 38
  
- Alignment No. 9461
- gi No. 2253166
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1251: from 1 to 63
  
- Alignment No. 9462
- gi No. 2253615

- % Identity 78.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9463
- gi No. 2909431
- % Identity 80.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
  
- Alignment No. 9464
- gi No. 2995216
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36
  
- Alignment No. 9465
- gi No. 2995219
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36
  
- Alignment No. 9466
- gi No. 2995225
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36
  
- Alignment No. 9467
- gi No. 2995264
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36
  
- Alignment No. 9468
- gi No. 3002595
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9469
- gi No. 3002597
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9470
- gi No. 3002603
- % Identity 87
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9471
- gi No. 3002613
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9472
- gi No. 3002621
- % Identity 86.8

- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9473
- gi No. 3002633
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9474
- gi No. 3002635
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9475
- gi No. 3002637
- % Identity 88.9
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1251: from 16 to 105
  
- Alignment No. 9476
- gi No. 3002643
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9477
- gi No. 3002647
- % Identity 90
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1251: from 15 to 104
  
- Alignment No. 9478
- gi No. 3002649
- % Identity 87.6
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1251: from 15 to 103
  
- Alignment No. 9479
- gi No. 3002657
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9480
- gi No. 3002663
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
  
- Alignment No. 9481
- gi No. 3219788
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
  
- Alignment No. 9482
- gi No. 3219789
- % Identity 82.1
- Alignment Length 112

- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9483
- gi No. 3219790
- % Identity 85.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9484
- gi No. 3219791
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9485
- gi No. 3219792
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9486
- gi No. 3219803
- % Identity 81.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9487
- gi No. 3219805
- % Identity 82.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9488
- gi No. 352175
- % Identity 83.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9489
- gi No. 3745758
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 21 to 128
- Alignment No. 9490
- gi No. 386772
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9491
- gi No. 3875420
- % Identity 82.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
- Alignment No. 9492
- gi No. 3875421
- % Identity 76.4
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9493
- gi No. 3880527
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9494
- gi No. 3880606
- % Identity 83.3
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1251: from 57 to 128
  
- Alignment No. 9495
- gi No. 3979986
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9496
- gi No. 404466
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9497
- gi No. 4139869
- % Identity 90.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1251: from 44 to 128
  
- Alignment No. 9498
- gi No. 417103
- % Identity 95.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9499
- gi No. 422605
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9500
- gi No. 422606
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9501
- gi No. 4388695
- % Identity 89.7
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1251: from 61 to 128
  
- Alignment No. 9502
- gi No. 4504279
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9503
- gi No. 4504281
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9504
- gi No. 4504283
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9505
- gi No. 4504299
- % Identity 88.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9506
- gi No. 4574208
- % Identity 97.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 22 to 128
  
- Alignment No. 9507
- gi No. 4761212
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 8 to 119
  
- Alignment No. 9508
- gi No. 484441
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9509
- gi No. 484530
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
  
- Alignment No. 9510
- gi No. 484531
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
  
- Alignment No. 9511
- gi No. 4883733
- % Identity 89.6
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1251: from 11 to 116
  
- Alignment No. 9512
- gi No. 4883734
- % Identity 90.7
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 10 to 116
  
- Alignment No. 9513



- gi No. 4883735
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9514
- gi No. 4883736
- % Identity 89.5
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1251: from 11 to 115
  
- Alignment No. 9515
- gi No. 4883737
- % Identity 90.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115
  
- Alignment No. 9516
- gi No. 4883738
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1251: from 17 to 109
  
- Alignment No. 9517
- gi No. 4883739
- % Identity 90.4
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1251: from 13 to 116
  
- Alignment No. 9518
- gi No. 4883740
- % Identity 89.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115
  
- Alignment No. 9519
- gi No. 4883741
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
  
- Alignment No. 9520
- gi No. 4883743
- % Identity 88.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9521
- gi No. 4883744
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9522
- gi No. 4883745
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
  
- Alignment No. 9523
- gi No. 4883746

- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
  
- Alignment No. 9524
- gi No. 4883747
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9525
- gi No. 4883748
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9526
- gi No. 4883749
- % Identity 91.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1251: from 13 to 117
  
- Alignment No. 9527
- gi No. 4883751
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
  
- Alignment No. 9528
- gi No. 4883752
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 10 to 117
  
- Alignment No. 9529
- gi No. 4883753
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9530
- gi No. 4883754
- % Identity 88.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 9 to 115
  
- Alignment No. 9531
- gi No. 4883755
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115
  
- Alignment No. 9532
- gi No. 4883756
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9533
- gi No. 4883758
- % Identity 91.2

- Alignment Length 102
- Location of Alignment in SEQ ID NO 1251: from 13 to 114
  
- Alignment No. 9534
- gi No. 4883759
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9535
- gi No. 4883760
- % Identity 88.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
  
- Alignment No. 9536
- gi No. 4883762
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
  
- Alignment No. 9537
- gi No. 488571
- % Identity 95
- Alignment Length 119
- Location of Alignment in SEQ ID NO 1251: from 10 to 128
  
- Alignment No. 9538
- gi No. 488573
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
  
- Alignment No. 9539
- gi No. 529954
- % Identity 82.6
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9540
- gi No. 539427
- % Identity 91.7
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1251: from 2 to 49
  
- Alignment No. 9541
- gi No. 556612
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9542
- gi No. 559807
- % Identity 89.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9543
- gi No. 578470
- % Identity 88.2
- Alignment Length 68

- Location of Alignment in SEQ ID NO 1251: from 61 to 128
- Alignment No. 9544
- gi No. 630475
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1251: from 1 to 76
- Alignment No. 9545
- gi No. 630476
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1251: from 1 to 63
- Alignment No. 9546
- gi No. 631693
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1251: from 79 to 128
- Alignment No. 9547
- gi No. 70743
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9548
- gi No. 70747
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9549
- gi No. 70748
- % Identity 89.8
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9550
- gi No. 70749
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9551
- gi No. 70753
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9552
- gi No. 70755
- % Identity 87.4
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9553
- gi No. 70760
- % Identity 77.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 2 to 132

- Alignment No. 9554
- gi No. 729676
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9555
- gi No. 729677
- % Identity 82.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9556
- gi No. 81850
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 18 to 128
  
- Alignment No. 9557
- gi No. 84300
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41
  
- Alignment No. 9558
- gi No. 84329
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
  
- Alignment No. 9559
- gi No. 85000
- % Identity 91.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 2 to 116
  
- Alignment No. 9560
- gi No. 85001
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9561
- gi No. 90622
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
  
- Alignment No. 9562
- gi No. 995959
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1251: from 1 to 40
  
- Alignment No. 9563
- gi No. 99980
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1251: from 85 to 116

- Alignment No. 9564
- gi No. 99980
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1251: from 2 to 45
  
- Alignment No. 9565
- gi No. 99981
- % Identity 78.1
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1251: from 2 to 65

Maximum Length Sequence corresponding to clone ID 253173

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1252
- Ceres seq\_id 1499960

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1253
- Ceres seq\_id 1499961
- Location of start within SEQ ID NO 1252: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9566
- O-methyltransferase
- Location within SEQ ID NO 1253: from 97 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9567
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
  
- Alignment No. 9568
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1253: from 1 to 363
  
- Alignment No. 9569
- gi No. 1184041
- % Identity 78.4
- Alignment Length 343
- Location of Alignment in SEQ ID NO 1253: from 21 to 363
  
- Alignment No. 9570
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
  
- Alignment No. 9571
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
  
- Alignment No. 9572
- gi No. 170277
- % Identity 81.6

- Alignment Length 114
- Location of Alignment in SEQ ID NO 1253: from 231 to 344
  
- Alignment No. 9573
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1253: from 15 to 361
  
- Alignment No. 9574
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
  
- Alignment No. 9575
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1253: from 163 to 182
  
- Alignment No. 9576
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 363
  
- Alignment No. 9577
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
  
- Alignment No. 9578
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
  
- Alignment No. 9579
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
  
- Alignment No. 9580
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
  
- Alignment No. 9581
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1253: from 222 to 361
  
- Alignment No. 9582
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365

- Location of Alignment in SEQ ID NO 1253: from 1 to 363
- Alignment No. 9583
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9584
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1253: from 136 to 361
- Alignment No. 9585
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1253: from 1 to 344
- Alignment No. 9586
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1253: from 1 to 344
- Alignment No. 9587
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9588
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9589
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9590
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9591
- gi No. 4808530
- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9592
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361



- Alignment No. 9593
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
  
- Alignment No. 9594
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1253: from 16 to 361
  
- Alignment No. 9595
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
  
- Alignment No. 9596
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1254
- Ceres seq\_id 1499962
- Location of start within SEQ ID NO 1252: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9597
- O-methyltransferase
- Location within SEQ ID NO 1254: from 74 to 315 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9598
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9599
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1254: from 1 to 340
  
- Alignment No. 9600
- gi No. 1184041
- % Identity 78.4
- Alignment Length 343
- Location of Alignment in SEQ ID NO 1254: from 1 to 340
  
- Alignment No. 9601
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9602
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339
  
- Alignment No. 9603
- gi No. 170277
- % Identity 81.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1254: from 208 to 321
  
- Alignment No. 9604
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9605
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339
  
- Alignment No. 9606
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1254: from 140 to 159
  
- Alignment No. 9607
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 340
  
- Alignment No. 9608
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9609
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9610
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339
  
- Alignment No. 9611
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9612

- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1254: from 199 to 338
  
- Alignment No. 9613
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1254: from 1 to 340
  
- Alignment No. 9614
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9615
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1254: from 113 to 338
  
- Alignment No. 9616
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1254: from 1 to 321
  
- Alignment No. 9617
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1254: from 1 to 321
  
- Alignment No. 9618
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9619
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9620
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9621
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9622
- gi No. 4808530

- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9623
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9624
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9625
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9626
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339
  
- Alignment No. 9627
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1255
- Ceres seq\_id 1499963
- Location of start within SEQ ID NO 1252: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9628
- O-methyltransferase
- Location within SEQ ID NO 1255: from 64 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9629
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9630
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
  
- Alignment No. 9631
- gi No. 1184041
- % Identity 78.4

- Alignment Length 343
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
  
- Alignment No. 9632
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
  
- Alignment No. 9633
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
  
- Alignment No. 9634
- gi No. 170277
- % Identity 81.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1255: from 198 to 311
  
- Alignment No. 9635
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9636
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
  
- Alignment No. 9637
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1255: from 130 to 149
  
- Alignment No. 9638
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
  
- Alignment No. 9639
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9640
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9641
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364

- Location of Alignment in SEQ ID NO 1255: from 1 to 329
- Alignment No. 9642
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9643
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1255: from 189 to 328
- Alignment No. 9644
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
- Alignment No. 9645
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9646
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1255: from 103 to 328
- Alignment No. 9647
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1255: from 1 to 311
- Alignment No. 9648
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1255: from 1 to 311
- Alignment No. 9649
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9650
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9651
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9652
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9653
- gi No. 4808530
- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9654
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9655
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9656
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9657
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
  
- Alignment No. 9658
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

Maximum Length Sequence corresponding to clone ID 253258

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1256
- Ceres seq\_id 1499964

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1257
- Ceres seq\_id 1499965
- Location of start within SEQ ID NO 1256: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9659
- gi No. 3785990
- % Identity 84.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1257: from 15 to 99

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1258
  - Ceres seq\_id 1499966
  - Location of start within SEQ ID NO 1256: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1259
  - Ceres seq\_id 1499967
  - Location of start within SEQ ID NO 1256: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9660
  - gi No. 3785990
  - % Identity 98.9
  - Alignment Length 95
  - Location of Alignment in SEQ ID NO 1259: from 1 to 92

Maximum Length Sequence corresponding to clone ID 253262

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1260
  - Ceres seq\_id 1499968
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1261
  - Ceres seq\_id 1499969
  - Location of start within SEQ ID NO 1260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9661
  - gi No. 3152605
  - % Identity 98.8
  - Alignment Length 83
  - Location of Alignment in SEQ ID NO 1261: from 4 to 84
- Alignment No. 9662
  - gi No. 4006889
  - % Identity 83.1
  - Alignment Length 83
  - Location of Alignment in SEQ ID NO 1261: from 4 to 84

Maximum Length Sequence corresponding to clone ID 253359

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1262
  - Ceres seq\_id 1499970
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1263
  - Ceres seq\_id 1499971
  - Location of start within SEQ ID NO 1262: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9663
  - Hsp90 protein
  - Location within SEQ ID NO 1263: from 36 to 110 aa.



- Alignment No. 9664
- Hsp90 protein
- Location within SEQ ID NO 1263: from 39 to 138 aa.
  
- Alignment No. 9665
- Hsp90 protein
- Location within SEQ ID NO 1263: from 131 to 181 aa.
  
- Alignment No. 9666
- 11-S plant seed storage protein
- Location within SEQ ID NO 1263: from 14 to 95 aa.
  
- Alignment No. 9667
- Troponin
- Location within SEQ ID NO 1263: from 25 to 123 aa.
  
- Alignment No. 9668
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 7 to 85 aa.
  
- Alignment No. 9669
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 7 to 88 aa.
  
- Alignment No. 9670
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 9 to 86 aa.
  
- Alignment No. 9671
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 17 to 133 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253404

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1264
- Ceres seq\_id 1499972

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1265
- Ceres seq\_id 1499973
- Location of start within SEQ ID NO 1264: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9672
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1265: from 58 to 514 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1266
- Ceres seq\_id 1499974
- Location of start within SEQ ID NO 1264: at 479 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9673
- Glycosyl hydrolase family 9

- Location within SEQ ID NO 1266: from 1 to 398 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1267
- Ceres seq\_id 1499975
- Location of start within SEQ ID NO 1264: at 533 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9674
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1267: from 1 to 380 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253420

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1268
- Ceres seq\_id 1499976

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1269
- Ceres seq\_id 1499977
- Location of start within SEQ ID NO 1268: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9675
- gi No. 3928150
- % Identity 78.6
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1269: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1270
- Ceres seq\_id 1499978
- Location of start within SEQ ID NO 1268: at 563 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1271
- Ceres seq\_id 1499979
- Location of start within SEQ ID NO 1268: at 638 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253499

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1272
- Ceres seq\_id 1499984

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1273
- Ceres seq\_id 1499985
- Location of start within SEQ ID NO 1272: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9676
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1273: from 96 to 318 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1274
- Ceres seq\_id 1499986
- Location of start within SEQ ID NO 1272: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9677
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1274: from 87 to 309 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253505

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1275
- Ceres seq\_id 1499989

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1276
- Ceres seq\_id 1499990
- Location of start within SEQ ID NO 1275: at 206 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9678
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1276: from 83 to 360 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9679
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1276: from 1 to 391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1277
- Ceres seq\_id 1499991
- Location of start within SEQ ID NO 1275: at 356 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1277: from 33 to 310 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9681
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1277: from 1 to 341

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1278
- Ceres seq\_id 1499992
- Location of start within SEQ ID NO 1275: at 422 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9682
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1278: from 11 to 288 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9683
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1278: from 1 to 319

Maximum Length Sequence corresponding to clone ID 253633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1279
- Ceres seq\_id 1499993

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1280
- Ceres seq\_id 1499994
- Location of start within SEQ ID NO 1279: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9684
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1280: from 3 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253648

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1281
- Ceres seq\_id 1499995

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1282
- Ceres seq\_id 1499996
- Location of start within SEQ ID NO 1281: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1283
- Ceres seq\_id 1499997
- Location of start within SEQ ID NO 1281: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9685
- gi No. 1209262
- % Identity 71
- Alignment Length 63

- Location of Alignment in SEQ ID NO 1283: from 5 to 66
- Alignment No. 9686
- gi No. 125408
- % Identity 92.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1283: from 1 to 66
- Alignment No. 9687
- gi No. 167146
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1283: from 5 to 66
- Alignment No. 9688
- gi No. 399298
- % Identity 100
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1283: from 1 to 66
- Alignment No. 9689
- gi No. 4493273
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9690
- gi No. 4493276
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9691
- gi No. 4494076
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9692
- gi No. 4538893
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1284
- Ceres seq\_id 1499998
- Location of start within SEQ ID NO 1281: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253653

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1285
- Ceres seq\_id 1499999

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1286
- Ceres seq\_id 1500000
- Location of start within SEQ ID NO 1285: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9693
- Plant lipid transfer protein family
- Location within SEQ ID NO 1286: from 45 to 76 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1287
- Ceres seq\_id 1500001
- Location of start within SEQ ID NO 1285: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9694
- Plant lipid transfer protein family
- Location within SEQ ID NO 1287: from 33 to 64 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1288
- Ceres seq\_id 1500002
- Location of start within SEQ ID NO 1285: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 9695
- Plant lipid transfer protein family
- Location within SEQ ID NO 1288: from 17 to 48 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253679

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1289
- Ceres seq\_id 1500003

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1290
- Ceres seq\_id 1500004
- Location of start within SEQ ID NO 1289: at 603 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9696
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1290: from 37 to 214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1291
- Ceres seq\_id 1500005
- Location of start within SEQ ID NO 1289: at 606 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9697
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1291: from 36 to 213

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1292
- Ceres seq\_id 1500006
- Location of start within SEQ ID NO 1289: at 711 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9698
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1292: from 1 to 178

Maximum Length Sequence corresponding to clone ID 253698

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1293
- Ceres seq\_id 1500007

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1294
- Ceres seq\_id 1500008
- Location of start within SEQ ID NO 1293: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9699
- Cytochrome P450
- Location within SEQ ID NO 1294: from 31 to 481 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9700
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1294: from 314 to 492
  
- Alignment No. 9701
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1294: from 1 to 494
  
- Alignment No. 9702
- gi No. 4468802
- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1294: from 1 to 492
  
- Alignment No. 9703
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1294: from 1 to 494

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1295
- Ceres seq\_id 1500009
- Location of start within SEQ ID NO 1293: at 365 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9704
- Cytochrome P450
- Location within SEQ ID NO 1295: from 1 to 366 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9705
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1295: from 199 to 377
- Alignment No. 9706
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1295: from 1 to 379
- Alignment No. 9707
- gi No. 4468802
- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1295: from 1 to 377
- Alignment No. 9708
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1295: from 1 to 379

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1296
- Ceres seq\_id 1500010
- Location of start within SEQ ID NO 1293: at 536 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9709
- Cytochrome P450
- Location within SEQ ID NO 1296: from 1 to 309 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9710
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1296: from 142 to 320
- Alignment No. 9711
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1296: from 1 to 322
- Alignment No. 9712
- gi No. 4468802



- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1296: from 1 to 320
  
- Alignment No. 9713
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1296: from 1 to 322

Maximum Length Sequence corresponding to clone ID 253770

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1297
- Ceres seq\_id 1500011

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1298
- Ceres seq\_id 1500012
- Location of start within SEQ ID NO 1297: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9714
- Inositol monophosphatase family
- Location within SEQ ID NO 1298: from 122 to 327 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9715
- gi No. 1354510
- % Identity 100
- Alignment Length 373
- Location of Alignment in SEQ ID NO 1298: from 1 to 373
  
- Alignment No. 9716
- gi No. 2736075
- % Identity 99.5
- Alignment Length 373
- Location of Alignment in SEQ ID NO 1298: from 1 to 373

Maximum Length Sequence corresponding to clone ID 253849

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1299
- Ceres seq\_id 1500017

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1300
- Ceres seq\_id 1500018
- Location of start within SEQ ID NO 1299: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9717
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1300: from 201 to 241 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9718
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1300: from 1 to 354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1301
- Ceres seq\_id 1500019
- Location of start within SEQ ID NO 1299: at 325 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9719
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1301: from 128 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9720
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1301: from 1 to 281

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1302
- Ceres seq\_id 1500020
- Location of start within SEQ ID NO 1299: at 472 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9721
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1302: from 79 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9722
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1302: from 1 to 232

Maximum Length Sequence corresponding to clone ID 254111

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1303
- Ceres seq\_id 1500025

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1304
- Ceres seq\_id 1500026
- Location of start within SEQ ID NO 1303: at 381 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9723
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1304: from 18 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1305
- Ceres seq\_id 1500027
- Location of start within SEQ ID NO 1303: at 522 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9724
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1305: from 1 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1306
- Ceres seq\_id 1500028
- Location of start within SEQ ID NO 1303: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9725
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1306: from 1 to 125

Maximum Length Sequence corresponding to clone ID 254513

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1307
- Ceres seq\_id 1500036

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1308
- Ceres seq\_id 1500037
- Location of start within SEQ ID NO 1307: at 613 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9726
- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1308: from 1 to 373

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1309
- Ceres seq\_id 1500038
- Location of start within SEQ ID NO 1307: at 718 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9727
- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1309: from 1 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1310
- Ceres seq\_id 1500039
- Location of start within SEQ ID NO 1307: at 868 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9728

- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1310: from 1 to 288

Maximum Length Sequence corresponding to clone ID 254633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1311
- Ceres seq\_id 1500040

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1312
- Ceres seq\_id 1500041
- Location of start within SEQ ID NO 1311: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9729
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1312: from 101 to 317
  
- Alignment No. 9730
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1312: from 76 to 309
  
- Alignment No. 9731
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1312: from 1 to 317

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1313
- Ceres seq\_id 1500042
- Location of start within SEQ ID NO 1311: at 242 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9732
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1313: from 53 to 269
  
- Alignment No. 9733
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1313: from 28 to 261
  
- Alignment No. 9734
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1313: from 1 to 269

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1314
  - Ceres seq\_id 1500043
  - Location of start within SEQ ID NO 1311: at 323 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9735
  - gi No. 2935529
  - % Identity 76
  - Alignment Length 217
  - Location of Alignment in SEQ ID NO 1314: from 26 to 242
  - Alignment No. 9736
  - gi No. 3687238
  - % Identity 100
  - Alignment Length 234
  - Location of Alignment in SEQ ID NO 1314: from 1 to 234
  - Alignment No. 9737
  - gi No. 4539422
  - % Identity 73.9
  - Alignment Length 319
  - Location of Alignment in SEQ ID NO 1314: from 1 to 242

Maximum Length Sequence corresponding to clone ID 254758

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1315
  - Ceres seq\_id 1500050
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1316
  - Ceres seq\_id 1500051
  - Location of start within SEQ ID NO 1315: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9738
- TBC domain
- Location within SEQ ID NO 1316: from 156 to 275 aa.
- (D) Related Amino Acid Sequences
  - Alignment No. 9739
  - gi No. 2880048
  - % Identity 96.9
  - Alignment Length 254
  - Location of Alignment in SEQ ID NO 1316: from 143 to 275

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1317
  - Ceres seq\_id 1500052
  - Location of start within SEQ ID NO 1315: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9740
- TBC domain
- Location within SEQ ID NO 1317: from 140 to 259 aa.
- (D) Related Amino Acid Sequences
  - Alignment No. 9741

- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1317: from 127 to 259

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1318
- Ceres seq\_id 1500053
- Location of start within SEQ ID NO 1315: at 408 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9742
- TBC domain
- Location within SEQ ID NO 1318: from 21 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9743
- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1318: from 8 to 140

Maximum Length Sequence corresponding to clone ID 254801

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1319
- Ceres seq\_id 1500054

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1320
- Ceres seq\_id 1500055
- Location of start within SEQ ID NO 1319: at 401 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9744
- Ubiquitin family
- Location within SEQ ID NO 1320: from 1 to 76 aa.

- Alignment No. 9745
- Ubiquitin family
- Location within SEQ ID NO 1320: from 77 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9746
- gi No. 100490
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9747
- gi No. 100490
- % Identity 100
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1320: from 10 to 146
  
- Alignment No. 9748
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9749
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9750
- gi No. 100524
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9751
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9752
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9753
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9754
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9755
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9756
- gi No. 100525
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 1 to 106
  
- Alignment No. 9757
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9758
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9759

- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9760
- gi No. 100598
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9761
- gi No. 100598
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9762
- gi No. 100599
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9763
- gi No. 100599
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9764
- gi No. 100812
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9765
- gi No. 100812
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9766
- gi No. 100934
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9767
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9768
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9769
- gi No. 100934



- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9770
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9771
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9772
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9773
- gi No. 100981
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1320: from 113 to 146
  
- Alignment No. 9774
- gi No. 100981
- % Identity 100
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 37 to 76
  
- Alignment No. 9775
- gi No. 102062
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9776
- gi No. 102062
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9777
- gi No. 102278
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9778
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9779
- gi No. 102278
- % Identity 94.5

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9780
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9781
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9782
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9783
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9784
- gi No. 102279
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9785
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9786
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9787
- gi No. 102280
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9788
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9789
- gi No. 102280
- % Identity 93.2
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9790
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9791
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9792
- gi No. 102281
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9793
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9794
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9795
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9796
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9797
- gi No. 102389
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9798
- gi No. 102389
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 9799
- gi No. 103436
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9800
- gi No. 103436
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9801
- gi No. 1044940
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9802
- gi No. 1044940
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9803
- gi No. 104829
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9804
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9805
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9806
- gi No. 1050930
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9807
- gi No. 1050930
- % Identity 95
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1320: from 1 to 100
  
- Alignment No. 9808
- gi No. 10673
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9809
- gi No. 10673
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 9810
- gi No. 1070590
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9811
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9812
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9813
- gi No. 1070591
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9814
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9815
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9816
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9817
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9818
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9819
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9820

- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9821
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9822
- gi No. 1076678
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9823
- gi No. 1076678
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 54 to 146
  
- Alignment No. 9824
- gi No. 1076708
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9825
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9826
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9827
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9828
- gi No. 1078777
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9829
- gi No. 1078777
- % Identity 88.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9830
- gi No. 1078813

- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9831
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9832
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9833
- gi No. 1083758
- % Identity 88
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 9834
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9835
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9836
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9837
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9838
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9839
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9840
- gi No. 1083758
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9841
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9842
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9843
- gi No. 1101011
- % Identity 84.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9844
- gi No. 1101011
- % Identity 87.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 68 to 146
  
- Alignment No. 9845
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9846
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9847
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9848
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9849
- gi No. 1101011
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9850
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146



- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9851
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9852
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9853
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9854
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9855
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9856
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9857
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9858
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9859
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9860
- gi No. 1101021
- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1320: from 1 to 46

- Alignment No. 9861
- gi No. 1101021
- % Identity 84.4
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1320: from 83 to 146
  
- Alignment No. 9862
- gi No. 1101021
- % Identity 86.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1320: from 7 to 122
  
- Alignment No. 9863
- gi No. 1101023
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 114 to 146
  
- Alignment No. 9864
- gi No. 1101023
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 38 to 87
  
- Alignment No. 9865
- gi No. 1107481
- % Identity 97.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 1 to 96
  
- Alignment No. 9866
- gi No. 1107481
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9867
- gi No. 1143188
- % Identity 94.5
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 77 to 149
  
- Alignment No. 9868
- gi No. 1143188
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9869
- gi No. 1143188
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9870
- gi No. 1143188
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9871
- gi No. 1167510
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9872
- gi No. 1167510
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1320: from 1 to 103
  
- Alignment No. 9873
- gi No. 1174858
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9874
- gi No. 1174858
- % Identity 76.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9875
- gi No. 1174859
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9876
- gi No. 1174859
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9877
- gi No. 1174860
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9878
- gi No. 1174860
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9879
- gi No. 1174861
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9880
- gi No. 1174861
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9881

- gi No. 1184755
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9882
- gi No. 1184755
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9883
- gi No. 1197093
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9884
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9885
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9886
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9887
- gi No. 1304128
- % Identity 96.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 1 to 79
  
- Alignment No. 9888
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9889
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9890
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9891
- gi No. 1304128

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9892
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9893
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9894
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9895
- gi No. 1304357
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9896
- gi No. 1304357
- % Identity 82.9
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9897
- gi No. 1321735
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9898
- gi No. 1321735
- % Identity 95.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1320: from 1 to 139
  
- Alignment No. 9899
- gi No. 1326021
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146
  
- Alignment No. 9900
- gi No. 1326021
- % Identity 97
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 44 to 76
  
- Alignment No. 9901
- gi No. 1326022
- % Identity 96.1

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9902
- gi No. 1326022
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
  
- Alignment No. 9903
- gi No. 1326022
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9904
- gi No. 1332579
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9905
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9906
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9907
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9908
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9909
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9910
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9911
- gi No. 1332579
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9912
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9913
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9914
- gi No. 1351348
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9915
- gi No. 1351348
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9916
- gi No. 1351349
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9917
- gi No. 1351349
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9918
- gi No. 1353755
- % Identity 95.2
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 1 to 83
- Alignment No. 9919
- gi No. 1353755
- % Identity 95.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1320: from 42 to 146
- Alignment No. 9920
- gi No. 1353757
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1320: from 1 to 46
- Alignment No. 9921
- gi No. 1353757
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 78 to 146

- Alignment No. 9922
- gi No. 1353757
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1320: from 2 to 122
  
- Alignment No. 9923
- gi No. 1362008
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9924
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9925
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9926
- gi No. 1362008
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9927
- gi No. 1362008
- % Identity 92.5
- Alignment Length 159
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9928
- gi No. 1362009
- % Identity 79.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 1320: from 1 to 148
  
- Alignment No. 9929
- gi No. 1362010
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9930
- gi No. 1362010
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9931
- gi No. 1362010
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146



- Alignment No. 9932
- gi No. 1362010
- % Identity 92.5
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9933
- gi No. 1362012
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9934
- gi No. 1362012
- % Identity 76.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1320: from 1 to 147
  
- Alignment No. 9935
- gi No. 1362012
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1320: from 1 to 145
  
- Alignment No. 9936
- gi No. 1362012
- % Identity 71.1
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9937
- gi No. 136665
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9938
- gi No. 136665
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9939
- gi No. 136666
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9940
- gi No. 136666
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9941
- gi No. 136667
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9942

- gi No. 136667
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9943
- gi No. 136668
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9944
- gi No. 136668
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9945
- gi No. 136669
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9946
- gi No. 136669
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9947
- gi No. 136670
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9948
- gi No. 136670
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9949
- gi No. 136671
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9950
- gi No. 136671
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9951
- gi No. 136672
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9952
- gi No. 136672

- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9953
- gi No. 136673
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9954
- gi No. 136673
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9955
- gi No. 136674
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9956
- gi No. 136674
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9957
- gi No. 136675
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9958
- gi No. 136675
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9959
- gi No. 136676
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9960
- gi No. 136676
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9961
- gi No. 136677
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9962
- gi No. 136677
- % Identity 97.4

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9963
- gi No. 136678
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9964
- gi No. 136678
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9965
- gi No. 1421797
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9966
- gi No. 1421797
- % Identity 96.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 1 to 79
  
- Alignment No. 9967
- gi No. 1480012
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1320: from 93 to 146
  
- Alignment No. 9968
- gi No. 1480012
- % Identity 95.1
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1320: from 17 to 77
  
- Alignment No. 9969
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1320: from 1 to 37
  
- Alignment No. 9970
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1320: from 77 to 113
  
- Alignment No. 9971
- gi No. 158759
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9972
- gi No. 158759
- % Identity 94.7
- Alignment Length 76

- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9973
- gi No. 158763
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9974
- gi No. 158763
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9975
- gi No. 158765
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9976
- gi No. 158765
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9977
- gi No. 158767
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9978
- gi No. 158767
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9979
- gi No. 158769
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9980
- gi No. 158769
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9981
- gi No. 158771
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9982
- gi No. 158771
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9983
- gi No. 161281
- % Identity 94.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 77 to 147
  
- Alignment No. 9984
- gi No. 161281
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9985
- gi No. 163575
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9986
- gi No. 163575
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146
  
- Alignment No. 9987
- gi No. 163575
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9988
- gi No. 166336
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9989
- gi No. 166336
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9990
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9991
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9992
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9993
- gi No. 166336
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9994
- gi No. 1666175
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9995
- gi No. 1666175
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9996
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1320: from 1 to 41
  
- Alignment No. 9997
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1320: from 77 to 117
  
- Alignment No. 9998
- gi No. 167935
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9999
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10000
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10001
- gi No. 167935
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10002
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10003

- gi No. 167941
- % Identity 92.8
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 78 to 146
  
- Alignment No. 10004
- gi No. 167941
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 2 to 76
  
- Alignment No. 10005
- gi No. 167945
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10006
- gi No. 167945
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10007
- gi No. 167945
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10008
- gi No. 167947
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10009
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10010
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10011
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10012
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10013
- gi No. 167947



- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10014
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10015
- gi No. 167949
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10016
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10017
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10018
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10019
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10020
- gi No. 1684855
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10021
- gi No. 1684855
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1320: from 16 to 146
  
- Alignment No. 10022
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10023
- gi No. 1684855
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10024
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10025
- gi No. 1684857
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10026
- gi No. 1684857
- % Identity 100
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1320: from 15 to 146
  
- Alignment No. 10027
- gi No. 1684857
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10028
- gi No. 170352
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10029
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10030
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10031
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10032
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10033
- gi No. 170352
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10034
- gi No. 170354
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10035
- gi No. 170354
- % Identity 100
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1320: from 5 to 146
- Alignment No. 10036
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10037
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10038
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10039
- gi No. 1762374
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10040
- gi No. 1762374
- % Identity 95.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 1 to 71
- Alignment No. 10041
- gi No. 1762935
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10042
- gi No. 1762935
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10043
- gi No. 1763015
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10044
- gi No. 1763015
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10045
- gi No. 1771780
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10046
- gi No. 1771780
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10047
- gi No. 1778712
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10048
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10049
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10050
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10051
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10052
- gi No. 1800281
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10053
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10054
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10055
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10056
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10057
- gi No. 1805696
- % Identity 95.2
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1320: from 84 to 146
  
- Alignment No. 10058
- gi No. 1805696
- % Identity 95.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 1 to 65
  
- Alignment No. 10059
- gi No. 1805696
- % Identity 95.5
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1320: from 8 to 141
  
- Alignment No. 10060
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 1 to 38
  
- Alignment No. 10061
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 77 to 114
  
- Alignment No. 10062
- gi No. 1841849
- % Identity 100
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1320: from 1 to 16
  
- Alignment No. 10063
- gi No. 1841849
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146
  
- Alignment No. 10064

- gi No. 1841849
- % Identity 100
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1320: from 36 to 92
  
- Alignment No. 10065
- gi No. 208558
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10066
- gi No. 208558
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10067
- gi No. 208560
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10068
- gi No. 208560
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10069
- gi No. 208562
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10070
- gi No. 208562
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10071
- gi No. 208564
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10072
- gi No. 208564
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10073
- gi No. 208566
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10074
- gi No. 208566

- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10075
- gi No. 208568
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10076
- gi No. 208568
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10077
- gi No. 208891
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 72 to 146
  
- Alignment No. 10078
- gi No. 208891
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 1 to 98
  
- Alignment No. 10079
- gi No. 209603
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10080
- gi No. 209603
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10081
- gi No. 2118958
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10082
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10083
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10084
- gi No. 2118958
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10085
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10086
- gi No. 2118959
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 1 to 112
  
- Alignment No. 10087
- gi No. 2118959
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10088
- gi No. 2118959
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10089
- gi No. 2118960
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10090
- gi No. 2118960
- % Identity 96.5
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 62 to 146
  
- Alignment No. 10091
- gi No. 2118960
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10092
- gi No. 2118961
- % Identity 94.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 73 to 146
  
- Alignment No. 10093
- gi No. 2118961
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10094
- gi No. 2118961
- % Identity 95.2
- Alignment Length 146



- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10095
- gi No. 2118962
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 73 to 146
- Alignment No. 10096
- gi No. 2118962
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10097
- gi No. 2118962
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10098
- gi No. 2118963
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
- Alignment No. 10099
- gi No. 2118963
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146
- Alignment No. 10100
- gi No. 2118964
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10101
- gi No. 2118964
- % Identity 96.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1320: from 37 to 146
- Alignment No. 10102
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10103
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10104
- gi No. 2118965
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10105
- gi No. 2118965
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146
  
- Alignment No. 10106
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10107
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10108
- gi No. 2129452
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10109
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10110
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10111
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10112
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10113
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10114
- gi No. 2133278
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10115
- gi No. 2133278
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10116
- gi No. 2133549
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146
  
- Alignment No. 10117
- gi No. 2133549
- % Identity 95.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
  
- Alignment No. 10118
- gi No. 2133549
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 97 to 146
  
- Alignment No. 10119
- gi No. 2133549
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 21 to 76
  
- Alignment No. 10120
- gi No. 2133549
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 44 to 124
  
- Alignment No. 10121
- gi No. 2144011
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10122
- gi No. 2144011
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10123
- gi No. 2144275
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10124
- gi No. 2144275
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10125

- gi No. 2144734
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10126
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10127
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10128
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10129
- gi No. 2149467
- % Identity 87.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 68 to 146
  
- Alignment No. 10130
- gi No. 2149467
- % Identity 83.3
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10131
- gi No. 2209091
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10132
- gi No. 2209091
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10133
- gi No. 223061
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10134
- gi No. 223061
- % Identity 94.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
  
- Alignment No. 10135
- gi No. 224321

- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10136
- gi No. 224321
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
  
- Alignment No. 10137
- gi No. 224321
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10138
- gi No. 225317
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10139
- gi No. 225317
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153
  
- Alignment No. 10140
- gi No. 225319
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10141
- gi No. 225319
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153
  
- Alignment No. 10142
- gi No. 225320
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10143
- gi No. 225320
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153
  
- Alignment No. 10144
- gi No. 2281952
- % Identity 95.2
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 8 to 69
  
- Alignment No. 10145
- gi No. 2281952
- % Identity 95.2

- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 84 to 145
  
- Alignment No. 10146
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 8 to 69
  
- Alignment No. 10147
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 84 to 145
  
- Alignment No. 10148
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1320: from 8 to 52
  
- Alignment No. 10149
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1320: from 84 to 128
  
- Alignment No. 10150
- gi No. 2281959
- % Identity 90.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1320: from 83 to 146
  
- Alignment No. 10151
- gi No. 2281959
- % Identity 90.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 7 to 71
  
- Alignment No. 10152
- gi No. 2330875
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10153
- gi No. 2330875
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10154
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1320: from 6 to 63
  
- Alignment No. 10155
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58

- Location of Alignment in SEQ ID NO 1320: from 82 to 139
- Alignment No. 10156
- gi No. 2408009
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10157
- gi No. 2408009
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10158
- gi No. 2437825
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10159
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10160
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10161
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10162
- gi No. 247308
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10163
- gi No. 247308
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10164
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 1 to 20
- Alignment No. 10165
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 77 to 96

- Alignment No. 10166
- gi No. 2558539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10167
- gi No. 2558539
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10168
- gi No. 2627129
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10169
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10170
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10171
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10172
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10173
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10174
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10175
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146



- Alignment No. 10176
- gi No. 2627131
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 10177
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10178
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10179
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10180
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10181
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10182
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10183
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10184
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10185
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10186

- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10187
- gi No. 2627133
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 10188
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10189
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10190
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10191
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10192
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10193
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10194
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10195
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10196
- gi No. 2627133

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10197
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10198
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10199
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10200
- gi No. 2641213
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10201
- gi No. 2641213
- % Identity 98.6
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1320: from 1 to 139
  
- Alignment No. 10202
- gi No. 2654141
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10203
- gi No. 2654141
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10204
- gi No. 2654141
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10205
- gi No. 2654141
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10206
- gi No. 2654141
- % Identity 89.7

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10207
- gi No. 2707837
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10208
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10209
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10210
- gi No. 2707837
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10211
- gi No. 2739333
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10212
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10213
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10214
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10215
- gi No. 2760345
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10216
- gi No. 2760345
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10217
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10218
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10219
- gi No. 2760347
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10220
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10221
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10222
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10223
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10224
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10225
- gi No. 2760349
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10226
- gi No. 2760349
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10227
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10228
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10229
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10230
- gi No. 279635
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10231
- gi No. 279635
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10232
- gi No. 279636
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10233
- gi No. 279636
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10234
- gi No. 280386
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10235
- gi No. 280386
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10236
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 1 to 20

- Alignment No. 10237
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 77 to 96
  
- Alignment No. 10238
- gi No. 283496
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10239
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10240
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10241
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10242
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10243
- gi No. 2894304
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10244
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10245
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10246
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10247

- gi No. 2894306
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10248
- gi No. 2894306
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10249
- gi No. 2894308
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10250
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10251
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10252
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10253
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10254
- gi No. 2995277
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1320: from 124 to 146
  
- Alignment No. 10255
- gi No. 2995277
- % Identity 96.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1320: from 48 to 77
  
- Alignment No. 10256
- gi No. 2995949
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10257
- gi No. 2995949



- % Identity 100
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1320: from 43 to 146
  
- Alignment No. 10258
- gi No. 3047314
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10259
- gi No. 3047314
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10260
- gi No. 3047316
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10261
- gi No. 3047316
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10262
- gi No. 3047318
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10263
- gi No. 3047318
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10264
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10265
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10266
- gi No. 3047318
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10267
- gi No. 3091264
- % Identity 98.7

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10268
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10269
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10270
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10271
- gi No. 3126967
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10272
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10273
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10274
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10275
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10276
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10277
- gi No. 3152950
- % Identity 97.1
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10278
- gi No. 3152950
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10279
- gi No. 3158372
- % Identity 100
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 49 to 146
- Alignment No. 10280
- gi No. 3158372
- % Identity 99.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1320: from 1 to 109
- Alignment No. 10281
- gi No. 320608
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10282
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10283
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10284
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10285
- gi No. 322750
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10286
- gi No. 322750
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10287
- gi No. 323071
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10288
- gi No. 323071
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10289
- gi No. 323157
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10290
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10291
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10292
- gi No. 323157
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10293
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10294
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10295
- gi No. 323208
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10296
- gi No. 323208
- % Identity 82.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1320: from 4 to 146
  
- Alignment No. 10297
- gi No. 323230
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10298
- gi No. 323230
- % Identity 83.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10299
- gi No. 3265058
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10300
- gi No. 3265058
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10301
- gi No. 3319208
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10302
- gi No. 3319208
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10303
- gi No. 3335355
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1320: from 132 to 146
  
- Alignment No. 10304
- gi No. 3335355
- % Identity 100
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1320: from 56 to 76
  
- Alignment No. 10305
- gi No. 3335355
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 1 to 129
  
- Alignment No. 10306
- gi No. 3335355
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10307
- gi No. 3335355
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10308

- gi No. 340062
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1320: from 81 to 146
  
- Alignment No. 10309
- gi No. 340062
- % Identity 95.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1320: from 5 to 76
  
- Alignment No. 10310
- gi No. 3452083
- % Identity 93.1
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1320: from 1 to 29
  
- Alignment No. 10311
- gi No. 3452083
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 99 to 146
  
- Alignment No. 10312
- gi No. 3452083
- % Identity 96.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 23 to 105
  
- Alignment No. 10313
- gi No. 348148
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146
  
- Alignment No. 10314
- gi No. 348148
- % Identity 95.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
  
- Alignment No. 10315
- gi No. 348148
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 44 to 124
  
- Alignment No. 10316
- gi No. 348149
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 97 to 146
  
- Alignment No. 10317
- gi No. 348149
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 21 to 76
  
- Alignment No. 10318
- gi No. 3603456

- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10319
- gi No. 3603456
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 41 to 146
  
- Alignment No. 10320
- gi No. 3603456
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10321
- gi No. 3603456
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10322
- gi No. 3687425
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10323
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10324
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10325
- gi No. 3738185
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10326
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10327
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10328
- gi No. 3738185
- % Identity 97.3

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10329
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10330
- gi No. 3776536
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10331
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10332
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10333
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10334
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10335
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10336
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10337
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10338
- gi No. 3789940
- % Identity 100
- Alignment Length 76



- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10339
- gi No. 3789940
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10340
- gi No. 3789940
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10341
- gi No. 3789940
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10342
- gi No. 3789942
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10343
- gi No. 3789942
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10344
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10345
- gi No. 3789942
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10346
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10347
- gi No. 3822277
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10348
- gi No. 3822277
- % Identity 77.6
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10349
- gi No. 385076
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10350
- gi No. 385076
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10351
- gi No. 3882081
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10352
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10353
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10354
- gi No. 3885463
- % Identity 94
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1320: from 80 to 146
  
- Alignment No. 10355
- gi No. 3885463
- % Identity 86.6
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1320: from 4 to 85
  
- Alignment No. 10356
- gi No. 3892189
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10357
- gi No. 3892189
- % Identity 84.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10358
- gi No. 402242
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10359
- gi No. 402242
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10360
- gi No. 4049712
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10361
- gi No. 4049712
- % Identity 84.6
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
  
- Alignment No. 10362
- gi No. 4102845
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 82 to 146
  
- Alignment No. 10363
- gi No. 4102845
- % Identity 87.3
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 6 to 76
  
- Alignment No. 10364
- gi No. 4105408
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10365
- gi No. 4105408
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1320: from 10 to 146
  
- Alignment No. 10366
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10367
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10368
- gi No. 4115337
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10369

- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10370
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10371
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10372
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10373
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10374
- gi No. 4150898
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10375
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10376
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10377
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10378
- gi No. 4150912
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10379
- gi No. 4150912

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10380
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10381
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10382
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10383
- gi No. 4150914
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10384
- gi No. 4150914
- % Identity 95.7
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1320: from 7 to 146
  
- Alignment No. 10385
- gi No. 4151082
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10386
- gi No. 4151082
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10387
- gi No. 418854
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10388
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10389
- gi No. 418854
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10390
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10391
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10392
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10393
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1320: from 1 to 19
  
- Alignment No. 10394
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1320: from 77 to 95
  
- Alignment No. 10395
- gi No. 421867
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10396
- gi No. 421867
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10397
- gi No. 421929
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10398
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10399
- gi No. 421929
- % Identity 99.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10400
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10401
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10402
- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10403
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10404
- gi No. 422248
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10405
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10406
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10407
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10408
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10409
- gi No. 422269
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10410
- gi No. 422269
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10411
- gi No. 422270
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10412
- gi No. 422270
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10413
- gi No. 422271
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10414
- gi No. 422271
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10415
- gi No. 433970
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10416
- gi No. 433970
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146
  
- Alignment No. 10417
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10418
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10419
- gi No. 433970
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146



- Alignment No. 10420
- gi No. 433970
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10421
- gi No. 444791
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10422
- gi No. 444791
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10423
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10424
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10425
- gi No. 4506713
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10426
- gi No. 4506713
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10427
- gi No. 4507761
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10428
- gi No. 4507761
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10429
- gi No. 4510359
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146
  
- Alignment No. 10430

- gi No. 4510359
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1320: from 36 to 77
  
- Alignment No. 10431
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 1 to 25
  
- Alignment No. 10432
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 77 to 101
  
- Alignment No. 10433
- gi No. 4586594
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10434
- gi No. 4586594
- % Identity 100
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 10435
- gi No. 4587232
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10436
- gi No. 4587232
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10437
- gi No. 4587234
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10438
- gi No. 4587234
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10439
- gi No. 4587236
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10440
- gi No. 4587236

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10441
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10442
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10443
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10444
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10445
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10446
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10447
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10448
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10449
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10450
- gi No. 4587236
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10451
- gi No. 4587534
- % Identity 75.3
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 1 to 73
  
- Alignment No. 10452
- gi No. 4589760
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10453
- gi No. 4589760
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10454
- gi No. 463363
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10455
- gi No. 463363
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10456
- gi No. 463365
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10457
- gi No. 463365
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10458
- gi No. 463367
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10459
- gi No. 463367
- % Identity 89.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10460
- gi No. 463369
- % Identity 91.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10461
- gi No. 463369
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10462
- gi No. 463371
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10463
- gi No. 463371
- % Identity 88.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10464
- gi No. 463373
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10465
- gi No. 463373
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10466
- gi No. 463375
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10467
- gi No. 463375
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10468
- gi No. 464989
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10469
- gi No. 464989
- % Identity 80.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10470
- gi No. 464990
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10471
- gi No. 464990
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10472
- gi No. 468272
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10473
- gi No. 468272
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10474
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1320: from 1 to 47
  
- Alignment No. 10475
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1320: from 77 to 123
  
- Alignment No. 10476
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 3 to 27
  
- Alignment No. 10477
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 79 to 103
  
- Alignment No. 10478
- gi No. 477630
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10479
- gi No. 477630
- % Identity 94.4
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1320: from 21 to 146
  
- Alignment No. 10480
- gi No. 477815
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10481
- gi No. 477815
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10482
- gi No. 478811
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10483
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10484
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10485
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10486
- gi No. 4809266
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10487
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10488
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10489
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10490
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10491

- gi No. 481477
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10492
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10493
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10494
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10495
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10496
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10497
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10498
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10499
- gi No. 485518
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10500
- gi No. 485518
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10501
- gi No. 49586



- % Identity 95.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 1 to 71
  
- Alignment No. 10502
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10503
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10504
- gi No. 510473
- % Identity 85.4
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1320: from 1 to 89
  
- Alignment No. 10505
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10506
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10507
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10508
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10509
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10510
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10511
- gi No. 510473
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10512
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10513
- gi No. 510476
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10514
- gi No. 510476
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10515
- gi No. 5107695
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10516
- gi No. 5107695
- % Identity 86.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10517
- gi No. 539404
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10518
- gi No. 539404
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10519
- gi No. 539935
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10520
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10521
- gi No. 539935
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10522
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10523
- gi No. 541546
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10524
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10525
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10526
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10527
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10528
- gi No. 541953
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10529
- gi No. 541953
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10530
- gi No. 541954
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10531
- gi No. 541954
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10532
- gi No. 542395
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 99 to 146
  
- Alignment No. 10533
- gi No. 542395
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1320: from 23 to 76
  
- Alignment No. 10534
- gi No. 5441519
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10535
- gi No. 5441519
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10536
- gi No. 552237
- % Identity 97.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146
  
- Alignment No. 10537
- gi No. 552237
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1320: from 1 to 36
  
- Alignment No. 10538
- gi No. 552237
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 36 to 112
  
- Alignment No. 10539
- gi No. 5523967
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10540
- gi No. 5523967
- % Identity 96.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1320: from 60 to 146
  
- Alignment No. 10541
- gi No. 5523969
- % Identity 95.1
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1320: from 65 to 146

- Alignment No. 10542
- gi No. 5523969
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10543
- gi No. 5523969
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10544
- gi No. 5523971
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10545
- gi No. 5523971
- % Identity 95.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1320: from 58 to 146
  
- Alignment No. 10546
- gi No. 5523973
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10547
- gi No. 5523973
- % Identity 87.6
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1320: from 26 to 146
  
- Alignment No. 10548
- gi No. 5523975
- % Identity 95.9
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 74 to 146
  
- Alignment No. 10549
- gi No. 5523975
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10550
- gi No. 5523977
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10551
- gi No. 5523977
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1320: from 33 to 146
  
- Alignment No. 10552

- gi No. 5523979
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10553
- gi No. 5523979
- % Identity 72.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
  
- Alignment No. 10554
- gi No. 5523979
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10555
- gi No. 5523981
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10556
- gi No. 5523981
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1320: from 50 to 146
  
- Alignment No. 10557
- gi No. 5523983
- % Identity 94.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1320: from 79 to 146
  
- Alignment No. 10558
- gi No. 5523983
- % Identity 86.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 3 to 85
  
- Alignment No. 10559
- gi No. 5523985
- % Identity 87.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10560
- gi No. 5523985
- % Identity 94.9
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1320: from 29 to 146
  
- Alignment No. 10561
- gi No. 5523987
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10562
- gi No. 5523987

- % Identity 96.6
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1320: from 29 to 146
  
- Alignment No. 10563
- gi No. 5531273
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10564
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10565
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10566
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10567
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10568
- gi No. 5531278
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10569
- gi No. 5531278
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10570
- gi No. 5531281
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10571
- gi No. 5531281
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10572
- gi No. 554564
- % Identity 93.2

- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 74 to 146
  
- Alignment No. 10573
- gi No. 554564
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10574
- gi No. 567767
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10575
- gi No. 567767
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1320: from 47 to 146
  
- Alignment No. 10576
- gi No. 567767
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10577
- gi No. 571519
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10578
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10579
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10580
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10581
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10582
- gi No. 571519
- % Identity 95.9
- Alignment Length 146



- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10583
- gi No. 576773
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10584
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10585
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10586
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10587
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10588
- gi No. 576775
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10589
- gi No. 576775
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10590
- gi No. 578545
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
- Alignment No. 10591
- gi No. 578545
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10592
- gi No. 578545
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10593
- gi No. 578545
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10594
- gi No. 578545
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10595
- gi No. 578546
- % Identity 85.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
  
- Alignment No. 10596
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10597
- gi No. 578546
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10598
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10599
- gi No. 578546
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10600
- gi No. 578549
- % Identity 81.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
  
- Alignment No. 10601
- gi No. 578549
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10602
- gi No. 578549
- % Identity 84.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10603
- gi No. 578549
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10604
- gi No. 578551
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
  
- Alignment No. 10605
- gi No. 578551
- % Identity 86.8
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1320: from 3 to 146
  
- Alignment No. 10606
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10607
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10608
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10609
- gi No. 600539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10610
- gi No. 600539
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10611
- gi No. 602076
- % Identity 100
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1320: from 1 to 113
  
- Alignment No. 10612
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10613

- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10614
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10615
- gi No. 625174
- % Identity 86.7
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 1 to 89
  
- Alignment No. 10616
- gi No. 625174
- % Identity 95.3
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 18 to 146
  
- Alignment No. 10617
- gi No. 625174
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10618
- gi No. 625509
- % Identity 100
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 57 to 146
  
- Alignment No. 10619
- gi No. 625509
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 1 to 129
  
- Alignment No. 10620
- gi No. 625509
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10621
- gi No. 625509
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10622
- gi No. 630455
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10623
- gi No. 630455

- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10624
- gi No. 630479
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10625
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10626
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10627
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10628
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10629
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10630
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10631
- gi No. 70637
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10632
- gi No. 70637
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 1 to 74
  
- Alignment No. 10633
- gi No. 70639
- % Identity 97.4

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10634
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10635
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10636
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10637
- gi No. 70640
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10638
- gi No. 70640
- % Identity 97.4
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
  
- Alignment No. 10639
- gi No. 70642
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10640
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10641
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10642
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10643
- gi No. 70642
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10644
- gi No. 70643
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10645
- gi No. 70643
- % Identity 100
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146
- Alignment No. 10646
- gi No. 70644
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10647
- gi No. 70644
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1320: from 48 to 146
- Alignment No. 10648
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10649
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10650
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10651
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10652
- gi No. 70645
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10653
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10654
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10655
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10656
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10657
- gi No. 70646
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10658
- gi No. 70646
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10659
- gi No. 70647
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10660
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10661
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10662
- gi No. 70648
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10663
- gi No. 70648
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77



- Alignment No. 10664
- gi No. 70650
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10665
- gi No. 70650
- % Identity 76.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10666
- gi No. 70653
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10667
- gi No. 70653
- % Identity 92.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
  
- Alignment No. 10668
- gi No. 70654
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10669
- gi No. 70654
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10670
- gi No. 70657
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10671
- gi No. 70657
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10672
- gi No. 70658
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10673
- gi No. 70658
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10674

- gi No. 70659
- % Identity 96.9
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 82 to 146
  
- Alignment No. 10675
- gi No. 70659
- % Identity 97.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 6 to 76
  
- Alignment No. 10676
- gi No. 70660
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10677
- gi No. 70660
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10678
- gi No. 726391
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10679
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10680
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10681
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10682
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10683
- gi No. 726391
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10684
- gi No. 726391

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10685
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10686
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10687
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10688
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10689
- gi No. 82040
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146
  
- Alignment No. 10690
- gi No. 82040
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 1 to 112
  
- Alignment No. 10691
- gi No. 82040
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10692
- gi No. 82040
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10693
- gi No. 82284
- % Identity 100
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 1 to 56
  
- Alignment No. 10694
- gi No. 82284
- % Identity 100

- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 77 to 132
  
- Alignment No. 10695
- gi No. 82286
- % Identity 100
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1320: from 133 to 146
  
- Alignment No. 10696
- gi No. 82286
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 57 to 76
  
- Alignment No. 10697
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
  
- Alignment No. 10698
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 77 to 124
  
- Alignment No. 10699
- gi No. 82288
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1320: from 113 to 146
  
- Alignment No. 10700
- gi No. 82288
- % Identity 100
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 37 to 76
  
- Alignment No. 10701
- gi No. 82426
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10702
- gi No. 82426
- % Identity 100
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 59 to 146
  
- Alignment No. 10703
- gi No. 82426
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10704
- gi No. 82512
- % Identity 98.7
- Alignment Length 77

- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10705
- gi No. 82512
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 41 to 146
- Alignment No. 10706
- gi No. 82512
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10707
- gi No. 825728
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1320: from 116 to 146
- Alignment No. 10708
- gi No. 825728
- % Identity 94.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 40 to 77
- Alignment No. 10709
- gi No. 82733
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10710
- gi No. 82733
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10711
- gi No. 82734
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10712
- gi No. 82734
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 35 to 146
- Alignment No. 10713
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10714
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10715
- gi No. 829173
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1320: from 89 to 146
  
- Alignment No. 10716
- gi No. 829173
- % Identity 90.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1320: from 13 to 78
  
- Alignment No. 10717
- gi No. 83594
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10718
- gi No. 83594
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10719
- gi No. 83596
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10720
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10721
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10722
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10723
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10724
- gi No. 84151
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10725
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10726
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10727
- gi No. 84152
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10728
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10729
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10730
- gi No. 84152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10731
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10732
- gi No. 84336
- % Identity 94.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1320: from 95 to 146
  
- Alignment No. 10733
- gi No. 84336
- % Identity 93.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1320: from 19 to 78
  
- Alignment No. 10734
- gi No. 84337
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10735

- gi No. 84337
- % Identity 93.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1320: from 1 to 95
  
- Alignment No. 10736
- gi No. 84478
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10737
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10738
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10739
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10740
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10741
- gi No. 84478
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10742
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10743
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10744
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10745
- gi No. 84478



- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10746
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10747
- gi No. 84834
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10748
- gi No. 84834
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10749
- gi No. 84834
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1320: from 1 to 92
  
- Alignment No. 10750
- gi No. 84834
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1320: from 54 to 146
  
- Alignment No. 10751
- gi No. 85106
- % Identity 94.9
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
  
- Alignment No. 10752
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10753
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10754
- gi No. 86473
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1320: from 121 to 146
  
- Alignment No. 10755
- gi No. 86473
- % Identity 93.8

- Alignment Length 32
- Location of Alignment in SEQ ID NO 1320: from 45 to 76
  
- Alignment No. 10756
- gi No. 86474
- % Identity 94.4
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1320: from 60 to 77
  
- Alignment No. 10757
- gi No. 870794
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10758
- gi No. 870794
- % Identity 75.5
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1320: from 1 to 147
  
- Alignment No. 10759
- gi No. 870794
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1320: from 1 to 145
  
- Alignment No. 10760
- gi No. 870794
- % Identity 70.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10761
- gi No. 89311
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10762
- gi No. 89311
- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 51 to 146
  
- Alignment No. 10763
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10764
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10765
- gi No. 899115
- % Identity 100
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10766
- gi No. 899115
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1320: from 1 to 99
- Alignment No. 10767
- gi No. 899608
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10768
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10769
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10770
- gi No. 899608
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10771
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10772
- gi No. 902525
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10773
- gi No. 902525
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10774
- gi No. 902584
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10775
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10776
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10777
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10778
- gi No. 902584
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10779
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10780
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10781
- gi No. 902586
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10782
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10783
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10784
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10785
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10786
- gi No. 91870
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 72 to 146
  
- Alignment No. 10787
- gi No. 91870
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 1 to 98
  
- Alignment No. 10788
- gi No. 91871
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10789
- gi No. 91871
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10790
- gi No. 9295
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1320: from 84 to 146
  
- Alignment No. 10791
- gi No. 9295
- % Identity 87
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 8 to 76
  
- Alignment No. 10792
- gi No. 940395
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 10793
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10794
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10795
- gi No. 940395
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10796

- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10797
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10798
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10799
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10800
- gi No. 967985
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10801
- gi No. 967985
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10802
- gi No. 99469
- % Identity 100
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 114 to 146
  
- Alignment No. 10803
- gi No. 99469
- % Identity 100
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1320: from 38 to 79
  
- Alignment No. 10804
- gi No. 99771
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10805
- gi No. 99771
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10806
- gi No. 99772

- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10807
- gi No. 99772
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10808
- gi No. 99975
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10809
- gi No. 99975
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1321
- Ceres seq\_id 1500056
- Location of start within SEQ ID NO 1319: at 629 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 10810
- Ubiquitin family
- Location within SEQ ID NO 1321: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 10811
- gi No. 100490
- % Identity 100
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10812
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10813
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10814
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10815
- gi No. 100524
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10816
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10817
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10818
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10819
- gi No. 100525
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 30
- Alignment No. 10820
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10821
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10822
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10823
- gi No. 100598
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10824
- gi No. 100599
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10825
- gi No. 100812
- % Identity 100
- Alignment Length 70



- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10826
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10827
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10828
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10829
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10830
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10831
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10832
- gi No. 100981
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1321: from 37 to 70
- Alignment No. 10833
- gi No. 102062
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10834
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10835
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10836
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10837
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10838
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10839
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10840
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10841
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10842
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10843
- gi No. 102280
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10844
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10845
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10846
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10847
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10848
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10849
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10850
- gi No. 102389
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10851
- gi No. 102389
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 10852
- gi No. 103436
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10853
- gi No. 1044940
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10854
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10855
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10856

- gi No. 1050930
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10857
- gi No. 1050930
- % Identity 95
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1321: from 1 to 24
  
- Alignment No. 10858
- gi No. 10673
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10859
- gi No. 10673
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 10860
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10861
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10862
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10863
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10864
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10865
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10866
- gi No. 1070591

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10867
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10868
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10869
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10870
- gi No. 1076678
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10871
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10872
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10873
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10874
- gi No. 1078777
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10875
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10876
- gi No. 1078813
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10877
- gi No. 1083758
- % Identity 88
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
  
- Alignment No. 10878
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10879
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10880
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10881
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10882
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10883
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10884
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10885
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10886
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10887
- gi No. 1101011
- % Identity 87.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10888
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10889
- gi No. 1101011
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10890
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10891
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10892
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10893
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10894
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10895
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10896
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10897
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46
  
- Alignment No. 10898
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46
  
- Alignment No. 10899
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46
  
- Alignment No. 10900
- gi No. 1101021
- % Identity 84.4
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1321: from 7 to 70
  
- Alignment No. 10901
- gi No. 1101021
- % Identity 86.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1321: from 1 to 46
  
- Alignment No. 10902
- gi No. 1101023
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1321: from 38 to 70
  
- Alignment No. 10903
- gi No. 1101023
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 10904
- gi No. 1107481
- % Identity 97.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 20
  
- Alignment No. 10905
- gi No. 1107481
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10906
- gi No. 1143188
- % Identity 94.5
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 73



- Alignment No. 10907
- gi No. 1143188
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10908
- gi No. 1143188
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10909
- gi No. 1167510
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10910
- gi No. 1167510
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1321: from 1 to 27
  
- Alignment No. 10911
- gi No. 1174858
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10912
- gi No. 1174859
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10913
- gi No. 1174860
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10914
- gi No. 1174861
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10915
- gi No. 1184755
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10916
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10917

- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10918
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10919
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10920
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10921
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10922
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10923
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10924
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10925
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10926
- gi No. 1304357
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10927
- gi No. 1321735

- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10928
- gi No. 1321735
- % Identity 95.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1321: from 1 to 63
  
- Alignment No. 10929
- gi No. 1326021
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70
  
- Alignment No. 10930
- gi No. 1326022
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10931
- gi No. 1326022
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10932
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10933
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10934
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10935
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10936
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10937
- gi No. 1332579
- % Identity 98.6

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10938
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10939
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10940
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10941
- gi No. 1351348
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10942
- gi No. 1351349
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10943
- gi No. 1353755
- % Identity 95.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10944
- gi No. 1353757
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1321: from 2 to 70
  
- Alignment No. 10945
- gi No. 1353757
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1321: from 1 to 46
  
- Alignment No. 10946
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10947
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10948
- gi No. 1362008
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10949
- gi No. 1362008
- % Identity 92.5
- Alignment Length 159
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10950
- gi No. 1362009
- % Identity 79.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 1321: from 1 to 72
- Alignment No. 10951
- gi No. 1362010
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10952
- gi No. 1362010
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10953
- gi No. 1362010
- % Identity 92.5
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10954
- gi No. 1362012
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10955
- gi No. 1362012
- % Identity 76.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1321: from 1 to 71
- Alignment No. 10956
- gi No. 1362012
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1321: from 1 to 69
- Alignment No. 10957
- gi No. 1362012
- % Identity 71.1
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10958
- gi No. 136665
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10959
- gi No. 136666
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10960
- gi No. 136667
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10961
- gi No. 136668
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10962
- gi No. 136669
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10963
- gi No. 136670
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10964
- gi No. 136671
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10965
- gi No. 136672
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10966
- gi No. 136673
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10967
- gi No. 136674
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10968
- gi No. 136675
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10969
- gi No. 136676
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10970
- gi No. 136677
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10971
- gi No. 136678
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10972
- gi No. 1421797
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10973
- gi No. 1480012
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1321: from 17 to 70
  
- Alignment No. 10974
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1321: from 1 to 37
  
- Alignment No. 10975
- gi No. 158759
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10976
- gi No. 158763
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10977
- gi No. 158765
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10978

- gi No. 158767
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10979
- gi No. 158769
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10980
- gi No. 158771
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10981
- gi No. 161281
- % Identity 94.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1321: from 1 to 71
  
- Alignment No. 10982
- gi No. 163575
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10983
- gi No. 163575
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10984
- gi No. 166336
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10985
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10986
- gi No. 166336
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10987
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10988
- gi No. 166336



- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10989
- gi No. 1666175
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10990
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1321: from 1 to 41
  
- Alignment No. 10991
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10992
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10993
- gi No. 167935
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10994
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10995
- gi No. 167941
- % Identity 92.8
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1321: from 2 to 70
  
- Alignment No. 10996
- gi No. 167945
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10997
- gi No. 167945
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10998
- gi No. 167947
- % Identity 94.5

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 10999
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11000
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11001
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11002
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11003
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11004
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11005
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11006
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11007
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11008
- gi No. 1684855
- % Identity 81.7
- Alignment Length 131

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11009
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11010
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11011
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11012
- gi No. 1684857
- % Identity 100
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11013
- gi No. 1684857
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11014
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11015
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11016
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11017
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11018
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11019
- gi No. 170354
- % Identity 100
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11020
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11021
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11022
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11023
- gi No. 1762374
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11024
- gi No. 1762935
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11025
- gi No. 1763015
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11026
- gi No. 1771780
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11027
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11028
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11029
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11030
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11031
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11032
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11033
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11034
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11035
- gi No. 1805696
- % Identity 95.2
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1321: from 8 to 70
  
- Alignment No. 11036
- gi No. 1805696
- % Identity 95.5
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1321: from 1 to 65
  
- Alignment No. 11037
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1321: from 1 to 38
  
- Alignment No. 11038
- gi No. 1841849
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70
  
- Alignment No. 11039

- gi No. 1841849
- % Identity 100
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1321: from 1 to 16
  
- Alignment No. 11040
- gi No. 208558
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11041
- gi No. 208560
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11042
- gi No. 208562
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11043
- gi No. 208564
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11044
- gi No. 208566
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11045
- gi No. 208568
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11046
- gi No. 208891
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11047
- gi No. 208891
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 22
  
- Alignment No. 11048
- gi No. 209603
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11049
- gi No. 2118958

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11050
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11051
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11052
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11053
- gi No. 2118959
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 36
  
- Alignment No. 11054
- gi No. 2118959
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11055
- gi No. 2118959
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11056
- gi No. 2118960
- % Identity 96.5
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11057
- gi No. 2118960
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11058
- gi No. 2118961
- % Identity 94.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11059
- gi No. 2118961
- % Identity 95.2

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11060
- gi No. 2118962
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11061
- gi No. 2118962
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11062
- gi No. 2118963
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11063
- gi No. 2118964
- % Identity 96.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11064
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11065
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11066
- gi No. 2118965
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11067
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11068
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11069
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146



- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11070
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11071
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11072
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11073
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11074
- gi No. 2133278
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11075
- gi No. 2133549
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70
- Alignment No. 11076
- gi No. 2133549
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 21 to 70
- Alignment No. 11077
- gi No. 2133549
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 48
- Alignment No. 11078
- gi No. 2144011
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11079
- gi No. 2144275
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11080
- gi No. 2144734
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11081
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11082
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11083
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11084
- gi No. 2149467
- % Identity 87.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11085
- gi No. 2209091
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11086
- gi No. 223061
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11087
- gi No. 224321
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11088
- gi No. 224321
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11089
- gi No. 225317
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11090
- gi No. 225319
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77
  
- Alignment No. 11091
- gi No. 225320
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77
  
- Alignment No. 11092
- gi No. 2281952
- % Identity 95.2
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1321: from 8 to 69
  
- Alignment No. 11093
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1321: from 8 to 69
  
- Alignment No. 11094
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1321: from 8 to 52
  
- Alignment No. 11095
- gi No. 2281959
- % Identity 90.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1321: from 7 to 70
  
- Alignment No. 11096
- gi No. 2330875
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11097
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1321: from 6 to 63
  
- Alignment No. 11098
- gi No. 2408009
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11099
- gi No. 2408009
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11100

- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11101
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11102
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11103
- gi No. 247308
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11104
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1321: from 1 to 20
  
- Alignment No. 11105
- gi No. 2558539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11106
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11107
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11108
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11109
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11110
- gi No. 2627129

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11111
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11112
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11113
- gi No. 2627131
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
  
- Alignment No. 11114
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11115
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11116
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11117
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11118
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11119
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11120
- gi No. 2627131
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11121
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11122
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11123
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11124
- gi No. 2627133
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
  
- Alignment No. 11125
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11126
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11127
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11128
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11129
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11130
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11131
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11132
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11133
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11134
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11135
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11136
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11137
- gi No. 2641213
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11138
- gi No. 2641213
- % Identity 98.6
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1321: from 1 to 63
- Alignment No. 11139
- gi No. 2654141
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11140
- gi No. 2654141
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11141
- gi No. 2654141
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11142
- gi No. 2654141
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11143
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11144
- gi No. 2707837
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11145
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11146
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11147
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11148
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11149
- gi No. 2760345
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11150
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70



- Alignment No. 11151
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11152
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11153
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11154
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11155
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11156
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11157
- gi No. 2760349
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11158
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11159
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11160
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11161

- gi No. 279635
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11162
- gi No. 279636
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11163
- gi No. 280386
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11164
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1321: from 1 to 20
  
- Alignment No. 11165
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11166
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11167
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11168
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11169
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11170
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11171
- gi No. 2894304

- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11172
- gi No. 2894306
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11173
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11174
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11175
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11176
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11177
- gi No. 2995277
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1321: from 48 to 70
  
- Alignment No. 11178
- gi No. 2995949
- % Identity 100
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11179
- gi No. 3047314
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11180
- gi No. 3047314
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11181
- gi No. 3047316
- % Identity 97.1

- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11182
- gi No. 3047318
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11183
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11184
- gi No. 3047318
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11185
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11186
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11187
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11188
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11189
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11190
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11191
- gi No. 3126967
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11192
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11193
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11194
- gi No. 3152950
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11195
- gi No. 3158372
- % Identity 100
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11196
- gi No. 3158372
- % Identity 99.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1321: from 1 to 33
- Alignment No. 11197
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11198
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11199
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11200
- gi No. 322750
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11201
- gi No. 323071
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11202
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11203
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11204
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11205
- gi No. 323157
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11206
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11207
- gi No. 323208
- % Identity 82.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11208
- gi No. 323230
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11209
- gi No. 3265058
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11210
- gi No. 3319208
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11211
- gi No. 3335355
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1321: from 56 to 70

- Alignment No. 11212
- gi No. 3335355
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 53
  
- Alignment No. 11213
- gi No. 3335355
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11214
- gi No. 3335355
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11215
- gi No. 340062
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1321: from 5 to 70
  
- Alignment No. 11216
- gi No. 3452083
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 23 to 70
  
- Alignment No. 11217
- gi No. 3452083
- % Identity 96.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1321: from 1 to 29
  
- Alignment No. 11218
- gi No. 348148
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70
  
- Alignment No. 11219
- gi No. 348148
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 48
  
- Alignment No. 11220
- gi No. 348149
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 21 to 70
  
- Alignment No. 11221
- gi No. 3603456
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11222

- gi No. 3603456
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11223
- gi No. 3603456
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11224
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11225
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11226
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11227
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11228
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11229
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11230
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11231
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11232
- gi No. 3776536



- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11233
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11234
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11235
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11236
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11237
- gi No. 3789940
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11238
- gi No. 3789940
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11239
- gi No. 3789940
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11240
- gi No. 3789942
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11241
- gi No. 3789942
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11242
- gi No. 3789942
- % Identity 98.6

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11243
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11244
- gi No. 3822277
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11245
- gi No. 385076
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11246
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11247
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11248
- gi No. 3885463
- % Identity 94
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1321: from 4 to 70
  
- Alignment No. 11249
- gi No. 3892189
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11250
- gi No. 3892189
- % Identity 84.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11251
- gi No. 402242
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11252
- gi No. 4049712
- % Identity 85.7
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11253
- gi No. 4102845
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1321: from 6 to 70
- Alignment No. 11254
- gi No. 4105408
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11255
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11256
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11257
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11258
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11259
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11260
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11261
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11262
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11263
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11264
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11265
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11266
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11267
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11268
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11269
- gi No. 4150914
- % Identity 95.7
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11270
- gi No. 4151082
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11271
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11272
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11273
  - gi No. 418854
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11274
  - gi No. 418854
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11275
  - gi No. 418854
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11276
  - gi No. 421735
  - % Identity 94.7
  - Alignment Length 19
  - Location of Alignment in SEQ ID NO 1321: from 1 to 19
- Alignment No. 11277
  - gi No. 421867
  - % Identity 100
  - Alignment Length 70
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11278
  - gi No. 421929
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11279
  - gi No. 421929
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11280
  - gi No. 421929
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11281
  - gi No. 421929
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11282
  - gi No. 421929
  - % Identity 99.3
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11283

- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11284
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11285
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11286
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11287
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11288
- gi No. 422269
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11289
- gi No. 422270
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11290
- gi No. 422271
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11291
- gi No. 433970
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11292
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11293
- gi No. 433970

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11294
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11295
- gi No. 433970
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11296
- gi No. 444791
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11297
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11298
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11299
- gi No. 4506713
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11300
- gi No. 4507761
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11301
- gi No. 4510359
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70
  
- Alignment No. 11302
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1321: from 1 to 25
  
- Alignment No. 11303
- gi No. 4586594
- % Identity 100

- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11304
- gi No. 4586594
- % Identity 100
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
  
- Alignment No. 11305
- gi No. 4587232
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11306
- gi No. 4587234
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11307
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11308
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11309
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11310
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11311
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11312
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11313
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146



- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11314
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11315
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11316
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11317
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11318
- gi No. 4589760
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11319
- gi No. 463363
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11320
- gi No. 463365
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11321
- gi No. 463367
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11322
- gi No. 463369
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11323
- gi No. 463371
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11324
- gi No. 463373
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11325
- gi No. 463375
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11326
- gi No. 464989
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11327
- gi No. 464990
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11328
- gi No. 468272
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11329
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1321: from 1 to 47
  
- Alignment No. 11330
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1321: from 3 to 27
  
- Alignment No. 11331
- gi No. 477630
- % Identity 94.4
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11332
- gi No. 477815
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11333
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11334
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11335
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11336
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11337
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11338
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11339
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11340
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11341
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11342
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11343
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11344

- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11345
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11346
- gi No. 485518
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11347
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11348
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11349
- gi No. 510473
- % Identity 85.4
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1321: from 1 to 13
  
- Alignment No. 11350
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11351
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11352
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11353
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11354
- gi No. 510473

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11355
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11356
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11357
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11358
- gi No. 510476
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11359
- gi No. 5107695
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11360
- gi No. 539404
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11361
- gi No. 539404
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11362
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11363
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11364
- gi No. 539935
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11365
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11366
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11367
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11368
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11369
- gi No. 541953
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11370
- gi No. 541954
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11371
- gi No. 542395
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 23 to 70
  
- Alignment No. 11372
- gi No. 5441519
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11373
- gi No. 552237
- % Identity 97.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70
  
- Alignment No. 11374
- gi No. 552237
- % Identity 94.8
- Alignment Length 77

- Location of Alignment in SEQ ID NO 1321: from 1 to 36
- Alignment No. 11375
- gi No. 5523967
- % Identity 96.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11376
- gi No. 5523969
- % Identity 95.1
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11377
- gi No. 5523969
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11378
- gi No. 5523971
- % Identity 95.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11379
- gi No. 5523973
- % Identity 87.6
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11380
- gi No. 5523975
- % Identity 95.9
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11381
- gi No. 5523977
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11382
- gi No. 5523979
- % Identity 72.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11383
- gi No. 5523979
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11384
- gi No. 5523981
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11385
- gi No. 5523983
- % Identity 94.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1321: from 3 to 70
  
- Alignment No. 11386
- gi No. 5523985
- % Identity 94.9
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11387
- gi No. 5523987
- % Identity 96.6
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11388
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11389
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11390
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11391
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11392
- gi No. 5531278
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11393
- gi No. 5531278
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11394
- gi No. 5531281
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70



- Alignment No. 11395
- gi No. 554564
- % Identity 93.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11396
- gi No. 567767
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11397
- gi No. 567767
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11398
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11399
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11400
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11401
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11402
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11403
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11404
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11405

- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11406
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11407
- gi No. 576775
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11408
- gi No. 576775
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11409
- gi No. 578545
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11410
- gi No. 578545
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11411
- gi No. 578545
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11412
- gi No. 578545
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11413
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11414
- gi No. 578546
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11415
- gi No. 578546

- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11416
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11417
- gi No. 578549
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11418
- gi No. 578549
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11419
- gi No. 578549
- % Identity 84.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11420
- gi No. 578551
- % Identity 86.8
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11421
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11422
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11423
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11424
- gi No. 600539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11425
- gi No. 602076
- % Identity 100

- Alignment Length 113
- Location of Alignment in SEQ ID NO 1321: from 1 to 37
  
- Alignment No. 11426
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11427
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11428
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11429
- gi No. 625174
- % Identity 86.7
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1321: from 1 to 13
  
- Alignment No. 11430
- gi No. 625174
- % Identity 95.3
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11431
- gi No. 625174
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11432
- gi No. 625509
- % Identity 100
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11433
- gi No. 625509
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 53
  
- Alignment No. 11434
- gi No. 625509
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11435
- gi No. 625509
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11436
- gi No. 630455
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11437
- gi No. 630479
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11438
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11439
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11440
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11441
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11442
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11443
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11444
- gi No. 70637
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11445
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11446
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11447
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11448
- gi No. 70640
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11449
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11450
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11451
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11452
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11453
- gi No. 70643
- % Identity 100
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11454
- gi No. 70644
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11455
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11456
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11457
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11458
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11459
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11460
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11461
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11462
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11463
- gi No. 70646
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11464
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11465
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11466

- gi No. 70648
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11467
- gi No. 70650
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11468
- gi No. 70653
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11469
- gi No. 70654
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11470
- gi No. 70657
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11471
- gi No. 70658
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11472
- gi No. 70659
- % Identity 96.9
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1321: from 6 to 70
  
- Alignment No. 11473
- gi No. 70660
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11474
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11475
- gi No. 726391
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11476
- gi No. 726391



- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11477
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11478
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11479
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11480
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11481
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11482
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11483
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11484
- gi No. 82040
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11485
- gi No. 82040
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 36
  
- Alignment No. 11486
- gi No. 82040
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11487
- gi No. 82040
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11488
- gi No. 82284
- % Identity 100
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1321: from 1 to 56
  
- Alignment No. 11489
- gi No. 82286
- % Identity 100
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1321: from 57 to 70
  
- Alignment No. 11490
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 1 to 48
  
- Alignment No. 11491
- gi No. 82288
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1321: from 37 to 70
  
- Alignment No. 11492
- gi No. 82426
- % Identity 100
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11493
- gi No. 82426
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11494
- gi No. 82512
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11495
- gi No. 82512
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11496
- gi No. 825728
- % Identity 96.8
- Alignment Length 31

- Location of Alignment in SEQ ID NO 1321: from 40 to 70
- Alignment No. 11497
- gi No. 82733
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11498
- gi No. 82734
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11499
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11500
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11501
- gi No. 829173
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1321: from 13 to 70
- Alignment No. 11502
- gi No. 83594
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11503
- gi No. 83594
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
- Alignment No. 11504
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11505
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11506
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11507
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11508
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11509
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11510
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11511
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11512
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11513
- gi No. 84152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11514
- gi No. 84336
- % Identity 94.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1321: from 19 to 70
  
- Alignment No. 11515
- gi No. 84337
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11516
- gi No. 84337
- % Identity 93.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1321: from 1 to 19

- Alignment No. 11517
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11518
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11519
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11520
- gi No. 84478
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11521
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11522
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11523
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11524
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11525
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11526
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11527

- gi No. 84834
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11528
- gi No. 84834
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1321: from 1 to 16
  
- Alignment No. 11529
- gi No. 84834
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11530
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11531
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11532
- gi No. 86473
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1321: from 45 to 70
  
- Alignment No. 11533
- gi No. 870794
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11534
- gi No. 870794
- % Identity 75.5
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1321: from 1 to 71
  
- Alignment No. 11535
- gi No. 870794
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1321: from 1 to 69
  
- Alignment No. 11536
- gi No. 870794
- % Identity 70.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11537
- gi No. 89311

- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11538
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11539
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11540
- gi No. 899115
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11541
- gi No. 899115
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1321: from 1 to 23
  
- Alignment No. 11542
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11543
- gi No. 899608
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11544
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11545
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11546
- gi No. 902525
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11547
- gi No. 902584
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11548
- gi No. 902584
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11549
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11550
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11551
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11552
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11553
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11554
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11555
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11556
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11557
- gi No. 91870
- % Identity 96
- Alignment Length 75



- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11558
- gi No. 91870
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 22
- Alignment No. 11559
- gi No. 91871
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11560
- gi No. 9295
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1321: from 8 to 70
- Alignment No. 11561
- gi No. 940395
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
- Alignment No. 11562
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11563
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11564
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11565
- gi No. 940395
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11566
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11567
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11568
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11569
- gi No. 967985
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11570
- gi No. 99469
- % Identity 100
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1321: from 38 to 70
  
- Alignment No. 11571
- gi No. 99771
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11572
- gi No. 99772
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11573
- gi No. 99975
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

Maximum Length Sequence corresponding to clone ID 254904

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1322
- Ceres seq\_id 1500057

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1323
- Ceres seq\_id 1500058
- Location of start within SEQ ID NO 1322: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11574
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1323: from 144 to 304 aa.
  
- Alignment No. 11575
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1323: from 129 to 346 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1324
- Ceres seq\_id 1500059

- Location of start within SEQ ID NO 1322: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11576
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1324: from 105 to 265 aa.
- Alignment No. 11577
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1324: from 90 to 307 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1325
- Ceres seq\_id 1500060
- Location of start within SEQ ID NO 1322: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11578
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1325: from 97 to 257 aa.
- Alignment No. 11579
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1325: from 82 to 299 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255048

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1326
- Ceres seq\_id 1500065

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1327
- Ceres seq\_id 1500066
- Location of start within SEQ ID NO 1326: at 199 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11580
- gi No. 1041702
- % Identity 86.6
- Alignment Length 236
- Location of Alignment in SEQ ID NO 1327: from 19 to 118
- Alignment No. 11581
- gi No. 1778097
- % Identity 71.4
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1327: from 4 to 87
- Alignment No. 11582
- gi No. 1778107
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1327: from 1 to 82

- Alignment No. 11583
- gi No. 1778109
- % Identity 71.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1327: from 1 to 77
  
- Alignment No. 11584
- gi No. 3461833
- % Identity 73.8
- Alignment Length 241
- Location of Alignment in SEQ ID NO 1327: from 14 to 118
  
- Alignment No. 11585
- gi No. 4027897
- % Identity 70.2
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1327: from 1 to 118

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1328
- Ceres seq\_id 1500067
- Location of start within SEQ ID NO 1326: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11586
- gi No. 1041702
- % Identity 86.6
- Alignment Length 236
- Location of Alignment in SEQ ID NO 1328: from 5 to 104
  
- Alignment No. 11587
- gi No. 1778097
- % Identity 71.4
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1328: from 1 to 73
  
- Alignment No. 11588
- gi No. 1778107
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1328: from 1 to 68
  
- Alignment No. 11589
- gi No. 1778109
- % Identity 71.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1328: from 1 to 63
  
- Alignment No. 11590
- gi No. 3461833
- % Identity 73.8
- Alignment Length 241
- Location of Alignment in SEQ ID NO 1328: from 1 to 104
  
- Alignment No. 11591
- gi No. 4027897
- % Identity 70.2
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1328: from 1 to 104

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1329
  - Ceres seq\_id 1500068
  - Location of start within SEQ ID NO 1326: at 740 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255050

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1330
  - Ceres seq\_id 1500069
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1331
  - Ceres seq\_id 1500070
  - Location of start within SEQ ID NO 1330: at 200 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11592
- TBC domain
- Location within SEQ ID NO 1331: from 113 to 327 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1332
  - Ceres seq\_id 1500071
  - Location of start within SEQ ID NO 1330: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11593
- TBC domain
- Location within SEQ ID NO 1332: from 102 to 316 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1333
  - Ceres seq\_id 1500072
  - Location of start within SEQ ID NO 1330: at 659 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11594
- TBC domain
- Location within SEQ ID NO 1333: from 1 to 174 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255298

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1334
  - Ceres seq\_id 1500073
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1335
  - Ceres seq\_id 1500074
  - Location of start within SEQ ID NO 1334: at 363 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 11595
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1335: from 78 to 348 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11596
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1335: from 215 to 261
- Alignment No. 11597
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1335: from 189 to 262
- Alignment No. 11598
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1335: from 200 to 250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1336
- Ceres seq\_id 1500075
- Location of start within SEQ ID NO 1334: at 735 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 11599
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1336: from 1 to 224 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11600
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1336: from 91 to 137
- Alignment No. 11601
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1336: from 65 to 138
- Alignment No. 11602
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1336: from 76 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1337
- Ceres seq\_id 1500076
- Location of start within SEQ ID NO 1334: at 822 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11603
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1337: from 1 to 195 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11604
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1337: from 62 to 108
- Alignment No. 11605
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1337: from 36 to 109
- Alignment No. 11606
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1337: from 47 to 97

Maximum Length Sequence corresponding to clone ID 255307

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1338
- Ceres seq\_id 1500077

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1339
- Ceres seq\_id 1500078
- Location of start within SEQ ID NO 1338: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11607
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1339: from 97 to 436 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11608
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1339: from 1 to 444
- Alignment No. 11609
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1339: from 1 to 444
- Alignment No. 11610
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1339: from 1 to 444

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1340

- Ceres seq\_id 1500079
- Location of start within SEQ ID NO 1338: at 141 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11611
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1340: from 80 to 419 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11612
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

- Alignment No. 11613
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

- Alignment No. 11614
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1341
- Ceres seq\_id 1500080
- Location of start within SEQ ID NO 1338: at 420 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11615
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1341: from 1 to 326 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11616
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

- Alignment No. 11617
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

- Alignment No. 11618
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

Maximum Length Sequence corresponding to clone ID 255364

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1342



- Ceres seq\_id 1500081
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1343
  - Ceres seq\_id 1500082
  - Location of start within SEQ ID NO 1342: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11619
  - gi No. 4768976
  - % Identity 71.7
  - Alignment Length 92
  - Location of Alignment in SEQ ID NO 1343: from 246 to 337

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1344
  - Ceres seq\_id 1500083
  - Location of start within SEQ ID NO 1342: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11620
  - gi No. 4768976
  - % Identity 71.7
  - Alignment Length 92
  - Location of Alignment in SEQ ID NO 1344: from 215 to 306

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1345
  - Ceres seq\_id 1500084
  - Location of start within SEQ ID NO 1342: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11621
  - gi No. 4768976
  - % Identity 71.7
  - Alignment Length 92
  - Location of Alignment in SEQ ID NO 1345: from 154 to 245

Maximum Length Sequence corresponding to clone ID 255477

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1346
  - Ceres seq\_id 1500085
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1347
  - Ceres seq\_id 1500086
  - Location of start within SEQ ID NO 1346: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11622
  - gi No. 5430753
  - % Identity 81.9
  - Alignment Length 234
  - Location of Alignment in SEQ ID NO 1347: from 110 to 341

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1348
- Ceres seq\_id 1500087
- Location of start within SEQ ID NO 1346: at 613 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11623
- gi No. 5430753
- % Identity 81.9
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1348: from 1 to 232

Maximum Length Sequence corresponding to clone ID 255542

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1349
- Ceres seq\_id 1500088

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1350
- Ceres seq\_id 1500089
- Location of start within SEQ ID NO 1349: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11624
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11625
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11626
- gi No. 100216
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11627
- gi No. 102424
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 279 to 293
- Alignment No. 11628
- gi No. 102427
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11629
- gi No. 1061334
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 279 to 295

- Alignment No. 11630
- gi No. 1065941
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 282 to 294
  
- Alignment No. 11631
- gi No. 1065941
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11632
- gi No. 1065941
- % Identity 72.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1350: from 329 to 345
  
- Alignment No. 11633
- gi No. 1076555
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11634
- gi No. 108231
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11635
- gi No. 113210
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11636
- gi No. 1163054
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11637
- gi No. 1163054
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11638
- gi No. 1185397
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
  
- Alignment No. 11639
- gi No. 1185397
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11640
- gi No. 1185397
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
  
- Alignment No. 11641
- gi No. 119111
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11642
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11643
- gi No. 1326381
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 323 to 337
  
- Alignment No. 11644
- gi No. 1345537
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11645
- gi No. 134920
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
  
- Alignment No. 11646
- gi No. 134920
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 348
  
- Alignment No. 11647
- gi No. 1351865
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 281 to 293
  
- Alignment No. 11648
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11649
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11650

- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11651
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11652
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11653
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11654
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11655
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11656
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11657
- gi No. 1480413
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11658
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
  
- Alignment No. 11659
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
  
- Alignment No. 11660
- gi No. 1644461

- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
  
- Alignment No. 11661
- gi No. 1655699
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
  
- Alignment No. 11662
- gi No. 1655699
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11663
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11664
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11665
- gi No. 169345
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11666
- gi No. 1911629
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11667
- gi No. 1911629
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
  
- Alignment No. 11668
- gi No. 1914851
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11669
- gi No. 1914851
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 278 to 293
  
- Alignment No. 11670
- gi No. 1914851
- % Identity 77.8

- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 278 to 293
  
- Alignment No. 11671
- gi No. 1914851
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1350: from 278 to 293
  
- Alignment No. 11672
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11673
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11674
- gi No. 2129478
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11675
- gi No. 2147342
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 323 to 336
  
- Alignment No. 11676
- gi No. 2147342
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 323 to 338
  
- Alignment No. 11677
- gi No. 226743
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 348
  
- Alignment No. 11678
- gi No. 2494630
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 283 to 293
  
- Alignment No. 11679
- gi No. 2494630
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
  
- Alignment No. 11680
- gi No. 3204132
- % Identity 77.8
- Alignment Length 18

- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11681
- gi No. 3204132
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1350: from 327 to 346
- Alignment No. 11682
- gi No. 322758
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11683
- gi No. 322758
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 291
- Alignment No. 11684
- gi No. 347455
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1350: from 327 to 346
- Alignment No. 11685
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 324 to 334
- Alignment No. 11686
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 324 to 334
- Alignment No. 11687
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11688
- gi No. 4033606
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11689
- gi No. 4096360
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11690
- gi No. 4096360
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 293



- Alignment No. 11691
- gi No. 4096360
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
  
- Alignment No. 11692
- gi No. 4467884
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
  
- Alignment No. 11693
- gi No. 4522026
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 347
  
- Alignment No. 11694
- gi No. 4589678
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
  
- Alignment No. 11695
- gi No. 497413
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 283 to 293
  
- Alignment No. 11696
- gi No. 497413
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
  
- Alignment No. 11697
- gi No. 5302801
- % Identity 99.6
- Alignment Length 473
- Location of Alignment in SEQ ID NO 1350: from 1 to 473
  
- Alignment No. 11698
- gi No. 5441495
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
  
- Alignment No. 11699
- gi No. 5441495
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 331 to 343
  
- Alignment No. 11700
- gi No. 628112
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11701
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11702
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11703
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11704
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11705
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
  
- Alignment No. 11706
- gi No. 628185
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
  
- Alignment No. 11707
- gi No. 81870
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1351
- Ceres seq\_id 1500090
- Location of start within SEQ ID NO 1349: at 492 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11708
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11709
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11710
- gi No. 100216
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11711
- gi No. 102424
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 132 to 146
  
- Alignment No. 11712
- gi No. 102427
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11713
- gi No. 1061334
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 132 to 148
  
- Alignment No. 11714
- gi No. 1065941
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 135 to 147
  
- Alignment No. 11715
- gi No. 1065941
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11716
- gi No. 1065941
- % Identity 72.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1351: from 182 to 198
  
- Alignment No. 11717
- gi No. 1076555
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11718
- gi No. 108231
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11719
- gi No. 113210
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11720
- gi No. 1163054
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11721
- gi No. 1163054
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11722
- gi No. 1185397
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11723
- gi No. 1185397
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11724
- gi No. 1185397
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
  
- Alignment No. 11725
- gi No. 119111
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11726
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11727
- gi No. 1326381
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 176 to 190
  
- Alignment No. 11728
- gi No. 1345537
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11729
- gi No. 134920
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11730

- gi No. 134920
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 201
  
- Alignment No. 11731
- gi No. 1351865
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 134 to 146
  
- Alignment No. 11732
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11733
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11734
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11735
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11736
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11737
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11738
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11739
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11740
- gi No. 141279

- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11741
- gi No. 1480413
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11742
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11743
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11744
- gi No. 1644461
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11745
- gi No. 1655699
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11746
- gi No. 1655699
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11747
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11748
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11749
- gi No. 169345
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11750
- gi No. 1911629
- % Identity 78.6

- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11751
- gi No. 1911629
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
  
- Alignment No. 11752
- gi No. 1914851
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11753
- gi No. 1914851
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 131 to 146
  
- Alignment No. 11754
- gi No. 1914851
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 131 to 146
  
- Alignment No. 11755
- gi No. 1914851
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1351: from 131 to 146
  
- Alignment No. 11756
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11757
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11758
- gi No. 2129478
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11759
- gi No. 2147342
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 176 to 189
  
- Alignment No. 11760
- gi No. 2147342
- % Identity 75
- Alignment Length 16

- Location of Alignment in SEQ ID NO 1351: from 176 to 191
- Alignment No. 11761
- gi No. 226743
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 201
- Alignment No. 11762
- gi No. 2494630
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 136 to 146
- Alignment No. 11763
- gi No. 2494630
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
- Alignment No. 11764
- gi No. 3204132
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11765
- gi No. 3204132
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1351: from 180 to 199
- Alignment No. 11766
- gi No. 322758
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11767
- gi No. 322758
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 144
- Alignment No. 11768
- gi No. 347455
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1351: from 180 to 199
- Alignment No. 11769
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 177 to 187
- Alignment No. 11770
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 177 to 187



- Alignment No. 11771
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
  
- Alignment No. 11772
- gi No. 4033606
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11773
- gi No. 4096360
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
  
- Alignment No. 11774
- gi No. 4096360
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11775
- gi No. 4096360
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
  
- Alignment No. 11776
- gi No. 4467884
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
  
- Alignment No. 11777
- gi No. 4522026
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 200
  
- Alignment No. 11778
- gi No. 4589678
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
  
- Alignment No. 11779
- gi No. 497413
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 136 to 146
  
- Alignment No. 11780
- gi No. 497413
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193

- Alignment No. 11781
- gi No. 5302801
- % Identity 99.6
- Alignment Length 473
- Location of Alignment in SEQ ID NO 1351: from 1 to 326
  
- Alignment No. 11782
- gi No. 5441495
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
  
- Alignment No. 11783
- gi No. 5441495
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 184 to 196
  
- Alignment No. 11784
- gi No. 628112
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11785
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11786
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11787
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11788
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11789
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
  
- Alignment No. 11790
- gi No. 628185
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
  
- Alignment No. 11791

- gi No. 81870
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

Maximum Length Sequence corresponding to clone ID 255685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1352
- Ceres seq\_id 1500091

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1353
- Ceres seq\_id 1500092
- Location of start within SEQ ID NO 1352: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11792
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1353: from 1 to 80 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1354
- Ceres seq\_id 1500093
- Location of start within SEQ ID NO 1352: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255876

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1355
- Ceres seq\_id 1500097

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1356
- Ceres seq\_id 1500098
- Location of start within SEQ ID NO 1355: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11793
- Lyase
- Location within SEQ ID NO 1356: from 63 to 473 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11794
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1356: from 1 to 473

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1357
- Ceres seq\_id 1500099
- Location of start within SEQ ID NO 1355: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11795

- Lyase
- Location within SEQ ID NO 1357: from 17 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11796
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1357: from 1 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1358
- Ceres seq\_id 1500100
- Location of start within SEQ ID NO 1355: at 325 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11797
- Lyase
- Location within SEQ ID NO 1358: from 1 to 382 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11798
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1358: from 1 to 382

Maximum Length Sequence corresponding to clone ID 256052

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1359
- Ceres seq\_id 1500101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1360
- Ceres seq\_id 1500102
- Location of start within SEQ ID NO 1359: at 129 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11799
- NifU-like domain
- Location within SEQ ID NO 1360: from 89 to 155 aa.
- Alignment No. 11800
- NifU-like domain
- Location within SEQ ID NO 1360: from 171 to 233 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11801
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1360: from 13 to 236

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1361
- Ceres seq\_id 1500103
- Location of start within SEQ ID NO 1359: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11802
- NifU-like domain
- Location within SEQ ID NO 1361: from 77 to 143 aa.

- Alignment No. 11803
- NifU-like domain
- Location within SEQ ID NO 1361: from 159 to 221 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11804
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1361: from 1 to 224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1362
- Ceres seq\_id 1500104
- Location of start within SEQ ID NO 1359: at 372 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11805
- NifU-like domain
- Location within SEQ ID NO 1362: from 8 to 74 aa.

- Alignment No. 11806
- NifU-like domain
- Location within SEQ ID NO 1362: from 90 to 152 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11807
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1362: from 1 to 155

Maximum Length Sequence corresponding to clone ID 256076

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1363
- Ceres seq\_id 1500105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1364
- Ceres seq\_id 1500106
- Location of start within SEQ ID NO 1363: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11808
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1364: from 1 to 240 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11809
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11810
- gi No. 1076641

- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11811
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11812
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11813
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11814
- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11815
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244
  
- Alignment No. 11816
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11817
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11818
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11819
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11820
- gi No. 1617200
- % Identity 81.1

- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11821
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11822
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11823
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11824
- gi No. 1730039
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244
  
- Alignment No. 11825
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1364: from 76 to 245
  
- Alignment No. 11826
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1364: from 20 to 245
  
- Alignment No. 11827
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
  
- Alignment No. 11828
- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11829
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11830
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285

- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11831
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11832
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11833
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11834
- gi No. 2191169
- % Identity 78.7
- Alignment Length 300
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11835
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11836
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
- Alignment No. 11837
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1364: from 1 to 244
- Alignment No. 11838
- gi No. 2598601
- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11839
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11840
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244



- Alignment No. 11841
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11842
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11843
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11844
- gi No. 3236117
- % Identity 80
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11845
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
  
- Alignment No. 11846
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1364: from 176 to 245
  
- Alignment No. 11847
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
  
- Alignment No. 11848
- gi No. 3928148
- % Identity 81.6
- Alignment Length 266
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11849
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11850
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11851
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11852
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
  
- Alignment No. 11853
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1365
- Ceres seq\_id 1500107
- Location of start within SEQ ID NO 1363: at 433 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11854
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1365: from 1 to 237 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11855
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11856
- gi No. 1076641
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11857
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11858
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11859
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11860

- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11861
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11862
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11863
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11864
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11865
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11866
- gi No. 1617200
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11867
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11868
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11869
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11870
- gi No. 1730039

- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11871
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1365: from 73 to 242
  
- Alignment No. 11872
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1365: from 17 to 242
  
- Alignment No. 11873
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
  
- Alignment No. 11874
- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11875
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11876
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11877
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11878
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11879
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11880
- gi No. 2191169
- % Identity 78.7

- Alignment Length 300
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11881
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11882
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
  
- Alignment No. 11883
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11884
- gi No. 2598601
- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11885
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11886
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11887
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11888
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11889
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11890
- gi No. 3236117
- % Identity 80
- Alignment Length 285

- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11891
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11892
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1365: from 173 to 242
- Alignment No. 11893
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11894
- gi No. 3928148
- % Identity 81.6
- Alignment Length 266
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11895
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11896
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11897
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11898
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11899
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1366
- Ceres seq\_id 1500108
- Location of start within SEQ ID NO 1363: at 514 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 11900
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1366: from 1 to 210 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11901
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11902
- gi No. 1076641
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11903
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11904
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11905
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11906
- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11907
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
- Alignment No. 11908
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11909
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11910
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11911
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11912
- gi No. 1617200
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11913
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11914
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11915
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11916
- gi No. 1730039
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
  
- Alignment No. 11917
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1366: from 46 to 215
  
- Alignment No. 11918
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11919
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11920



- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11921
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11922
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11923
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11924
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11925
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11926
- gi No. 2191169
- % Identity 78.7
- Alignment Length 300
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11927
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11928
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11929
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
  
- Alignment No. 11930
- gi No. 2598601

- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11931
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11932
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
  
- Alignment No. 11933
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11934
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11935
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11936
- gi No. 3236117
- % Identity 80
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11937
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11938
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1366: from 146 to 215
  
- Alignment No. 11939
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11940
- gi No. 3928148
- % Identity 81.6

- Alignment Length 266
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11941
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11942
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11943
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11944
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11945
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

Maximum Length Sequence corresponding to clone ID 256152

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1367
- Ceres seq\_id 1500109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1368
- Ceres seq\_id 1500110
- Location of start within SEQ ID NO 1367: at 416 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11946
- gi No. 3386609
- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1368: from 1 to 348

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1369
- Ceres seq\_id 1500111
- Location of start within SEQ ID NO 1367: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11947
- gi No. 3386609

- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1369: from 1 to 342

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1370
- Ceres seq\_id 1500112
- Location of start within SEQ ID NO 1367: at 668 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11948
- gi No. 3386609
- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1370: from 1 to 264

Maximum Length Sequence corresponding to clone ID 256433

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1371
- Ceres seq\_id 1500115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1372
- Ceres seq\_id 1500116
- Location of start within SEQ ID NO 1371: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11949
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1372: from 82 to 185 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11950
- gi No. 3335372
- % Identity 89.8
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1372: from 29 to 185

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1373
- Ceres seq\_id 1500117
- Location of start within SEQ ID NO 1371: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11951
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1373: from 54 to 157 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11952
- gi No. 3335372
- % Identity 89.8
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1373: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1374
- Ceres seq\_id 1500118

- Location of start within SEQ ID NO 1371: at 662 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11953
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1374: from 1 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11954
- gi No. 3335372
- % Identity 99.5
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1374: from 1 to 161

Maximum Length Sequence corresponding to clone ID 256780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1375
- Ceres seq\_id 1500131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1376
- Ceres seq\_id 1500132
- Location of start within SEQ ID NO 1375: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11955
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1376: from 3 to 469
- Alignment No. 11956
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1376: from 1 to 469
- Alignment No. 11957
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1376: from 3 to 469
- Alignment No. 11958
- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1376: from 2 to 469
- Alignment No. 11959
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1376: from 3 to 469

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1377
- Ceres seq\_id 1500133
- Location of start within SEQ ID NO 1375: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11960
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11961
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11962
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11963
- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11964
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1378
- Ceres seq\_id 1500134
- Location of start within SEQ ID NO 1375: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11965
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11966
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11967
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11968

- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11969
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

Maximum Length Sequence corresponding to clone ID 257053

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1379
- Ceres seq\_id 1500135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1380
- Ceres seq\_id 1500136
- Location of start within SEQ ID NO 1379: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11970
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1380: from 267 to 301 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1381
- Ceres seq\_id 1500137
- Location of start within SEQ ID NO 1379: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11971
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1381: from 265 to 299 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1382
- Ceres seq\_id 1500138
- Location of start within SEQ ID NO 1379: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11972
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1382: from 222 to 256 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257278

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1383
- Ceres seq\_id 1500149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1384
- Ceres seq\_id 1500150

- Location of start within SEQ ID NO 1383: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1385
- Ceres seq\_id 1500151
- Location of start within SEQ ID NO 1383: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1386
- Ceres seq\_id 1500152
- Location of start within SEQ ID NO 1383: at 230 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11973
- gi No. 3717946
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86

- Alignment No. 11974
- gi No. 3717987
- % Identity 76.2
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86

- Alignment No. 11975
- gi No. 3717989
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86

Maximum Length Sequence corresponding to clone ID 257311

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1387
- Ceres seq\_id 1500153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1388
- Ceres seq\_id 1500154
- Location of start within SEQ ID NO 1387: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1389
- Ceres seq\_id 1500155
- Location of start within SEQ ID NO 1387: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)



(D) Related Amino Acid Sequences

- Alignment No. 11976
- gi No. 3834307
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1389: from 18 to 57

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1390
- Ceres seq\_id 1500156
- Location of start within SEQ ID NO 1387: at 323 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11977
- gi No. 3834307
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1390: from 1 to 40

Maximum Length Sequence corresponding to clone ID 257315

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1391
- Ceres seq\_id 1500157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1392
- Ceres seq\_id 1500158
- Location of start within SEQ ID NO 1391: at 264 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11978
- gi No. 3335359
- % Identity 70.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1392: from 1 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1393
- Ceres seq\_id 1500159
- Location of start within SEQ ID NO 1391: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11979
- gi No. 3335359
- % Identity 70.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1393: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1394
- Ceres seq\_id 1500160
- Location of start within SEQ ID NO 1391: at 351 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11980
- gi No. 3335359
- % Identity 70.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1394: from 1 to 56

Maximum Length Sequence corresponding to clone ID 257348

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1395
- Ceres seq\_id 1500165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1396
- Ceres seq\_id 1500166
- Location of start within SEQ ID NO 1395: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 11981
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1396: from 5 to 73 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11982
- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1396: from 22 to 73
  
- Alignment No. 11983
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11984
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11985
- gi No. 1076510
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11986
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
  
- Alignment No. 11987
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11988
- gi No. 118099
- % Identity 73.2

- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
  
- Alignment No. 11989
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11990
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11991
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1396: from 50 to 73
  
- Alignment No. 11992
- gi No. 1345921
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11993
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11994
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11995
- gi No. 1480465
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11996
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11997
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11998
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1396: from 5 to 73
- Alignment No. 11999
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
- Alignment No. 12000
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12001
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12002
- gi No. 1706248
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12003
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12004
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12005
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12006
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12007
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
- Alignment No. 12008
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12009
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
  
- Alignment No. 12010
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1396: from 2 to 73
  
- Alignment No. 12011
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
  
- Alignment No. 12012
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
  
- Alignment No. 12013
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12014
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12015
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12016
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12017
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
  
- Alignment No. 12018
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1396: from 25 to 73

- Alignment No. 12019
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12020
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12021
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12022
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
  
- Alignment No. 12023
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12024
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
  
- Alignment No. 12025
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1396: from 22 to 73
  
- Alignment No. 12026
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12027
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1396: from 2 to 73
  
- Alignment No. 12028
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1396: from 7 to 73
  
- Alignment No. 12029

- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12030
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12031
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12032
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12033
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1397
- Ceres seq\_id 1500167
- Location of start within SEQ ID NO 1395: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12034
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1397: from 1 to 64 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12035
- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1397: from 13 to 64
  
- Alignment No. 12036
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12037
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12038
- gi No. 1076510

- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12039
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12040
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12041
- gi No. 118099
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12042
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12043
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12044
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1397: from 41 to 64
  
- Alignment No. 12045
- gi No. 1345921
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12046
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12047
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12048
- gi No. 1480465
- % Identity 82.4



- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12049
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12050
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12051
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12052
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12053
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12054
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12055
- gi No. 1706248
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12056
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12057
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12058
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74

- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12059
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12060
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12061
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12062
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12063
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12064
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12065
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12066
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12067
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12068
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12069
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12070
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12071
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1397: from 16 to 64
  
- Alignment No. 12072
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12073
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12074
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12075
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12076
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12077
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12078
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1397: from 13 to 64

- Alignment No. 12079
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12080
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12081
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12082
- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12083
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12084
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12085
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12086
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1398
- Ceres seq\_id 1500168
- Location of start within SEQ ID NO 1395: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12087
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1398: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12088

- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12089
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12090
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12091
- gi No. 1076510
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12092
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12093
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12094
- gi No. 118099
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12095
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12096
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12097
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1398: from 29 to 52
  
- Alignment No. 12098
- gi No. 1345921

- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12099
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12100
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12101
- gi No. 1480465
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12102
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12103
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12104
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12105
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12106
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12107
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12108
- gi No. 1706248
- % Identity 73

- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12109
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12110
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12111
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12112
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12113
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12114
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12115
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12116
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12117
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12118
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71

- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12119
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12120
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12121
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12122
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12123
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12124
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1398: from 4 to 52
- Alignment No. 12125
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12126
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12127
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12128
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52



- Alignment No. 12129
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12130
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12131
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12132
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12133
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12134
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12135
- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12136
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12137
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12138
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12139
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

Maximum Length Sequence corresponding to clone ID 257355

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1399
- Ceres seq\_id 1500169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1400
- Ceres seq\_id 1500170
- Location of start within SEQ ID NO 1399: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12140
- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 1400: from 117 to 168 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257369

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1401
- Ceres seq\_id 1500179

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1402
- Ceres seq\_id 1500180
- Location of start within SEQ ID NO 1401: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1403
- Ceres seq\_id 1500181
- Location of start within SEQ ID NO 1401: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12141
- gi No. 2642158
- % Identity 70.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1403: from 11 to 155
- Alignment No. 12142
- gi No. 81286
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1403: from 4 to 17

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1404
- Ceres seq\_id 1500182
- Location of start within SEQ ID NO 1401: at 181 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12143
- gi No. 2642158
- % Identity 70.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1404: from 1 to 117

Maximum Length Sequence corresponding to clone ID 257391

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1405
- Ceres seq\_id 1500186

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1406
- Ceres seq\_id 1500187
- Location of start within SEQ ID NO 1405: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12144
- Syntaxin
- Location within SEQ ID NO 1406: from 51 to 178 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1407
- Ceres seq\_id 1500188
- Location of start within SEQ ID NO 1405: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12145
- Syntaxin
- Location within SEQ ID NO 1407: from 21 to 148 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1408
- Ceres seq\_id 1500189
- Location of start within SEQ ID NO 1405: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12146
- Syntaxin
- Location within SEQ ID NO 1408: from 1 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257556

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1409
- Ceres seq\_id 1500190

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1410
- Ceres seq\_id 1500191
- Location of start within SEQ ID NO 1409: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12147
- CTF/NF-I family
- Location within SEQ ID NO 1410: from 32 to 107 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12148
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 166 to 176
- Alignment No. 12149
- gi No. 3650031
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 163 to 173
- Alignment No. 12150
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 290 to 300

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1411
- Ceres seq\_id 1500192
- Location of start within SEQ ID NO 1409: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12151
- CTF/NF-I family
- Location within SEQ ID NO 1411: from 26 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12152
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 160 to 170
- Alignment No. 12153
- gi No. 3650031
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 157 to 167
- Alignment No. 12154
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 284 to 294

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1412
- Ceres seq\_id 1500193
- Location of start within SEQ ID NO 1409: at 612 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12155
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1412: from 87 to 97

Maximum Length Sequence corresponding to clone ID 257654

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1413
- Ceres seq\_id 1500198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1414
- Ceres seq\_id 1500199
- Location of start within SEQ ID NO 1413: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1415
- Ceres seq\_id 1500200
- Location of start within SEQ ID NO 1413: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

domain)

- Alignment No. 12156
- SRF-type transcription factor (DNA-binding and dimerisation
- Location within SEQ ID NO 1415: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12157
- gi No. 1001935
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12158
- gi No. 1049022
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12159
- gi No. 1076646
- % Identity 73.9
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12160
- gi No. 1076827
- % Identity 72.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 58

- Alignment No. 12161
- gi No. 1206003

- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12162
- gi No. 1208800
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1415: from 17 to 41
  
- Alignment No. 12163
- gi No. 1208802
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1415: from 17 to 41
  
- Alignment No. 12164
- gi No. 1208804
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1415: from 19 to 41
  
- Alignment No. 12165
- gi No. 1239961
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12166
- gi No. 1345965
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12167
- gi No. 1362195
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12168
- gi No. 1362196
- % Identity 78.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12169
- gi No. 1362197
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12170
- gi No. 1362198
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12171
- gi No. 1362199
- % Identity 76.3

- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12172
- gi No. 1362200
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12173
- gi No. 1362201
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1415: from 15 to 59
  
- Alignment No. 12174
- gi No. 1362202
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59
  
- Alignment No. 12175
- gi No. 1362203
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12176
- gi No. 1362204
- % Identity 81.8
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59
  
- Alignment No. 12177
- gi No. 1362205
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1415: from 16 to 60
  
- Alignment No. 12178
- gi No. 1362206
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59
  
- Alignment No. 12179
- gi No. 1362209
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12180
- gi No. 2160701
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1415: from 1 to 69
  
- Alignment No. 12181
- gi No. 2286109
- % Identity 71.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12182
- gi No. 2459835
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1415: from 1 to 56
- Alignment No. 12183
- gi No. 2463333
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12184
- gi No. 2979566
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12185
- gi No. 3023536
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12186
- gi No. 3114588
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12187
- gi No. 320596
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12188
- gi No. 322801
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1415: from 3 to 79
- Alignment No. 12189
- gi No. 3292820
- % Identity 71.8
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12190
- gi No. 3493647
- % Identity 80.2
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1415: from 1 to 81
- Alignment No. 12191
- gi No. 3646322
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1415: from 4 to 70



- Alignment No. 12192
- gi No. 3646340
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12193
- gi No. 3688591
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12194
- gi No. 3851331
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 16 to 71
  
- Alignment No. 12195
- gi No. 3851333
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1415: from 16 to 69
  
- Alignment No. 12196
- gi No. 4033710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
  
- Alignment No. 12197
- gi No. 4033721
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
  
- Alignment No. 12198
- gi No. 4033725
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1415: from 5 to 76
  
- Alignment No. 12199
- gi No. 4101710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
  
- Alignment No. 12200
- gi No. 4103486
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
  
- Alignment No. 12201
- gi No. 4322475
- % Identity 77.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1415: from 1 to 83

- Alignment No. 12202
- gi No. 497145
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35
  
- Alignment No. 12203
- gi No. 497147
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35
  
- Alignment No. 12204
- gi No. 497149
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35
  
- Alignment No. 12205
- gi No. 5002523
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1415: from 1 to 79
  
- Alignment No. 12206
- gi No. 5019431
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
  
- Alignment No. 12207
- gi No. 5031217
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12208
- gi No. 5051933
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
  
- Alignment No. 12209
- gi No. 5051935
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 12 to 70
  
- Alignment No. 12210
- gi No. 5070138
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12211
- gi No. 5295990
- % Identity 90.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
  
- Alignment No. 12212

- gi No. 542034
- % Identity 76.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1415: from 1 to 77
  
- Alignment No. 12213
- gi No. 542192
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 11 to 70
  
- Alignment No. 12214
- gi No. 5566279
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1415: from 12 to 51
  
- Alignment No. 12215
- gi No. 5712746
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1415: from 7 to 56
  
- Alignment No. 12216
- gi No. 5712748
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1415: from 7 to 56
  
- Alignment No. 12217
- gi No. 695686
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1415: from 1 to 69
  
- Alignment No. 12218
- gi No. 695688
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
  
- Alignment No. 12219
- gi No. 695690
- % Identity 73
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
  
- Alignment No. 12220
- gi No. 793906
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12221
- gi No. 81611
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1415: from 3 to 57
  
- Alignment No. 12222
- gi No. 862644

- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1415: from 7 to 79
  
- Alignment No. 12223
- gi No. 939779
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12224
- gi No. 939783
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1415: from 1 to 57
  
- Alignment No. 12225
- gi No. 951172
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1416
- Ceres seq\_id 1500201
- Location of start within SEQ ID NO 1413: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12226
- SRF-type transcription factor (DNA-binding and dimerisation domain)
- Location within SEQ ID NO 1416: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12227
- gi No. 1001935
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12228
- gi No. 1049022
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
  
- Alignment No. 12229
- gi No. 1076646
- % Identity 73.9
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
  
- Alignment No. 12230
- gi No. 1076827
- % Identity 72.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 51
  
- Alignment No. 12231
- gi No. 1206003

- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12232
- gi No. 1208800
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1416: from 10 to 34
  
- Alignment No. 12233
- gi No. 1208802
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1416: from 10 to 34
  
- Alignment No. 12234
- gi No. 1208804
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1416: from 12 to 34
  
- Alignment No. 12235
- gi No. 1239961
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12236
- gi No. 1345965
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12237
- gi No. 1362195
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12238
- gi No. 1362196
- % Identity 78.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12239
- gi No. 1362197
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12240
- gi No. 1362198
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12241
- gi No. 1362199
- % Identity 76.3

- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12242
- gi No. 1362200
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12243
- gi No. 1362201
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1416: from 8 to 52
  
- Alignment No. 12244
- gi No. 1362202
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52
  
- Alignment No. 12245
- gi No. 1362203
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12246
- gi No. 1362204
- % Identity 81.8
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52
  
- Alignment No. 12247
- gi No. 1362205
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1416: from 9 to 53
  
- Alignment No. 12248
- gi No. 1362206
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52
  
- Alignment No. 12249
- gi No. 1362209
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12250
- gi No. 2160701
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1416: from 1 to 62
  
- Alignment No. 12251
- gi No. 2286109
- % Identity 71.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12252
- gi No. 2459835
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
- Alignment No. 12253
- gi No. 2463333
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12254
- gi No. 2979566
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12255
- gi No. 3023536
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12256
- gi No. 3114588
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12257
- gi No. 320596
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12258
- gi No. 322801
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
- Alignment No. 12259
- gi No. 3292820
- % Identity 71.8
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12260
- gi No. 3493647
- % Identity 80.2
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1416: from 1 to 74
- Alignment No. 12261
- gi No. 3646322
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12262
- gi No. 3646340
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12263
- gi No. 3688591
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12264
- gi No. 3851331
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 9 to 64
  
- Alignment No. 12265
- gi No. 3851333
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1416: from 9 to 62
  
- Alignment No. 12266
- gi No. 4033710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12267
- gi No. 4033721
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12268
- gi No. 4033725
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12269
- gi No. 4101710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12270
- gi No. 4103486
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12271
- gi No. 4322475
- % Identity 77.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1416: from 1 to 76



- Alignment No. 12272
- gi No. 497145
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
  
- Alignment No. 12273
- gi No. 497147
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
  
- Alignment No. 12274
- gi No. 497149
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
  
- Alignment No. 12275
- gi No. 5002523
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
  
- Alignment No. 12276
- gi No. 5019431
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12277
- gi No. 5031217
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12278
- gi No. 5051933
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
  
- Alignment No. 12279
- gi No. 5051935
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 5 to 63
  
- Alignment No. 12280
- gi No. 5070138
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12281
- gi No. 5295990
- % Identity 90.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
  
- Alignment No. 12282

- gi No. 542034
- % Identity 76.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1416: from 1 to 70
  
- Alignment No. 12283
- gi No. 542192
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 4 to 63
  
- Alignment No. 12284
- gi No. 5566279
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1416: from 5 to 44
  
- Alignment No. 12285
- gi No. 5712746
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
  
- Alignment No. 12286
- gi No. 5712748
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
  
- Alignment No. 12287
- gi No. 695686
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1416: from 1 to 62
  
- Alignment No. 12288
- gi No. 695688
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12289
- gi No. 695690
- % Identity 73
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
  
- Alignment No. 12290
- gi No. 793906
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12291
- gi No. 81611
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1416: from 1 to 50
  
- Alignment No. 12292
- gi No. 862644

- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
  
- Alignment No. 12293
- gi No. 939779
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12294
- gi No. 939783
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1416: from 1 to 50
  
- Alignment No. 12295
- gi No. 951172
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

Maximum Length Sequence corresponding to clone ID 257713

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1417
- Ceres seq\_id 1500202

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1418
- Ceres seq\_id 1500203
- Location of start within SEQ ID NO 1417: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1419
- Ceres seq\_id 1500204
- Location of start within SEQ ID NO 1417: at 469 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12296
- gi No. 4680201
- % Identity 90.9
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1419: from 20 to 63
  
- Alignment No. 12297
- gi No. 4680489
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1419: from 1 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1420
- Ceres seq\_id 1500205
- Location of start within SEQ ID NO 1417: at 499 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12298
- gi No. 4680201
- % Identity 90.9
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1420: from 10 to 53
  
- Alignment No. 12299
- gi No. 4680489
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1420: from 1 to 53

Maximum Length Sequence corresponding to clone ID 257780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1421
- Ceres seq\_id 1500212

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1422
- Ceres seq\_id 1500213
- Location of start within SEQ ID NO 1421: at 351 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12300
- Ribosomal protein S17
- Location within SEQ ID NO 1422: from 1 to 57 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12301
- gi No. 1173221
- % Identity 85
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12302
- gi No. 1173223
- % Identity 88
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12303
- gi No. 133866
- % Identity 86.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12304
- gi No. 133867
- % Identity 92.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12305
- gi No. 166867
- % Identity 86.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12306
- gi No. 5708091
- % Identity 85.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
- Alignment No. 12307
- gi No. 81811
- % Identity 88.2
- Alignment Length 119
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

Maximum Length Sequence corresponding to clone ID 257928

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1423
- Ceres seq\_id 1500234

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1424
- Ceres seq\_id 1500235
- Location of start within SEQ ID NO 1423: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1425
- Ceres seq\_id 1500236
- Location of start within SEQ ID NO 1423: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1426
- Ceres seq\_id 1500237
- Location of start within SEQ ID NO 1423: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12308
- gi No. 2258365
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1426: from 46 to 92

- Alignment No. 12309

- gi No. 3342734
- % Identity 71.4
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1426: from 44 to 92

- Alignment No. 12310

- gi No. 3860916
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1426: from 49 to 92

Maximum Length Sequence corresponding to clone ID 257979

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1427
- Ceres seq\_id 1500246

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1428
- Ceres seq\_id 1500247
- Location of start within SEQ ID NO 1427: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12311
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1428: from 104 to 154 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12312
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1428: from 137 to 154
- Alignment No. 12313
- gi No. 403968
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1428: from 136 to 153
- Alignment No. 12314
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1428: from 135 to 154
- Alignment No. 12315
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1428: from 135 to 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1429
- Ceres seq\_id 1500248
- Location of start within SEQ ID NO 1427: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12316
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1429: from 85 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12317
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1429: from 118 to 135
- Alignment No. 12318
- gi No. 403968
- % Identity 77.8
- Alignment Length 18

- Location of Alignment in SEQ ID NO 1429: from 117 to 134
- Alignment No. 12319
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1429: from 116 to 135
- Alignment No. 12320
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1429: from 116 to 135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1430
- Ceres seq\_id 1500249
- Location of start within SEQ ID NO 1427: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12321
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1430: from 22 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12322
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1430: from 55 to 72
- Alignment No. 12323
- gi No. 403968
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1430: from 54 to 71
- Alignment No. 12324
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1430: from 53 to 72
- Alignment No. 12325
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1430: from 53 to 72

Maximum Length Sequence corresponding to clone ID 257985

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1431
- Ceres seq\_id 1500250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1432
- Ceres seq\_id 1500251
- Location of start within SEQ ID NO 1431: at 160 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12326
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1432: from 64 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12327
- gi No. 140346
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1432: from 45 to 57

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1433
- Ceres seq\_id 1500252
- Location of start within SEQ ID NO 1431: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 258340

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1434
- Ceres seq\_id 1500263

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1435
- Ceres seq\_id 1500264
- Location of start within SEQ ID NO 1434: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12328
- Syntaxin
- Location within SEQ ID NO 1435: from 5 to 306 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1436
- Ceres seq\_id 1500265
- Location of start within SEQ ID NO 1434: at 305 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12329
- Syntaxin
- Location within SEQ ID NO 1436: from 1 to 274 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1437
- Ceres seq\_id 1500266
- Location of start within SEQ ID NO 1434: at 401 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12330
- Syntaxin
- Location within SEQ ID NO 1437: from 1 to 242 aa.



(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 258706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1438
- Ceres seq\_id 1500283

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1439
- Ceres seq\_id 1500284
- Location of start within SEQ ID NO 1438: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1440
- Ceres seq\_id 1500285
- Location of start within SEQ ID NO 1438: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12331
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1440: from 42 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1441
- Ceres seq\_id 1500286
- Location of start within SEQ ID NO 1438: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12332
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1441: from 1 to 66

Maximum Length Sequence corresponding to clone ID 259439

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1442
- Ceres seq\_id 1500298

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1443
- Ceres seq\_id 1500299
- Location of start within SEQ ID NO 1442: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12333
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 1443: from 30 to 55 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1444
- Ceres seq\_id 1500300
- Location of start within SEQ ID NO 1442: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12334
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 1444: from 28 to 53 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1445
- Ceres seq\_id 1500301
- Location of start within SEQ ID NO 1442: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 259532

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1446
- Ceres seq\_id 1500305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1447
- Ceres seq\_id 1500306
- Location of start within SEQ ID NO 1446: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12335
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1447: from 95 to 166 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12336
- gi No. 1749748
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1447: from 127 to 166
- Alignment No. 12337
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
- Alignment No. 12338
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
- Alignment No. 12339
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12340
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1447: from 15 to 166
  
- Alignment No. 12341
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12342
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12343
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12344
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12345
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1448
- Ceres seq\_id 1500307
- Location of start within SEQ ID NO 1446: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12346
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1448: from 61 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12347
- gi No. 1749748
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1448: from 93 to 132
  
- Alignment No. 12348
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12349

- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12350
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12351
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1448: from 1 to 132
  
- Alignment No. 12352
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12353
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12354
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12355
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12356
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1449
- Ceres seq\_id 1500308
- Location of start within SEQ ID NO 1446: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12357
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1449: from 60 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12358
- gi No. 1749748

- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1449: from 92 to 131
- Alignment No. 12359
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12360
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12361
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12362
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1449: from 1 to 131
- Alignment No. 12363
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12364
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12365
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12366
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12367
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131

Maximum Length Sequence corresponding to clone ID 259555

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1450

- Ceres seq\_id 1500313  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 1451  
- Ceres seq\_id 1500314  
- Location of start within SEQ ID NO 1450: at 481 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
- Alignment No. 12368  
- gi No. 1708463  
- % Identity 77.8  
- Alignment Length 262  
- Location of Alignment in SEQ ID NO 1451: from 1 to 203

(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 1452  
- Ceres seq\_id 1500315  
- Location of start within SEQ ID NO 1450: at 514 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
- Alignment No. 12369  
- gi No. 1708463  
- % Identity 77.8  
- Alignment Length 262  
- Location of Alignment in SEQ ID NO 1452: from 1 to 192

(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 1453  
- Ceres seq\_id 1500316  
- Location of start within SEQ ID NO 1450: at 622 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
- Alignment No. 12370  
- gi No. 1708463  
- % Identity 77.8  
- Alignment Length 262  
- Location of Alignment in SEQ ID NO 1453: from 1 to 156

Maximum Length Sequence corresponding to clone ID 259571  
(A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 1454  
- Ceres seq\_id 1500321  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 1455  
- Ceres seq\_id 1500322  
- Location of start within SEQ ID NO 1454: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 1456  
- Ceres seq\_id 1500323  
- Location of start within SEQ ID NO 1454: at 158 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12371
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1456: from 38 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1457
- Ceres seq\_id 1500324
- Location of start within SEQ ID NO 1454: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12372
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1457: from 9 to 61 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260361

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1458
- Ceres seq\_id 1500367

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1459
- Ceres seq\_id 1500368
- Location of start within SEQ ID NO 1458: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12373
- Nuclear transition protein 2
- Location within SEQ ID NO 1459: from 17 to 102 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12374
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1459: from 74 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1460
- Ceres seq\_id 1500369
- Location of start within SEQ ID NO 1458: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12375
- gi No. 347455
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1460: from 27 to 37

Maximum Length Sequence corresponding to clone ID 260368

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1461
- Ceres seq\_id 1500370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1462
- Ceres seq\_id 1500371
- Location of start within SEQ ID NO 1461: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12376
- Zinc finger, C2H2 type
- Location within SEQ ID NO 1462: from 25 to 47 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12377
- gi No. 1361986
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1462: from 15 to 51
- Alignment No. 12378
- gi No. 1362015
- % Identity 76.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1462: from 22 to 51
- Alignment No. 12379
- gi No. 1362017
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51
- Alignment No. 12380
- gi No. 1362018
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1462: from 27 to 51
- Alignment No. 12381
- gi No. 1362020
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51
- Alignment No. 12382
- gi No. 1871188
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51
- Alignment No. 12383
- gi No. 790687
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1463
- Ceres seq\_id 1500372
- Location of start within SEQ ID NO 1461: at 347 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)



(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1464
- Ceres seq\_id 1500373
- Location of start within SEQ ID NO 1461: at 460 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1465
- Ceres seq\_id 1500374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1466
- Ceres seq\_id 1500375
- Location of start within SEQ ID NO 1465: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1467
- Ceres seq\_id 1500376
- Location of start within SEQ ID NO 1465: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12384
- Ubiquitin family
- Location within SEQ ID NO 1467: from 1 to 38 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12385
- gi No. 100525
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1467: from 1 to 31
- Alignment No. 12386
- gi No. 1050930
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24
- Alignment No. 12387
- gi No. 208891
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1467: from 1 to 23
- Alignment No. 12388
- gi No. 456779
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24
- Alignment No. 12389

- gi No. 899115
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24
- Alignment No. 12390
- gi No. 91870
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1467: from 1 to 23

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1468
- Ceres seq\_id 1500377
- Location of start within SEQ ID NO 1465: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260615

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1469
- Ceres seq\_id 1500387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1470
- Ceres seq\_id 1500388
- Location of start within SEQ ID NO 1469: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12391
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 23 to 223 aa.
- Alignment No. 12392
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 37 to 322 aa.
- Alignment No. 12393
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 146 to 327 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1471
- Ceres seq\_id 1500389
- Location of start within SEQ ID NO 1469: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12394
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 21 to 221 aa.
- Alignment No. 12395
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 35 to 320 aa.
- Alignment No. 12396

- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 144 to 325 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1472
- Ceres seq\_id 1500390
- Location of start within SEQ ID NO 1469: at 342 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12397
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 1 to 157 aa.
- Alignment No. 12398
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 1 to 256 aa.
- Alignment No. 12399
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 80 to 261 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260891

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1473
- Ceres seq\_id 1500391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1474
- Ceres seq\_id 1500392
- Location of start within SEQ ID NO 1473: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12400
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1474: from 5 to 108 aa.
- Alignment No. 12401
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1474: from 10 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1475
- Ceres seq\_id 1500393
- Location of start within SEQ ID NO 1473: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12402
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1475: from 1 to 100 aa.
- Alignment No. 12403
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1475: from 2 to 100 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1476
- Ceres seq\_id 1500394
- Location of start within SEQ ID NO 1473: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12404
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1476: from 1 to 69 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1477
- Ceres seq\_id 1500395

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1478
- Ceres seq\_id 1500396
- Location of start within SEQ ID NO 1477: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1479
- Ceres seq\_id 1500397
- Location of start within SEQ ID NO 1477: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12405
- Sperm histone P2
- Location within SEQ ID NO 1479: from 15 to 73 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1480
- Ceres seq\_id 1500398
- Location of start within SEQ ID NO 1477: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261148

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1481
- Ceres seq\_id 1500407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1482
- Ceres seq\_id 1500408
- Location of start within SEQ ID NO 1481: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1483
- Ceres seq\_id 1500409
- Location of start within SEQ ID NO 1481: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12406
- GTP cyclohydrolase I
- Location within SEQ ID NO 1483: from 80 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1484
- Ceres seq\_id 1500410
- Location of start within SEQ ID NO 1481: at 128 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12407
- GTP cyclohydrolase I
- Location within SEQ ID NO 1484: from 38 to 89 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1485
- Ceres seq\_id 1500422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1486
- Ceres seq\_id 1500423
- Location of start within SEQ ID NO 1485: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12408
- Ribosomal protein L21e
- Location within SEQ ID NO 1486: from 28 to 108 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12409
- gi No. 2851508
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1486: from 27 to 108

- Alignment No. 12410

- gi No. 3885884

- % Identity 92.7

- Alignment Length 82

- Location of Alignment in SEQ ID NO 1486: from 27 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1487
- Ceres seq\_id 1500424

- Location of start within SEQ ID NO 1485: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1488
- Ceres seq\_id 1500425
- Location of start within SEQ ID NO 1485: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12411
- Ribosomal protein L21e
- Location within SEQ ID NO 1488: from 2 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12412
- gi No. 2851508
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1488: from 1 to 82
- Alignment No. 12413
- gi No. 3885884
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1488: from 1 to 82

Maximum Length Sequence corresponding to clone ID 261674

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1489
- Ceres seq\_id 1500464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1490
- Ceres seq\_id 1500465
- Location of start within SEQ ID NO 1489: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12414
- gi No. 2145062
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1490: from 82 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1491
- Ceres seq\_id 1500466
- Location of start within SEQ ID NO 1489: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12415
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1491: from 11 to 59 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1492
  - Ceres seq\_id 1500467
  - Location of start within SEQ ID NO 1489: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 12416
  - gi No. 3875441
  - % Identity 70.6
  - Alignment Length 17
  - Location of Alignment in SEQ ID NO 1492: from 81 to 97

Maximum Length Sequence corresponding to clone ID 261748

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1493
  - Ceres seq\_id 1500468
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1494
  - Ceres seq\_id 1500469
  - Location of start within SEQ ID NO 1493: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12417
- Sm protein
- Location within SEQ ID NO 1494: from 94 to 155 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1495
  - Ceres seq\_id 1500470
  - Location of start within SEQ ID NO 1493: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12418
- Sm protein
- Location within SEQ ID NO 1495: from 35 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261790

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1496
  - Ceres seq\_id 1500474
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1497
  - Ceres seq\_id 1500475
  - Location of start within SEQ ID NO 1496: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1498
  - Ceres seq\_id 1500476
  - Location of start within SEQ ID NO 1496: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12419
- Cytochrome P450
- Location within SEQ ID NO 1498: from 59 to 127 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1499
- Ceres seq\_id 1500477
- Location of start within SEQ ID NO 1496: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12420
- Cytochrome P450
- Location within SEQ ID NO 1499: from 36 to 104 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261801

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1500
- Ceres seq\_id 1500478

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1501
- Ceres seq\_id 1500479
- Location of start within SEQ ID NO 1500: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12421
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1501: from 49 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1502
- Ceres seq\_id 1500480
- Location of start within SEQ ID NO 1500: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1503
- Ceres seq\_id 1500481

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1504
- Ceres seq\_id 1500482
- Location of start within SEQ ID NO 1503: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12422
- Metallo-beta-lactamase superfamily



- Location within SEQ ID NO 1504: from 56 to 160 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1505
- Ceres seq\_id 1500483
- Location of start within SEQ ID NO 1503: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12423
- Metallo-beta-lactamase superfamily
- Location within SEQ ID NO 1505: from 34 to 138 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261831

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1506
- Ceres seq\_id 1500487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1507
- Ceres seq\_id 1500488
- Location of start within SEQ ID NO 1506: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1508
- Ceres seq\_id 1500489
- Location of start within SEQ ID NO 1506: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12424
- gi No. 132933
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1508: from 26 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1509
- Ceres seq\_id 1500490
- Location of start within SEQ ID NO 1506: at 221 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261853

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1510
- Ceres seq\_id 1500491

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1511
- Ceres seq\_id 1500492
- Location of start within SEQ ID NO 1510: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12425
- gi No. 3834316
- % Identity 96.9
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1511: from 1 to 173

Maximum Length Sequence corresponding to clone ID 261966

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1512
- Ceres seq\_id 1500495

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1513
- Ceres seq\_id 1500496
- Location of start within SEQ ID NO 1512: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12426
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1513: from 1 to 135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1514
- Ceres seq\_id 1500497
- Location of start within SEQ ID NO 1512: at 93 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12427
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1514: from 1 to 130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1515
- Ceres seq\_id 1500498
- Location of start within SEQ ID NO 1512: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12428
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1515: from 1 to 122

Maximum Length Sequence corresponding to clone ID 261978

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1516
- Ceres seq\_id 1500501

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1517
- Ceres seq\_id 1500502
- Location of start within SEQ ID NO 1516: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12429
- gi No. 1321924
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1517: from 100 to 122
  
- Alignment No. 12430
- gi No. 1944132
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1517: from 101 to 122
  
- Alignment No. 12431
- gi No. 2894607
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1517: from 101 to 125
  
- Alignment No. 12432
- gi No. 4218537
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1517: from 96 to 122
  
- Alignment No. 12433
- gi No. 5091624
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1517: from 103 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1518
- Ceres seq\_id 1500503
- Location of start within SEQ ID NO 1516: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261997

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1519
- Ceres seq\_id 1500504

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1520
- Ceres seq\_id 1500505
- Location of start within SEQ ID NO 1519: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12434
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1520: from 64 to 161 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12435
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1520: from 28 to 161
  
- Alignment No. 12436
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1520: from 138 to 161
  
- Alignment No. 12437
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1520: from 138 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1521
- Ceres seq\_id 1500506
- Location of start within SEQ ID NO 1519: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12438
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1521: from 50 to 147 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12439
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1521: from 14 to 147
  
- Alignment No. 12440
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1521: from 124 to 147
  
- Alignment No. 12441
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1521: from 124 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1522
- Ceres seq\_id 1500507
- Location of start within SEQ ID NO 1519: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12442
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1522: from 7 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12443
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1522: from 1 to 104
  
- Alignment No. 12444
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1522: from 81 to 104
  
- Alignment No. 12445
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1522: from 81 to 104

Maximum Length Sequence corresponding to clone ID 262057

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1523
- Ceres seq\_id 1500516

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1524
- Ceres seq\_id 1500517
- Location of start within SEQ ID NO 1523: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1525
- Ceres seq\_id 1500518
- Location of start within SEQ ID NO 1523: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12446
- gi No. 4966357
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1525: from 32 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1526
- Ceres seq\_id 1500519
- Location of start within SEQ ID NO 1523: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 262215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1527
- Ceres seq\_id 1500539

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1528
- Ceres seq\_id 1500540

- Location of start within SEQ ID NO 1527: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12447
- gi No. 2342684
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1528: from 1 to 16
- Alignment No. 12448
- gi No. 3540195
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1528: from 3 to 30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1529
- Ceres seq\_id 1500541
- Location of start within SEQ ID NO 1527: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1530
- Ceres seq\_id 1500542
- Location of start within SEQ ID NO 1527: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 262351

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1531
- Ceres seq\_id 1500554

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1532
- Ceres seq\_id 1500555
- Location of start within SEQ ID NO 1531: at 189 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12449
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1532: from 1 to 363
- Alignment No. 12450
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1532: from 313 to 363
- Alignment No. 12451
- gi No. 4539340

- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1532: from 1 to 363
  
- Alignment No. 12452
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1532: from 293 to 363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1533
- Ceres seq\_id 1500556
- Location of start within SEQ ID NO 1531: at 246 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12453
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1533: from 1 to 344
  
- Alignment No. 12454
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1533: from 294 to 344
  
- Alignment No. 12455
- gi No. 4539340
- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1533: from 1 to 344
  
- Alignment No. 12456
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1533: from 274 to 344

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1534
- Ceres seq\_id 1500557
- Location of start within SEQ ID NO 1531: at 585 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12457
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1534: from 1 to 231
  
- Alignment No. 12458
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1534: from 181 to 231

- Alignment No. 12459
- gi No. 4539340
- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1534: from 1 to 231
  
- Alignment No. 12460
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1534: from 161 to 231

Maximum Length Sequence corresponding to clone ID 262550

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1535
- Ceres seq\_id 1500558

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1536
- Ceres seq\_id 1500559
- Location of start within SEQ ID NO 1535: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12461
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1536: from 123 to 178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1537
- Ceres seq\_id 1500560
- Location of start within SEQ ID NO 1535: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12462
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1537: from 119 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1538
- Ceres seq\_id 1500561
- Location of start within SEQ ID NO 1535: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12463
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1538: from 89 to 144

Maximum Length Sequence corresponding to clone ID 262802

(A) Polynucleotide Sequence



- Pat. Appln. SEQ ID NO 1539
- Ceres seq\_id 1500562

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1540
- Ceres seq\_id 1500563
- Location of start within SEQ ID NO 1539: at 843 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12464
- Cytochrome P450
- Location within SEQ ID NO 1540: from 1 to 226 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1541
- Ceres seq\_id 1500564
- Location of start within SEQ ID NO 1539: at 960 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12465
- Cytochrome P450
- Location within SEQ ID NO 1541: from 1 to 187 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1542
- Ceres seq\_id 1500565
- Location of start within SEQ ID NO 1539: at 1095 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12466
- Cytochrome P450
- Location within SEQ ID NO 1542: from 1 to 142 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 263816

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1543
- Ceres seq\_id 1500614

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1544
- Ceres seq\_id 1500615
- Location of start within SEQ ID NO 1543: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12467
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1544: from 51 to 308 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12468
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277

- Location of Alignment in SEQ ID NO 1544: from 37 to 313

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1545
- Ceres seq\_id 1500616
- Location of start within SEQ ID NO 1543: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12469
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1545: from 24 to 281 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12470
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 1545: from 10 to 286

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1546
- Ceres seq\_id 1500617
- Location of start within SEQ ID NO 1543: at 339 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12471
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1546: from 1 to 196 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12472
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 1546: from 1 to 201

Maximum Length Sequence corresponding to clone ID 264799

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1547
- Ceres seq\_id 1500618

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1548
- Ceres seq\_id 1500619
- Location of start within SEQ ID NO 1547: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12473
- Jacalin-like lectin domain
- Location within SEQ ID NO 1548: from 107 to 244 aa.

- Alignment No. 12474
- Jacalin-like lectin domain
- Location within SEQ ID NO 1548: from 264 to 391 aa.

- Alignment No. 12475
- von Willebrand factor type A domain
- Location within SEQ ID NO 1548: from 104 to 212 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12476
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1548: from 92 to 402
  
- Alignment No. 12477
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1548: from 92 to 404

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1549
- Ceres seq\_id 1500620
- Location of start within SEQ ID NO 1547: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12478
- Jacalin-like lectin domain
- Location within SEQ ID NO 1549: from 63 to 200 aa.
  
- Alignment No. 12479
- Jacalin-like lectin domain
- Location within SEQ ID NO 1549: from 220 to 347 aa.
  
- Alignment No. 12480
- von Willebrand factor type A domain
- Location within SEQ ID NO 1549: from 60 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12481
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1549: from 48 to 358
  
- Alignment No. 12482
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1549: from 48 to 360

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1550
- Ceres seq\_id 1500621
- Location of start within SEQ ID NO 1547: at 274 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12483
- Jacalin-like lectin domain
- Location within SEQ ID NO 1550: from 16 to 153 aa.
  
- Alignment No. 12484
- Jacalin-like lectin domain
- Location within SEQ ID NO 1550: from 173 to 300 aa.
  
- Alignment No. 12485

- von Willebrand factor type A domain
- Location within SEQ ID NO 1550: from 13 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12486
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1550: from 1 to 311
- Alignment No. 12487
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1550: from 1 to 313

Maximum Length Sequence corresponding to clone ID 264837

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1551
- Ceres seq\_id 1500622

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1552
- Ceres seq\_id 1500623
- Location of start within SEQ ID NO 1551: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12488
- gi No. 4586265
- % Identity 70.6
- Alignment Length 143
- Location of Alignment in SEQ ID NO 1552: from 1 to 136
- Alignment No. 12489
- gi No. 5123937
- % Identity 100
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1552: from 1 to 136

Maximum Length Sequence corresponding to clone ID 265926

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1553
- Ceres seq\_id 1500633

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1554
- Ceres seq\_id 1500634
- Location of start within SEQ ID NO 1553: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12490
- gi No. 1171429
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1554: from 7 to 36
- Alignment No. 12491
- gi No. 2129537
- % Identity 80

- Alignment Length 30
- Location of Alignment in SEQ ID NO 1554: from 7 to 36
- Alignment No. 12492
- gi No. 2652938
- % Identity 80.6
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1554: from 6 to 36
- Alignment No. 12493
- gi No. 4836931
- % Identity 77.4
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1554: from 6 to 36

Maximum Length Sequence corresponding to clone ID 266518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1555
- Ceres seq\_id 1500645

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1556
- Ceres seq\_id 1500646
- Location of start within SEQ ID NO 1555: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12494
- short chain dehydrogenase
- Location within SEQ ID NO 1556: from 72 to 264 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12495
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1556: from 50 to 353
- Alignment No. 12496
- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1556: from 50 to 376
- Alignment No. 12497
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1556: from 1 to 232
- Alignment No. 12498
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1556: from 201 to 376
- Alignment No. 12499
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1556: from 72 to 376

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1557
- Ceres seq\_id 1500647
- Location of start within SEQ ID NO 1555: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12500
- short chain dehydrogenase
- Location within SEQ ID NO 1557: from 50 to 242 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12501
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1557: from 28 to 331
- Alignment No. 12502
- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1557: from 28 to 354
- Alignment No. 12503
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1557: from 1 to 210
- Alignment No. 12504
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1557: from 179 to 354
- Alignment No. 12505
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1557: from 50 to 354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1558
- Ceres seq\_id 1500648
- Location of start within SEQ ID NO 1555: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12506
- short chain dehydrogenase
- Location within SEQ ID NO 1558: from 47 to 239 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12507
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1558: from 25 to 328
- Alignment No. 12508

- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1558: from 25 to 351
  
- Alignment No. 12509
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1558: from 1 to 207
  
- Alignment No. 12510
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1558: from 176 to 351
  
- Alignment No. 12511
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1558: from 47 to 351

Maximum Length Sequence corresponding to clone ID 266520

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1559
- Ceres seq\_id 1500649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1560
- Ceres seq\_id 1500650
- Location of start within SEQ ID NO 1559: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12512
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1560: from 14 to 332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1561
- Ceres seq\_id 1500651
- Location of start within SEQ ID NO 1559: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12513
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1561: from 1 to 247

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1562
- Ceres seq\_id 1500652
- Location of start within SEQ ID NO 1559: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12514
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1562: from 1 to 244

Maximum Length Sequence corresponding to clone ID 266544

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1563
- Ceres seq\_id 1500653

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1564
- Ceres seq\_id 1500654
- Location of start within SEQ ID NO 1563: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12515
- Regulator of chromosome condensation (RCC1)
- Location within SEQ ID NO 1564: from 34 to 92 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1565
- Ceres seq\_id 1500655
- Location of start within SEQ ID NO 1563: at 218 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1566
- Ceres seq\_id 1500656
- Location of start within SEQ ID NO 1563: at 247 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12516
- Regulator of chromosome condensation (RCC1)
- Location within SEQ ID NO 1566: from 1 to 49 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266710

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1567
- Ceres seq\_id 1500661

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1568
- Ceres seq\_id 1500662
- Location of start within SEQ ID NO 1567: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12517



- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1568: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1569
- Ceres seq\_id 1500663
- Location of start within SEQ ID NO 1567: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12518
- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1569: from 1 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1570
- Ceres seq\_id 1500664
- Location of start within SEQ ID NO 1567: at 36 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12519
- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1570: from 1 to 154

Maximum Length Sequence corresponding to clone ID 266712

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1571
- Ceres seq\_id 1500665

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1572
- Ceres seq\_id 1500666
- Location of start within SEQ ID NO 1571: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12520
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1572: from 8 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12521
- gi No. 1076672
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
- Alignment No. 12522
- gi No. 1076731
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

- Alignment No. 12523
  - gi No. 1076731
  - % Identity 72.4
  - Alignment Length 105
  - Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12524
  - gi No. 1229138
  - % Identity 72.3
  - Alignment Length 101
  - Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12525
  - gi No. 1346180
  - % Identity 78.4
  - Alignment Length 97
  - Location of Alignment in SEQ ID NO 1572: from 3 to 99
- Alignment No. 12526
  - gi No. 1346181
  - % Identity 76.3
  - Alignment Length 97
  - Location of Alignment in SEQ ID NO 1572: from 3 to 99
- Alignment No. 12527
  - gi No. 1710625
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 1572: from 86 to 99
- Alignment No. 12528
  - gi No. 1710626
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 1572: from 86 to 96
- Alignment No. 12529
  - gi No. 1710626
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 1572: from 86 to 99
- Alignment No. 12530
  - gi No. 1710626
  - % Identity 73.3
  - Alignment Length 15
  - Location of Alignment in SEQ ID NO 1572: from 86 to 100
- Alignment No. 12531
  - gi No. 1710627
  - % Identity 76.9
  - Alignment Length 13
  - Location of Alignment in SEQ ID NO 1572: from 88 to 100
- Alignment No. 12532
  - gi No. 1934994
  - % Identity 73.7
  - Alignment Length 99
  - Location of Alignment in SEQ ID NO 1572: from 2 to 100
- Alignment No. 12533

- gi No. 2119042
- % Identity 77.9
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12534
- gi No. 2119042
- % Identity 71.9
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12535
- gi No. 2119043
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12536
- gi No. 2119044
- % Identity 75.7
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
  
- Alignment No. 12537
- gi No. 2129944
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100
  
- Alignment No. 12538
- gi No. 2143460
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1572: from 87 to 98
  
- Alignment No. 12539
- gi No. 2226370
- % Identity 76.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12540
- gi No. 2267567
- % Identity 73.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
  
- Alignment No. 12541
- gi No. 2267593
- % Identity 70.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12542
- gi No. 2293480
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12543
- gi No. 2293480

- % Identity 70.4
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1572: from 3 to 100
  
- Alignment No. 12544
- gi No. 2331131
- % Identity 72.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12545
- gi No. 2331133
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12546
- gi No. 2624326
- % Identity 74.5
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12547
- gi No. 2668742
- % Identity 71.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
  
- Alignment No. 12548
- gi No. 2674201
- % Identity 71.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
  
- Alignment No. 12549
- gi No. 283664
- % Identity 70.6
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1572: from 84 to 100
  
- Alignment No. 12550
- gi No. 3914466
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1572: from 59 to 78
  
- Alignment No. 12551
- gi No. 423560
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1572: from 87 to 98
  
- Alignment No. 12552
- gi No. 4567236
- % Identity 82.5
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1572: from 39 to 101
  
- Alignment No. 12553
- gi No. 4567236
- % Identity 73.2

- Alignment Length 71
- Location of Alignment in SEQ ID NO 1572: from 39 to 101
  
- Alignment No. 12554
- gi No. 4587684
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1572: from 49 to 65
  
- Alignment No. 12555
- gi No. 469072
- % Identity 76.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12556
- gi No. 4938296
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
  
- Alignment No. 12557
- gi No. 4938296
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
  
- Alignment No. 12558
- gi No. 5031693
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100
  
- Alignment No. 12559
- gi No. 542649
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 86 to 99
  
- Alignment No. 12560
- gi No. 544416
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
  
- Alignment No. 12561
- gi No. 544416
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12562
- gi No. 544421
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1572: from 22 to 100
  
- Alignment No. 12563
- gi No. 544423
- % Identity 74
- Alignment Length 100

- Location of Alignment in SEQ ID NO 1572: from 2 to 101
- Alignment No. 12564
- gi No. 544424
- % Identity 79.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
- Alignment No. 12565
- gi No. 544424
- % Identity 73.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
- Alignment No. 12566
- gi No. 544425
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 88 to 101
- Alignment No. 12567
- gi No. 544425
- % Identity 94.1
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12568
- gi No. 544425
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12569
- gi No. 544426
- % Identity 82.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12570
- gi No. 544426
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1572: from 1 to 99
- Alignment No. 12571
- gi No. 5726567
- % Identity 70
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
- Alignment No. 12572
- gi No. 82696
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 2 to 100
- Alignment No. 12573
- gi No. 974605
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

- Alignment No. 12574
- gi No. 974605
- % Identity 73.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

Maximum Length Sequence corresponding to clone ID 266730

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1573
- Ceres seq\_id 1500667

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1574
- Ceres seq\_id 1500668
- Location of start within SEQ ID NO 1573: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1575
- Ceres seq\_id 1500669
- Location of start within SEQ ID NO 1573: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1576
- Ceres seq\_id 1500670
- Location of start within SEQ ID NO 1573: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12575
- gi No. 1513292
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1576: from 9 to 49

- Alignment No. 12576
- gi No. 4539026
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1576: from 12 to 45

Maximum Length Sequence corresponding to clone ID 266771

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1577
- Ceres seq\_id 1500675

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1578
- Ceres seq\_id 1500676
- Location of start within SEQ ID NO 1577: at 450 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12577

- Zinc finger, C2H2 type
- Location within SEQ ID NO 1578: from 57 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12578
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1578: from 3 to 202

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1579
- Ceres seq\_id 1500677
- Location of start within SEQ ID NO 1577: at 645 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12579
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1579: from 1 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1580
- Ceres seq\_id 1500678
- Location of start within SEQ ID NO 1577: at 675 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12580
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1580: from 1 to 127

Maximum Length Sequence corresponding to clone ID 266884

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1581
- Ceres seq\_id 1500679

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1582
- Ceres seq\_id 1500680
- Location of start within SEQ ID NO 1581: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12581
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1582: from 69 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12582
- gi No. 4914417
- % Identity 72.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1582: from 15 to 129

(B) Polypeptide Sequence



- Pat. Appln. SEQ ID NO 1583
- Ceres seq\_id 1500681
- Location of start within SEQ ID NO 1581: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12583
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1583: from 55 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12584
- gi No. 4914417
- % Identity 72.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1583: from 1 to 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1584
- Ceres seq\_id 1500682
- Location of start within SEQ ID NO 1581: at 345 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266907

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1585
- Ceres seq\_id 1500683

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1586
- Ceres seq\_id 1500684
- Location of start within SEQ ID NO 1585: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12585
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1586: from 17 to 171

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1587
- Ceres seq\_id 1500685
- Location of start within SEQ ID NO 1585: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12586
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1587: from 1 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1588
- Ceres seq\_id 1500686

- Location of start within SEQ ID NO 1585: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12587
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1588: from 1 to 115

Maximum Length Sequence corresponding to clone ID 267121

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1589
- Ceres seq\_id 1500687

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1590
- Ceres seq\_id 1500688
- Location of start within SEQ ID NO 1589: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12588
- Myb-like DNA-binding domain
- Location within SEQ ID NO 1590: from 5 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12589
- gi No. 2832480
- % Identity 100
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
- Alignment No. 12590
- gi No. 2832554
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
- Alignment No. 12591
- gi No. 3063725
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
- Alignment No. 12592
- gi No. 3941468
- % Identity 98.4
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1590: from 1 to 249
- Alignment No. 12593
- gi No. 3941496
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 1590: from 66 to 108
- Alignment No. 12594
- gi No. 4490312
- % Identity 77.1
- Alignment Length 109

- Location of Alignment in SEQ ID NO 1590: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1591
- Ceres seq\_id 1500689
- Location of start within SEQ ID NO 1589: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12595
- Myb-like DNA-binding domain
- Location within SEQ ID NO 1591: from 4 to 50 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12596
- gi No. 2832480
- % Identity 100
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12597
- gi No. 2832554
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12598
- gi No. 3063725
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12599
- gi No. 3941468
- % Identity 98.4
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1591: from 1 to 248
- Alignment No. 12600
- gi No. 3941496
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 1591: from 65 to 107
- Alignment No. 12601
- gi No. 4490312
- % Identity 77.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1591: from 1 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1592
- Ceres seq\_id 1500690
- Location of start within SEQ ID NO 1589: at 452 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12602
- gi No. 3941468
- % Identity 98.4

- Alignment Length 249
- Location of Alignment in SEQ ID NO 1592: from 1 to 148

Maximum Length Sequence corresponding to clone ID 267357

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1593
- Ceres seq\_id 1500693

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1594
- Ceres seq\_id 1500694
- Location of start within SEQ ID NO 1593: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12603
- Ribosomal protein L36e
- Location within SEQ ID NO 1594: from 6 to 93 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12604
- gi No. 3236242
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1594: from 1 to 102

Maximum Length Sequence corresponding to clone ID 267559

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1595
- Ceres seq\_id 1500695

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1596
- Ceres seq\_id 1500696
- Location of start within SEQ ID NO 1595: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12605
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1596: from 11 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1597
- Ceres seq\_id 1500697
- Location of start within SEQ ID NO 1595: at 252 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12606
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1597: from 3 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1598
- Ceres seq\_id 1500698
- Location of start within SEQ ID NO 1595: at 255 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12607
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1598: from 2 to 89

Maximum Length Sequence corresponding to clone ID 268117

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1599
- Ceres seq\_id 1500703

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1600
- Ceres seq\_id 1500704
- Location of start within SEQ ID NO 1599: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12608
- gi No. 2924518
- % Identity 71.5
- Alignment Length 258
- Location of Alignment in SEQ ID NO 1600: from 13 to 264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1601
- Ceres seq\_id 1500705
- Location of start within SEQ ID NO 1599: at 569 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12609
- gi No. 2924518
- % Identity 71.5
- Alignment Length 258
- Location of Alignment in SEQ ID NO 1601: from 1 to 187

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1602
- Ceres seq\_id 1500706
- Location of start within SEQ ID NO 1599: at 659 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12610
- gi No. 2924518
- % Identity 71.5
- Alignment Length 258
- Location of Alignment in SEQ ID NO 1602: from 1 to 157

Maximum Length Sequence corresponding to clone ID 268199

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1603
- Ceres seq\_id 1500707

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1604
- Ceres seq\_id 1500708
- Location of start within SEQ ID NO 1603: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12611
- Asparaginase
- Location within SEQ ID NO 1604: from 20 to 182 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1605
- Ceres seq\_id 1500709
- Location of start within SEQ ID NO 1603: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12612
- Asparaginase
- Location within SEQ ID NO 1605: from 2 to 164 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1606
- Ceres seq\_id 1500710
- Location of start within SEQ ID NO 1603: at 292 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12613
- Asparaginase
- Location within SEQ ID NO 1606: from 1 to 85 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268536

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1607
- Ceres seq\_id 1500719

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1608
- Ceres seq\_id 1500720
- Location of start within SEQ ID NO 1607: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12614
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1608: from 117 to 222 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1609
- Ceres seq\_id 1500721
- Location of start within SEQ ID NO 1607: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12615
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1609: from 105 to 210 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1610
- Ceres seq\_id 1500722
- Location of start within SEQ ID NO 1607: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12616
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1610: from 23 to 128 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268621

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1611
- Ceres seq\_id 1500734

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1612
- Ceres seq\_id 1500735
- Location of start within SEQ ID NO 1611: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12617
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1612: from 23 to 78

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1613
- Ceres seq\_id 1500736
- Location of start within SEQ ID NO 1611: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12618
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1613: from 1 to 56

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1614
- Ceres seq\_id 1500737
- Location of start within SEQ ID NO 1611: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12619
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1614: from 1 to 50

Maximum Length Sequence corresponding to clone ID 268835

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1615
- Ceres seq\_id 1500742

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1616
- Ceres seq\_id 1500743
- Location of start within SEQ ID NO 1615: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12620
- gi No. 3510256
- % Identity 98.9
- Alignment Length 174
- Location of Alignment in SEQ ID NO 1616: from 1 to 174

Maximum Length Sequence corresponding to clone ID 268982

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1617
- Ceres seq\_id 1500748

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1618
- Ceres seq\_id 1500749
- Location of start within SEQ ID NO 1617: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12621
- Core histone H2A/H2B/H3/H4
- Location within SEQ ID NO 1618: from 17 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12622
- gi No. 10253
- % Identity 89
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12623
- gi No. 103198
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12624
- gi No. 104698
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1618: from 2 to 26

- Alignment No. 12625
- gi No. 1053045
- % Identity 95.3



- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12626
- gi No. 1053047
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12627
- gi No. 1053053
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12628
- gi No. 1053055
- % Identity 86.2
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1618: from 1 to 29
  
- Alignment No. 12629
- gi No. 1053057
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12630
- gi No. 1053059
- % Identity 93.7
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12631
- gi No. 1076583
- % Identity 95
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1618: from 1 to 60
  
- Alignment No. 12632
- gi No. 1079199
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12633
- gi No. 1085857
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1618: from 34 to 116
  
- Alignment No. 12634
- gi No. 1085858
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1618: from 34 to 116
  
- Alignment No. 12635
- gi No. 108593
- % Identity 76.2
- Alignment Length 21

- Location of Alignment in SEQ ID NO 1618: from 112 to 132
- Alignment No. 12636
- gi No. 109977
- % Identity 91.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1618: from 2 to 36
- Alignment No. 12637
- gi No. 1166436
- % Identity 81.4
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1618: from 36 to 94
- Alignment No. 12638
- gi No. 1197519
- % Identity 85.5
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1618: from 13 to 136
- Alignment No. 12639
- gi No. 1208642
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12640
- gi No. 1208644
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12641
- gi No. 1208646
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12642
- gi No. 1208656
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12643
- gi No. 1208658
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12644
- gi No. 1208664
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12645
- gi No. 1208668
- % Identity 92.9
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12646
- gi No. 1208699
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12647
- gi No. 1208701
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12648
- gi No. 1208707
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12649
- gi No. 1208715
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12650
- gi No. 1208725
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12651
- gi No. 1208727
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12652
- gi No. 1213291
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12653
- gi No. 1213307
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12654
- gi No. 1213313
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12655
- gi No. 1213315
- % Identity 89.3
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12656
- gi No. 122065
- % Identity 86
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12657
- gi No. 122066
- % Identity 84.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12658
- gi No. 122068
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12659
- gi No. 122070
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12660
- gi No. 122071
- % Identity 85.4
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
  
- Alignment No. 12661
- gi No. 122072
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
  
- Alignment No. 12662
- gi No. 122074
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12663
- gi No. 122076
- % Identity 85.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12664
- gi No. 122077
- % Identity 84.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12665
- gi No. 122078
- % Identity 77.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12666

- gi No. 122079
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12667
- gi No. 122080
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12668
- gi No. 122081
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12669
- gi No. 122082
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12670
- gi No. 122083
- % Identity 93.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12671
- gi No. 122084
- % Identity 96.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1618: from 57 to 136
  
- Alignment No. 12672
- gi No. 122085
- % Identity 94.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12673
- gi No. 122086
- % Identity 83.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12674
- gi No. 122087
- % Identity 94.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12675
- gi No. 122088
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12676
- gi No. 122089

- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12677
- gi No. 122090
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12678
- gi No. 122091
- % Identity 83.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12679
- gi No. 1360625
- % Identity 79.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12680
- gi No. 1360627
- % Identity 77.6
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1618: from 1 to 96
  
- Alignment No. 12681
- gi No. 1362108
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12682
- gi No. 1362171
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1618: from 105 to 136
  
- Alignment No. 12683
- gi No. 159967
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12684
- gi No. 161319
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12685
- gi No. 166384
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12686
- gi No. 1708108
- % Identity 91.9

- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12687
- gi No. 1708109
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12688
- gi No. 171637
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1618: from 3 to 35
  
- Alignment No. 12689
- gi No. 1723293
- % Identity 91.2
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 46 to 136
  
- Alignment No. 12690
- gi No. 1731925
- % Identity 91.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 3 to 117
  
- Alignment No. 12691
- gi No. 1762791
- % Identity 71.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1618: from 4 to 136
  
- Alignment No. 12692
- gi No. 1763308
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12693
- gi No. 1870700
- % Identity 91.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1618: from 1 to 111
  
- Alignment No. 12694
- gi No. 1881589
- % Identity 89.6
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1618: from 89 to 136
  
- Alignment No. 12695
- gi No. 1881594
- % Identity 91
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1618: from 1 to 87
  
- Alignment No. 12696
- gi No. 1881601
- % Identity 93.1
- Alignment Length 87

- Location of Alignment in SEQ ID NO 1618: from 1 to 87
- Alignment No. 12697
- gi No. 19611
- % Identity 94.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 1618: from 14 to 136
- Alignment No. 12698
- gi No. 19614
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1618: from 79 to 136
- Alignment No. 12699
- gi No. 208461
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1618: from 17 to 35
- Alignment No. 12700
- gi No. 208463
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1618: from 3 to 35
- Alignment No. 12701
- gi No. 2116601
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12702
- gi No. 211855
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12703
- gi No. 2119011
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12704
- gi No. 2119012
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12705
- gi No. 2119013
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12706
- gi No. 2119014
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 61 to 136



- Alignment No. 12707
- gi No. 2119018
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12708
- gi No. 2135356
- % Identity 92.6
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1618: from 1 to 27
  
- Alignment No. 12709
- gi No. 2136686
- % Identity 93.1
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1618: from 2 to 30
  
- Alignment No. 12710
- gi No. 2147399
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1618: from 1 to 39
  
- Alignment No. 12711
- gi No. 2252516
- % Identity 92.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1618: from 1 to 38
  
- Alignment No. 12712
- gi No. 2253166
- % Identity 87.1
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1618: from 1 to 62
  
- Alignment No. 12713
- gi No. 2253615
- % Identity 79.1
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12714
- gi No. 2909431
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12715
- gi No. 2995213
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12716
- gi No. 2995216
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36

- Alignment No. 12717
- gi No. 2995219
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12718
- gi No. 2995225
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12719
- gi No. 2995264
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12720
- gi No. 3002595
- % Identity 91.2
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12721
- gi No. 3002597
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12722
- gi No. 3002603
- % Identity 88
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12723
- gi No. 3002613
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12724
- gi No. 3002621
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12725
- gi No. 3002633
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12726
- gi No. 3002635
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12727

- gi No. 3002637
- % Identity 90
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1618: from 16 to 105
  
- Alignment No. 12728
- gi No. 3002643
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12729
- gi No. 3002647
- % Identity 91.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1618: from 15 to 104
  
- Alignment No. 12730
- gi No. 3002649
- % Identity 88.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1618: from 15 to 103
  
- Alignment No. 12731
- gi No. 3002657
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12732
- gi No. 3002663
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12733
- gi No. 3219788
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12734
- gi No. 3219789
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12735
- gi No. 3219790
- % Identity 85.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12736
- gi No. 3219791
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12737
- gi No. 3219792

- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12738
- gi No. 3219803
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12739
- gi No. 3219805
- % Identity 81.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12740
- gi No. 352175
- % Identity 84.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 2 to 135
  
- Alignment No. 12741
- gi No. 3745758
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1618: from 21 to 136
  
- Alignment No. 12742
- gi No. 386772
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 1 to 134
  
- Alignment No. 12743
- gi No. 3875420
- % Identity 84.6
- Alignment Length 123
- Location of Alignment in SEQ ID NO 1618: from 13 to 135
  
- Alignment No. 12744
- gi No. 3875421
- % Identity 75.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12745
- gi No. 3880527
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12746
- gi No. 3880606
- % Identity 85
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1618: from 57 to 136
  
- Alignment No. 12747
- gi No. 3979986
- % Identity 91.9

- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12748
- gi No. 404466
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12749
- gi No. 4139869
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1618: from 44 to 136
  
- Alignment No. 12750
- gi No. 417103
- % Identity 95.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12751
- gi No. 422605
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12752
- gi No. 422606
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12753
- gi No. 4388695
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 61 to 136
  
- Alignment No. 12754
- gi No. 4504279
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12755
- gi No. 4504281
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12756
- gi No. 4504283
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12757
- gi No. 4504299
- % Identity 89
- Alignment Length 136

- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12758
- gi No. 4574208
- % Identity 96.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 22 to 136
- Alignment No. 12759
- gi No. 4761212
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 8 to 119
- Alignment No. 12760
- gi No. 484441
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12761
- gi No. 484530
- % Identity 89.6
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
- Alignment No. 12762
- gi No. 484531
- % Identity 88.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
- Alignment No. 12763
- gi No. 4883733
- % Identity 90.6
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1618: from 11 to 116
- Alignment No. 12764
- gi No. 4883734
- % Identity 91.6
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1618: from 10 to 116
- Alignment No. 12765
- gi No. 4883735
- % Identity 91.7
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
- Alignment No. 12766
- gi No. 4883736
- % Identity 90.5
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1618: from 11 to 115
- Alignment No. 12767
- gi No. 4883737
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115

- Alignment No. 12768
- gi No. 4883738
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1618: from 17 to 109
  
- Alignment No. 12769
- gi No. 4883739
- % Identity 91.3
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1618: from 13 to 116
  
- Alignment No. 12770
- gi No. 4883740
- % Identity 90.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115
  
- Alignment No. 12771
- gi No. 4883741
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12772
- gi No. 4883743
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12773
- gi No. 4883744
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12774
- gi No. 4883745
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12775
- gi No. 4883746
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12776
- gi No. 4883747
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12777
- gi No. 4883748
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12778
- gi No. 4883749
- % Identity 92.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1618: from 13 to 117
  
- Alignment No. 12779
- gi No. 4883751
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12780
- gi No. 4883752
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 10 to 117
  
- Alignment No. 12781
- gi No. 4883753
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12782
- gi No. 4883754
- % Identity 89.7
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1618: from 9 to 115
  
- Alignment No. 12783
- gi No. 4883755
- % Identity 92.2
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115
  
- Alignment No. 12784
- gi No. 4883756
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12785
- gi No. 4883758
- % Identity 92.2
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1618: from 13 to 114
  
- Alignment No. 12786
- gi No. 4883759
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12787
- gi No. 4883760
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12788



- gi No. 4883762
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12789
- gi No. 488571
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 10 to 136
  
- Alignment No. 12790
- gi No. 488573
- % Identity 96
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1618: from 13 to 136
  
- Alignment No. 12791
- gi No. 529954
- % Identity 81.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12792
- gi No. 539427
- % Identity 91.7
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1618: from 2 to 49
  
- Alignment No. 12793
- gi No. 556612
- % Identity 83.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12794
- gi No. 559807
- % Identity 87.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12795
- gi No. 578470
- % Identity 90.3
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1618: from 61 to 132
  
- Alignment No. 12796
- gi No. 630475
- % Identity 86.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 1 to 76
  
- Alignment No. 12797
- gi No. 630476
- % Identity 88.7
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1618: from 1 to 62
  
- Alignment No. 12798
- gi No. 631693

- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1618: from 79 to 136
  
- Alignment No. 12799
- gi No. 70743
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12800
- gi No. 70747
- % Identity 91.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12801
- gi No. 70748
- % Identity 90.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12802
- gi No. 70749
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12803
- gi No. 70753
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12804
- gi No. 70755
- % Identity 88.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12805
- gi No. 70760
- % Identity 77.8
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12806
- gi No. 729676
- % Identity 86.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12807
- gi No. 729677
- % Identity 83.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12808
- gi No. 81850
- % Identity 96.6

- Alignment Length 118
- Location of Alignment in SEQ ID NO 1618: from 19 to 136
  
- Alignment No. 12809
- gi No. 84300
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
  
- Alignment No. 12810
- gi No. 84329
- % Identity 86.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 2 to 135
  
- Alignment No. 12811
- gi No. 85000
- % Identity 92.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 2 to 116
  
- Alignment No. 12812
- gi No. 85001
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12813
- gi No. 90622
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12814
- gi No. 995959
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1618: from 1 to 40
  
- Alignment No. 12815
- gi No. 99980
- % Identity 93.8
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1618: from 85 to 116
  
- Alignment No. 12816
- gi No. 99980
- % Identity 93.2
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1618: from 2 to 45
  
- Alignment No. 12817
- gi No. 99981
- % Identity 94.1
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1618: from 2 to 52

Maximum Length Sequence corresponding to clone ID 269337

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1619
- Ceres seq\_id 1500758

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1620
  - Ceres seq\_id 1500759
  - Location of start within SEQ ID NO 1619: at 1 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 12818
  - Dihydroorotase-like
  - Location within SEQ ID NO 1620: from 103 to 493 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1621
  - Ceres seq\_id 1500760
  - Location of start within SEQ ID NO 1619: at 19 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 12819
  - Dihydroorotase-like
  - Location within SEQ ID NO 1621: from 97 to 487 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1622
  - Ceres seq\_id 1500761
  - Location of start within SEQ ID NO 1619: at 310 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 12820
  - Dihydroorotase-like
  - Location within SEQ ID NO 1622: from 1 to 390 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269402

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1623
  - Ceres seq\_id 1500766
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1624
  - Ceres seq\_id 1500767
  - Location of start within SEQ ID NO 1623: at 519 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 12821
  - Fatty acid desaturase
  - Location within SEQ ID NO 1624: from 1 to 111 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1625
  - Ceres seq\_id 1500768
  - Location of start within SEQ ID NO 1623: at 558 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12822
- Fatty acid desaturase
- Location within SEQ ID NO 1625: from 1 to 98 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1626
- Ceres seq\_id 1500769
- Location of start within SEQ ID NO 1623: at 582 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12823
- Fatty acid desaturase
- Location within SEQ ID NO 1626: from 1 to 90 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1627
- Ceres seq\_id 1500778

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1628
- Ceres seq\_id 1500779
- Location of start within SEQ ID NO 1627: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12824
- Peroxidase
- Location within SEQ ID NO 1628: from 59 to 221 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12825
- gi No. 2342726
- % Identity 99.5
- Alignment Length 215
- Location of Alignment in SEQ ID NO 1628: from 7 to 221
- Alignment No. 12826
- gi No. 3643121
- % Identity 72.5
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1628: from 84 to 221
- Alignment No. 12827
- gi No. 538502
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1628: from 210 to 221

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1629
- Ceres seq\_id 1500780
- Location of start within SEQ ID NO 1627: at 19 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12828
- Peroxidase
- Location within SEQ ID NO 1629: from 53 to 215 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12829
- gi No. 2342726
- % Identity 99.5
- Alignment Length 215
- Location of Alignment in SEQ ID NO 1629: from 1 to 215
- Alignment No. 12830
- gi No. 3643121
- % Identity 72.5
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1629: from 78 to 215
- Alignment No. 12831
- gi No. 538502
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1629: from 204 to 215

Maximum Length Sequence corresponding to clone ID 269542

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1630
- Ceres seq\_id 1500785

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1631
- Ceres seq\_id 1500786
- Location of start within SEQ ID NO 1630: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12832
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1631: from 1 to 172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1632
- Ceres seq\_id 1500787
- Location of start within SEQ ID NO 1630: at 490 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12833
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1632: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1633
- Ceres seq\_id 1500788
- Location of start within SEQ ID NO 1630: at 547 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12834
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1633: from 1 to 127

Maximum Length Sequence corresponding to clone ID 269578

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1634
- Ceres seq\_id 1500793

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1635
- Ceres seq\_id 1500794
- Location of start within SEQ ID NO 1634: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12835
- gi No. 4220523
- % Identity 91.4
- Alignment Length 454
- Location of Alignment in SEQ ID NO 1635: from 1 to 254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1636
- Ceres seq\_id 1500795
- Location of start within SEQ ID NO 1634: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12836
- gi No. 4220523
- % Identity 91.4
- Alignment Length 454
- Location of Alignment in SEQ ID NO 1636: from 1 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1637
- Ceres seq\_id 1500796
- Location of start within SEQ ID NO 1634: at 835 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12837
- gi No. 4220523
- % Identity 91.4
- Alignment Length 454
- Location of Alignment in SEQ ID NO 1637: from 1 to 179

Maximum Length Sequence corresponding to clone ID 269582

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1638
- Ceres seq\_id 1500797

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1639
- Ceres seq\_id 1500798
- Location of start within SEQ ID NO 1638: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12838
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1639: from 11 to 272 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1640
- Ceres seq\_id 1500799
- Location of start within SEQ ID NO 1638: at 420 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12839
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1640: from 1 to 161 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1641
- Ceres seq\_id 1500800
- Location of start within SEQ ID NO 1638: at 462 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12840
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1641: from 1 to 147 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269610

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1642
- Ceres seq\_id 1500801

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1643
- Ceres seq\_id 1500802
- Location of start within SEQ ID NO 1642: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12841
- Polyphenyl synthetases
- Location within SEQ ID NO 1643: from 1 to 205 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12842
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1643: from 1 to 205

(B) Polypeptide Sequence



- Pat. Appln. SEQ ID NO 1644
- Ceres seq\_id 1500803
- Location of start within SEQ ID NO 1642: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12843
- Polyprenyl synthetases
- Location within SEQ ID NO 1644: from 1 to 196 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12844
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1644: from 1 to 196

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1645
- Ceres seq\_id 1500804
- Location of start within SEQ ID NO 1642: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12845
- Polyprenyl synthetases
- Location within SEQ ID NO 1645: from 1 to 179 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12846
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1645: from 1 to 179

Maximum Length Sequence corresponding to clone ID 269714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1646
- Ceres seq\_id 1500805

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1647
- Ceres seq\_id 1500806
- Location of start within SEQ ID NO 1646: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12847
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1647: from 81 to 129

- Alignment No. 12848
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1647: from 198 to 389

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1648

- Ceres seq\_id 1500807
- Location of start within SEQ ID NO 1646: at 427 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12849
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1648: from 76 to 124
- Alignment No. 12850
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1648: from 193 to 384

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1649
- Ceres seq\_id 1500808
- Location of start within SEQ ID NO 1646: at 556 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12851
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1649: from 33 to 81
- Alignment No. 12852
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1649: from 150 to 341

Maximum Length Sequence corresponding to clone ID 269772

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1650
- Ceres seq\_id 1500809

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1651
- Ceres seq\_id 1500810
- Location of start within SEQ ID NO 1650: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12853
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1651: from 59 to 179 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1652
- Ceres seq\_id 1500811
- Location of start within SEQ ID NO 1650: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12854
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1652: from 29 to 149 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269883

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1653
- Ceres seq\_id 1500820

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1654
- Ceres seq\_id 1500821
- Location of start within SEQ ID NO 1653: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12855
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1654: from 20 to 192 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12856
- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1654: from 7 to 192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1655
- Ceres seq\_id 1500822
- Location of start within SEQ ID NO 1653: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12857
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1655: from 12 to 184 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12858
- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1655: from 1 to 184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1656
- Ceres seq\_id 1500823
- Location of start within SEQ ID NO 1653: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12859
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1656: from 1 to 122 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12860

- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1656: from 1 to 122

Maximum Length Sequence corresponding to clone ID 270032

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1657
- Ceres seq\_id 1500828

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1658
- Ceres seq\_id 1500829
- Location of start within SEQ ID NO 1657: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12861
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1658: from 27 to 458 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12862
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12863
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1658: from 127 to 464
  
- Alignment No. 12864
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12865
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12866
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12867
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12868
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443

- Location of Alignment in SEQ ID NO 1658: from 22 to 464
- Alignment No. 12869
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
- Alignment No. 12870
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1658: from 74 to 464
- Alignment No. 12871
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
- Alignment No. 12872
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1659
- Ceres seq\_id 1500830
- Location of start within SEQ ID NO 1657: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12873
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1659: from 1 to 385 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12874
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
- Alignment No. 12875
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1659: from 54 to 391
- Alignment No. 12876
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
- Alignment No. 12877
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12878
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12879
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12880
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12881
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12882
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12883
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12884
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1660
- Ceres seq\_id 1500831
- Location of start within SEQ ID NO 1657: at 678 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12885
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1660: from 1 to 335 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12886
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341

- Alignment No. 12887
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1660: from 4 to 341
  
- Alignment No. 12888
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12889
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12890
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12891
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12892
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12893
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12894
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12895
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12896
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341

Maximum Length Sequence corresponding to clone ID 270102

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1661
- Ceres seq\_id 1500832

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1662
- Ceres seq\_id 1500833
- Location of start within SEQ ID NO 1661: at 298 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12897
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1662: from 183 to 292 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12898
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1662: from 2 to 292
- Alignment No. 12899
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1662: from 2 to 292

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1663
- Ceres seq\_id 1500834
- Location of start within SEQ ID NO 1661: at 349 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12900
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1663: from 166 to 275 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12901
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1663: from 1 to 275
- Alignment No. 12902
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1663: from 1 to 275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1664
- Ceres seq\_id 1500835
- Location of start within SEQ ID NO 1661: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12903
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1664: from 141 to 250 aa.



(D) Related Amino Acid Sequences

- Alignment No. 12904
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1664: from 1 to 250
- Alignment No. 12905
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1664: from 1 to 250

Maximum Length Sequence corresponding to clone ID 270115

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1665
- Ceres seq\_id 1500836

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1666
- Ceres seq\_id 1500837
- Location of start within SEQ ID NO 1665: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12906
- pfkB family carbohydrate kinase
- Location within SEQ ID NO 1666: from 59 to 124 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1667
- Ceres seq\_id 1500838
- Location of start within SEQ ID NO 1665: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270512

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1668
- Ceres seq\_id 1500847

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1669
- Ceres seq\_id 1500848
- Location of start within SEQ ID NO 1668: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12907
- gi No. 2341040
- % Identity 97
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1669: from 12 to 111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1670
- Ceres seq\_id 1500849

- Location of start within SEQ ID NO 1668: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12908
- gi No. 2341040
- % Identity 97
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1670: from 1 to 100

Maximum Length Sequence corresponding to clone ID 270714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1671
- Ceres seq\_id 1500854

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1672
- Ceres seq\_id 1500855
- Location of start within SEQ ID NO 1671: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12909
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1672: from 1 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1673
- Ceres seq\_id 1500856
- Location of start within SEQ ID NO 1671: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12910
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1673: from 1 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1674
- Ceres seq\_id 1500857
- Location of start within SEQ ID NO 1671: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12911
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1674: from 1 to 101

Maximum Length Sequence corresponding to clone ID 271327

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1675
- Ceres seq\_id 1500862

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1676
- Ceres seq\_id 1500863
- Location of start within SEQ ID NO 1675: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12912
- gi No. 3063449
- % Identity 100
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1676: from 1 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1677
- Ceres seq\_id 1500864
- Location of start within SEQ ID NO 1675: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12913
- gi No. 3063449
- % Identity 100
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1677: from 1 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1678
- Ceres seq\_id 1500865
- Location of start within SEQ ID NO 1675: at 360 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12914
- gi No. 3063449
- % Identity 100
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1678: from 1 to 84

Maximum Length Sequence corresponding to clone ID 271605

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1679
- Ceres seq\_id 1500866

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1680
- Ceres seq\_id 1500867
- Location of start within SEQ ID NO 1679: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12915
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1680: from 25 to 135
- Alignment No. 12916

- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1680: from 114 to 155
  
- Alignment No. 12917
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1680: from 121 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1681
- Ceres seq\_id 1500868
- Location of start within SEQ ID NO 1679: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12918
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1681: from 3 to 113
  
- Alignment No. 12919
- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1681: from 92 to 133
  
- Alignment No. 12920
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1681: from 99 to 133

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1682
- Ceres seq\_id 1500869
- Location of start within SEQ ID NO 1679: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12921
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1682: from 1 to 71
  
- Alignment No. 12922
- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1682: from 50 to 91
  
- Alignment No. 12923
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35

- Location of Alignment in SEQ ID NO 1682: from 57 to 91

Maximum Length Sequence corresponding to clone ID 272234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1683
- Ceres seq\_id 1500877

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1684
- Ceres seq\_id 1500878
- Location of start within SEQ ID NO 1683: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12924
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1684: from 66 to 160 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1685
- Ceres seq\_id 1500879
- Location of start within SEQ ID NO 1683: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12925
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1685: from 25 to 119 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1686
- Ceres seq\_id 1500880
- Location of start within SEQ ID NO 1683: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12926
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1686: from 1 to 91 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272243

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1687
- Ceres seq\_id 1500881

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1688
- Ceres seq\_id 1500882
- Location of start within SEQ ID NO 1687: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1689
- Ceres seq\_id 1500883

- Location of start within SEQ ID NO 1687: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12927
- Biotin-requiring enzymes
- Location within SEQ ID NO 1689: from 75 to 139 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12928
- gi No. 4210332
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1689: from 61 to 139
- Alignment No. 12929
- gi No. 4455214
- % Identity 76.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1689: from 72 to 131

Maximum Length Sequence corresponding to clone ID 272277

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1690
- Ceres seq\_id 1500884

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1691
- Ceres seq\_id 1500885
- Location of start within SEQ ID NO 1690: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1692
- Ceres seq\_id 1500886
- Location of start within SEQ ID NO 1690: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12930
- Mucin-like glycoprotein
- Location within SEQ ID NO 1692: from 25 to 90 aa.

- Alignment No. 12931
- Mucin-like glycoprotein
- Location within SEQ ID NO 1692: from 33 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1693
- Ceres seq\_id 1500887
- Location of start within SEQ ID NO 1690: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272304

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1694
- Ceres seq\_id 1500888

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1695
- Ceres seq\_id 1500889
- Location of start within SEQ ID NO 1694: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12932
- Protein phosphatase 2C
- Location within SEQ ID NO 1695: from 133 to 195 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12933
- gi No. 1914851
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1695: from 57 to 68
- Alignment No. 12934
- gi No. 3281853
- % Identity 75
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1695: from 126 to 196
- Alignment No. 12935
- gi No. 4808585
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1695: from 59 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1696
- Ceres seq\_id 1500890
- Location of start within SEQ ID NO 1694: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1697
- Ceres seq\_id 1500891
- Location of start within SEQ ID NO 1694: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12936
- Protein phosphatase 2C
- Location within SEQ ID NO 1697: from 82 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12937
- gi No. 1914851
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1697: from 6 to 17
- Alignment No. 12938

- gi No. 3281853
- % Identity 75
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1697: from 75 to 145
  
- Alignment No. 12939
- gi No. 4808585
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1697: from 8 to 18

Maximum Length Sequence corresponding to clone ID 272501

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1698
- Ceres seq\_id 1500900

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1699
- Ceres seq\_id 1500901
- Location of start within SEQ ID NO 1698: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12940
- gi No. 2130028
- % Identity 87.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1699: from 27 to 90
  
- Alignment No. 12941
- gi No. 2293568
- % Identity 93.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1699: from 28 to 90
  
- Alignment No. 12942
- gi No. 4530585
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1699: from 29 to 90
  
- Alignment No. 12943
- gi No. 5541720
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1699: from 27 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1700
- Ceres seq\_id 1500902
- Location of start within SEQ ID NO 1698: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12944
- gi No. 2130028
- % Identity 87.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1700: from 1 to 64



- Alignment No. 12945
- gi No. 2293568
- % Identity 93.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1700: from 2 to 64
  
- Alignment No. 12946
- gi No. 4530585
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1700: from 3 to 64
  
- Alignment No. 12947
- gi No. 5541720
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1700: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1701
- Ceres seq\_id 1500903
- Location of start within SEQ ID NO 1698: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12948
- gi No. 3377850
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1701: from 1 to 79

Maximum Length Sequence corresponding to clone ID 272512

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1702
- Ceres seq\_id 1500907

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1703
- Ceres seq\_id 1500908
- Location of start within SEQ ID NO 1702: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1704
- Ceres seq\_id 1500909
- Location of start within SEQ ID NO 1702: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12949
- gi No. 1531758
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1704: from 6 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1705

- Ceres seq\_id 1500910
- Location of start within SEQ ID NO 1702: at 316 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12950
- gi No. 1531758
- % Identity 71.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1705: from 1 to 49
  
- Alignment No. 12951
- gi No. 4803938
- % Identity 82.7
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1705: from 1 to 49

Maximum Length Sequence corresponding to clone ID 275375

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1706
- Ceres seq\_id 1500915

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1707
- Ceres seq\_id 1500916
- Location of start within SEQ ID NO 1706: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12952
- gi No. 3157951
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1707: from 147 to 181

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1708
- Ceres seq\_id 1500917
- Location of start within SEQ ID NO 1706: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12953
- gi No. 462338
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1708: from 57 to 77

Maximum Length Sequence corresponding to clone ID 275391

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1709
- Ceres seq\_id 1500926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1710
- Ceres seq\_id 1500927
- Location of start within SEQ ID NO 1709: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12954
- gi No. 2665536
- % Identity 90.5
- Alignment Length 179
- Location of Alignment in SEQ ID NO 1710: from 33 to 209

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1711
- Ceres seq\_id 1500928
- Location of start within SEQ ID NO 1709: at 227 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12955
- gi No. 2665536
- % Identity 90.5
- Alignment Length 179
- Location of Alignment in SEQ ID NO 1711: from 1 to 134

Maximum Length Sequence corresponding to clone ID 275392

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1712
- Ceres seq\_id 1500929

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1713
- Ceres seq\_id 1500930
- Location of start within SEQ ID NO 1712: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12956
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1713: from 21 to 101 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1714
- Ceres seq\_id 1500931
- Location of start within SEQ ID NO 1712: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1715
- Ceres seq\_id 1500932
- Location of start within SEQ ID NO 1712: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275421

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1716
- Ceres seq\_id 1500945

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1717
- Ceres seq\_id 1500946
- Location of start within SEQ ID NO 1716: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12957
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1717: from 34 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12958
- gi No. 3876261
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1717: from 113 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1718
- Ceres seq\_id 1500947
- Location of start within SEQ ID NO 1716: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12959
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1718: from 11 to 103 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12960
- gi No. 3876261
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1718: from 90 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1719
- Ceres seq\_id 1500948
- Location of start within SEQ ID NO 1716: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275764

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1720
- Ceres seq\_id 1500953

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1721
- Ceres seq\_id 1500954
- Location of start within SEQ ID NO 1720: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12961
- Beta-ketoacyl synthase
- Location within SEQ ID NO 1721: from 93 to 172 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12962

- gi No. 119784
- % Identity 75.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1721: from 58 to 172
- Alignment No. 12963
- gi No. 294668
- % Identity 83.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1721: from 78 to 172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1722
- Ceres seq\_id 1500955
- Location of start within SEQ ID NO 1720: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1723
- Ceres seq\_id 1500956
- Location of start within SEQ ID NO 1720: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12964
- Beta-ketoacyl synthase
- Location within SEQ ID NO 1723: from 49 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12965
- gi No. 119784
- % Identity 75.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1723: from 14 to 128
- Alignment No. 12966
- gi No. 294668
- % Identity 83.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1723: from 34 to 128

Maximum Length Sequence corresponding to clone ID 276068

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1724
- Ceres seq\_id 1500963

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1725
- Ceres seq\_id 1500964
- Location of start within SEQ ID NO 1724: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1726
- Ceres seq\_id 1500965
- Location of start within SEQ ID NO 1724: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1727
- Ceres seq\_id 1500966
- Location of start within SEQ ID NO 1724: at 141 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12967
- Mucin-like glycoprotein
- Location within SEQ ID NO 1727: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 276186

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1728
- Ceres seq\_id 1500974

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1729
- Ceres seq\_id 1500975
- Location of start within SEQ ID NO 1728: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12968
- gi No. 2425066
- % Identity 100
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1729: from 61 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1730
- Ceres seq\_id 1500976
- Location of start within SEQ ID NO 1728: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1731
- Ceres seq\_id 1500977
- Location of start within SEQ ID NO 1728: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 279386

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1732
- Ceres seq\_id 1500985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1733
- Ceres seq\_id 1500986

- Location of start within SEQ ID NO 1732: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1734
- Ceres seq\_id 1500987
- Location of start within SEQ ID NO 1732: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12969
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1734: from 12 to 77 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12970
- gi No. 1777312
- % Identity 71.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1734: from 1 to 77
- Alignment No. 12971
- gi No. 2980770
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1734: from 7 to 77
- Alignment No. 12972
- gi No. 3256035
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1734: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1735
- Ceres seq\_id 1500988
- Location of start within SEQ ID NO 1732: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12973
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1735: from 4 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12974
- gi No. 1777312
- % Identity 71.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1735: from 1 to 69
- Alignment No. 12975
- gi No. 2980770
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1735: from 1 to 69
- Alignment No. 12976

- gi No. 3256035
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1735: from 1 to 69

Maximum Length Sequence corresponding to clone ID 280780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1736
- Ceres seq\_id 1500992

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1737
- Ceres seq\_id 1500993
- Location of start within SEQ ID NO 1736: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12977
- gi No. 1041702
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12978
- gi No. 1778097
- % Identity 84.6
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1737: from 92 to 130
  
- Alignment No. 12979
- gi No. 1778099
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12980
- gi No. 1778101
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12981
- gi No. 1778107
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1737: from 92 to 129
  
- Alignment No. 12982
- gi No. 1778109
- % Identity 90.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1737: from 92 to 124
  
- Alignment No. 12983
- gi No. 1815681
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12984
- gi No. 3461833



- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12985
- gi No. 3510538
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12986
- gi No. 3510540
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12987
- gi No. 4027897
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12988
- gi No. 4027899
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12989
- gi No. 4138914
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12990
- gi No. 4138916
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12991
- gi No. 5524700
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12992
- gi No. 5714392
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1738
- Ceres seq\_id 1500994
- Location of start within SEQ ID NO 1736: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1739
- Ceres seq\_id 1500995
- Location of start within SEQ ID NO 1736: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12993
- gi No. 1041702
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 12994
- gi No. 1778097
- % Identity 84.6
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1739: from 66 to 104
  
- Alignment No. 12995
- gi No. 1778099
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 12996
- gi No. 1778101
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 12997
- gi No. 1778107
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1739: from 66 to 103
  
- Alignment No. 12998
- gi No. 1778109
- % Identity 90.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1739: from 66 to 98
  
- Alignment No. 12999
- gi No. 1815681
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13000
- gi No. 3461833
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13001
- gi No. 3510538
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13002
- gi No. 3510540
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13003
- gi No. 4027897
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13004
- gi No. 4027899
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13005
- gi No. 4138914
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13006
- gi No. 4138916
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13007
- gi No. 5524700
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13008
- gi No. 5714392
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

Maximum Length Sequence corresponding to clone ID 280829

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1740
- Ceres seq\_id 1501005

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1741
- Ceres seq\_id 1501006
- Location of start within SEQ ID NO 1740: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1742
- Ceres seq\_id 1501007
- Location of start within SEQ ID NO 1740: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13009
- Sugar (and other) transporter
- Location within SEQ ID NO 1742: from 33 to 111 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1743
- Ceres seq\_id 1501008
- Location of start within SEQ ID NO 1740: at 213 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13010
- Sugar (and other) transporter
- Location within SEQ ID NO 1743: from 1 to 73 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 280866

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1744
- Ceres seq\_id 1501016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1745
- Ceres seq\_id 1501017
- Location of start within SEQ ID NO 1744: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13011
- Histone-like transcription factors (CBF/NF-Y) and archaeal histones.
- Location within SEQ ID NO 1745: from 10 to 73 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1746
- Ceres seq\_id 1501018
- Location of start within SEQ ID NO 1744: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13012
- Histone-like transcription factors (CBF/NF-Y) and archaeal histones.
- Location within SEQ ID NO 1746: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 281118

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1747
- Ceres seq\_id 1501023

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1748
- Ceres seq\_id 1501024
- Location of start within SEQ ID NO 1747: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1749
- Ceres seq\_id 1501025
- Location of start within SEQ ID NO 1747: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13013
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1749: from 96 to 148 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1750
- Ceres seq\_id 1501026
- Location of start within SEQ ID NO 1747: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13014
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1750: from 42 to 94 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 281313

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1751
- Ceres seq\_id 1501027

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1752
- Ceres seq\_id 1501028
- Location of start within SEQ ID NO 1751: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13015
- gi No. 3153821
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1752: from 38 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1753
- Ceres seq\_id 1501029
- Location of start within SEQ ID NO 1751: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 282233

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1754

- Ceres seq\_id 1501037
  - (B) Polypeptide Sequence
    - Pat. Appln. SEQ ID NO 1755
    - Ceres seq\_id 1501038
    - Location of start within SEQ ID NO 1754: at 148 nt.
  - (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
    - Alignment No. 13016
    - Adaptor complexes medium subunit family
    - Location within SEQ ID NO 1755: from 8 to 121 aa.
  - (D) Related Amino Acid Sequences
    - Alignment No. 13017
    - gi No. 2271477
    - % Identity 95.9
    - Alignment Length 122
    - Location of Alignment in SEQ ID NO 1755: from 1 to 121
  - (B) Polypeptide Sequence
    - Pat. Appln. SEQ ID NO 1756
    - Ceres seq\_id 1501039
    - Location of start within SEQ ID NO 1754: at 238 nt.
  - (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
    - Alignment No. 13018
    - Adaptor complexes medium subunit family
    - Location within SEQ ID NO 1756: from 1 to 91 aa.
  - (D) Related Amino Acid Sequences
    - Alignment No. 13019
    - gi No. 2271477
    - % Identity 95.9
    - Alignment Length 122
    - Location of Alignment in SEQ ID NO 1756: from 1 to 91
  - (B) Polypeptide Sequence
    - Pat. Appln. SEQ ID NO 1757
    - Ceres seq\_id 1501040
    - Location of start within SEQ ID NO 1754: at 256 nt.
  - (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
    - Alignment No. 13020
    - Adaptor complexes medium subunit family
    - Location within SEQ ID NO 1757: from 1 to 85 aa.
  - (D) Related Amino Acid Sequences
    - Alignment No. 13021
    - gi No. 2271477
    - % Identity 95.9
    - Alignment Length 122
    - Location of Alignment in SEQ ID NO 1757: from 1 to 85
- Maximum Length Sequence corresponding to clone ID 282427
- (A) Polynucleotide Sequence
    - Pat. Appln. SEQ ID NO 1758
    - Ceres seq\_id 1501058
  - (B) Polypeptide Sequence
    - Pat. Appln. SEQ ID NO 1759

- Ceres seq\_id 1501059
- Location of start within SEQ ID NO 1758: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1760
- Ceres seq\_id 1501060
- Location of start within SEQ ID NO 1758: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13022
- Mucin-like glycoprotein
- Location within SEQ ID NO 1760: from 20 to 133 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1761
- Ceres seq\_id 1501061
- Location of start within SEQ ID NO 1758: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 282587

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1762
- Ceres seq\_id 1501090

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1763
- Ceres seq\_id 1501091
- Location of start within SEQ ID NO 1762: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13023
- BAH domain
- Location within SEQ ID NO 1763: from 30 to 115 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13024
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1763: from 30 to 115
  
- Alignment No. 13025
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1763: from 29 to 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1764
- Ceres seq\_id 1501092
- Location of start within SEQ ID NO 1762: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13026
- BAH domain
- Location within SEQ ID NO 1764: from 27 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13027
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1764: from 27 to 112
- Alignment No. 13028
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1764: from 26 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1765
- Ceres seq\_id 1501093
- Location of start within SEQ ID NO 1762: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13029
- BAH domain
- Location within SEQ ID NO 1765: from 1 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13030
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1765: from 1 to 81
- Alignment No. 13031
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1765: from 1 to 81

Maximum Length Sequence corresponding to clone ID 282710

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1766
- Ceres seq\_id 1501115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1767
- Ceres seq\_id 1501116
- Location of start within SEQ ID NO 1766: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13032
- gi No. 1742961
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 43 to 91



- Alignment No. 13033
- gi No. 1791309
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 43 to 91
  
- Alignment No. 13034
- gi No. 2198851
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1767: from 33 to 105
  
- Alignment No. 13035
- gi No. 2198851
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1767: from 80 to 107
  
- Alignment No. 13036
- gi No. 2198853
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1767: from 33 to 105
  
- Alignment No. 13037
- gi No. 2198853
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1767: from 80 to 107
  
- Alignment No. 13038
- gi No. 4959932
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 45 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1768
- Ceres seq\_id 1501117
- Location of start within SEQ ID NO 1766: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1769
- Ceres seq\_id 1501118
- Location of start within SEQ ID NO 1766: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13039
- gi No. 1742961
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 11 to 59
  
- Alignment No. 13040

- gi No. 1791309
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 11 to 59
  
- Alignment No. 13041
- gi No. 2198851
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1769: from 1 to 73
  
- Alignment No. 13042
- gi No. 2198851
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1769: from 48 to 75
  
- Alignment No. 13043
- gi No. 2198853
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1769: from 1 to 73
  
- Alignment No. 13044
- gi No. 2198853
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1769: from 48 to 75
  
- Alignment No. 13045
- gi No. 4959932
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 13 to 59

Maximum Length Sequence corresponding to clone ID 282723

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1770
- Ceres seq\_id 1501119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1771
- Ceres seq\_id 1501120
- Location of start within SEQ ID NO 1770: at 239 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13046
- Clathrin adaptor complex small chain
- Location within SEQ ID NO 1771: from 1 to 76 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1772
- Ceres seq\_id 1501121
- Location of start within SEQ ID NO 1770: at 254 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13047
- Clathrin adaptor complex small chain

- Location within SEQ ID NO 1772: from 1 to 71 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1773
- Ceres seq\_id 1501122
- Location of start within SEQ ID NO 1770: at 492 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13048
- Clathrin adaptor complex small chain
- Location within SEQ ID NO 1773: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13049
- gi No. 4835237
- % Identity 72.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1773: from 1 to 61

Maximum Length Sequence corresponding to clone ID 282725

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1774
- Ceres seq\_id 1501123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1775
- Ceres seq\_id 1501124
- Location of start within SEQ ID NO 1774: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1776
- Ceres seq\_id 1501125
- Location of start within SEQ ID NO 1774: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13050
- gi No. 2688824
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1776: from 74 to 111

Maximum Length Sequence corresponding to clone ID 282757

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1777
- Ceres seq\_id 1501137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1778
- Ceres seq\_id 1501138
- Location of start within SEQ ID NO 1777: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13051
- gi No. 103249
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13052
- gi No. 130831
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13053
- gi No. 1346784
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13054
- gi No. 2511580
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13055
- gi No. 2529567
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13056
- gi No. 266839
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13057
- gi No. 3024432
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13058
- gi No. 3334299
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13059
- gi No. 3421082
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13060
- gi No. 3805978
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13061

- gi No. 3874776
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13062
- gi No. 4092058
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13063
- gi No. 4506189
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13064
- gi No. 4586592
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13065
- gi No. 464459
- % Identity 82.6
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13066
- gi No. 485265
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

Maximum Length Sequence corresponding to clone ID 282828

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1779
- Ceres seq\_id 1501139

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1780
- Ceres seq\_id 1501140
- Location of start within SEQ ID NO 1779: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13067
- Fatty acid desaturase
- Location within SEQ ID NO 1780: from 93 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13068
- gi No. 2194093
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1780: from 99 to 144
  
- Alignment No. 13069
- gi No. 533082
- % Identity 71.2
- Alignment Length 52

- Location of Alignment in SEQ ID NO 1780: from 93 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1781
- Ceres seq\_id 1501141
- Location of start within SEQ ID NO 1779: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13070
- Fatty acid desaturase
- Location within SEQ ID NO 1781: from 40 to 91 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13071
- gi No. 2194093
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1781: from 46 to 91
- Alignment No. 13072
- gi No. 533082
- % Identity 71.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1781: from 40 to 91

Maximum Length Sequence corresponding to clone ID 282832

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1782
- Ceres seq\_id 1501142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1783
- Ceres seq\_id 1501143
- Location of start within SEQ ID NO 1782: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1784
- Ceres seq\_id 1501144
- Location of start within SEQ ID NO 1782: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1785
- Ceres seq\_id 1501145
- Location of start within SEQ ID NO 1782: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13073
- gi No. 2358287
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1785: from 38 to 48

- Alignment No. 13074
- gi No. 3928704
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1785: from 10 to 23
  
- Alignment No. 13075
- gi No. 4508019
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1785: from 10 to 23
  
- Alignment No. 13076
- gi No. 545067
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1785: from 139 to 151

Maximum Length Sequence corresponding to clone ID 282932

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1786
- Ceres seq\_id 1501163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1787
- Ceres seq\_id 1501164
- Location of start within SEQ ID NO 1786: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13077
- Histone deacetylase family
- Location within SEQ ID NO 1787: from 26 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13078
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1787: from 8 to 113
  
- Alignment No. 13079
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1787: from 1 to 113
  
- Alignment No. 13080
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1787: from 8 to 113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1788
- Ceres seq\_id 1501165
- Location of start within SEQ ID NO 1786: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13081

- Histone deacetylase family
- Location within SEQ ID NO 1788: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13082
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1788: from 1 to 70
- Alignment No. 13083
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1788: from 1 to 70
- Alignment No. 13084
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1788: from 1 to 70

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1789
- Ceres seq\_id 1501166
- Location of start within SEQ ID NO 1786: at 289 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13085
- Histone deacetylase family
- Location within SEQ ID NO 1789: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13086
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1789: from 1 to 63
- Alignment No. 13087
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1789: from 1 to 63
- Alignment No. 13088
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1789: from 1 to 63

Maximum Length Sequence corresponding to clone ID 283094

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1790
- Ceres seq\_id 1501167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1791
- Ceres seq\_id 1501168
- Location of start within SEQ ID NO 1790: at 3 nt.



(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13089
- gi No. 1170404
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1791: from 46 to 58
  
- Alignment No. 13090
- gi No. 1170404
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1791: from 44 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1792
- Ceres seq\_id 1501169
- Location of start within SEQ ID NO 1790: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13091
- gi No. 1170404
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1792: from 37 to 49
  
- Alignment No. 13092
- gi No. 1170404
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1792: from 35 to 49

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1793
- Ceres seq\_id 1501170
- Location of start within SEQ ID NO 1790: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283333

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1794
- Ceres seq\_id 1501203

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1795
- Ceres seq\_id 1501204
- Location of start within SEQ ID NO 1794: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1796
- Ceres seq\_id 1501205
- Location of start within SEQ ID NO 1794: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13093
- gi No. 102427
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31
  
- Alignment No. 13094
- gi No. 102427
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31
  
- Alignment No. 13095
- gi No. 4467884
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1796: from 19 to 29
  
- Alignment No. 13096
- gi No. 5123787
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1796: from 17 to 31
  
- Alignment No. 13097
- gi No. 553165
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1797
- Ceres seq\_id 1501206
- Location of start within SEQ ID NO 1794: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283840

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1798
- Ceres seq\_id 1501245

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1799
- Ceres seq\_id 1501246
- Location of start within SEQ ID NO 1798: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13098
- gi No. 322759
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1799: from 15 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1800
- Ceres seq\_id 1501247
- Location of start within SEQ ID NO 1798: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13099
- gi No. 688080
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1800: from 93 to 103
- Alignment No. 13100
- gi No. 688080
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1800: from 90 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1801
- Ceres seq\_id 1501248
- Location of start within SEQ ID NO 1798: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283927

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1802
- Ceres seq\_id 1501259

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1803
- Ceres seq\_id 1501260
- Location of start within SEQ ID NO 1802: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13101
- gi No. 1082871
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13102
- gi No. 1352426
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13103
- gi No. 1352427
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13104
- gi No. 1794151

- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1803: from 30 to 53
  
- Alignment No. 13105
- gi No. 2851524
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13106
- gi No. 3024017
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13107
- gi No. 3264536
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13108
- gi No. 3746340
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13109
- gi No. 3811355
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1803: from 28 to 56
  
- Alignment No. 13110
- gi No. 4503499
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13111
- gi No. 4587600
- % Identity 100
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13112
- gi No. 4758254
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13113
- gi No. 5690414
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
  
- Alignment No. 13114
- gi No. 626041
- % Identity 96

- Alignment Length 25
- Location of Alignment in SEQ ID NO 1803: from 29 to 53
- Alignment No. 13115
- gi No. 627817
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1803: from 29 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1804
- Ceres seq\_id 1501261
- Location of start within SEQ ID NO 1802: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13116
- gi No. 1082871
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13117
- gi No. 1352426
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13118
- gi No. 1352427
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13119
- gi No. 1794151
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13120
- gi No. 2851524
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13121
- gi No. 3024017
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13122
- gi No. 3264536
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13123
- gi No. 3746340

- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13124
- gi No. 3811355
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1804: from 56 to 75
  
- Alignment No. 13125
- gi No. 4503499
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13126
- gi No. 4587600
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13127
- gi No. 4758254
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13128
- gi No. 5690414
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13129
- gi No. 626041
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13130
- gi No. 627817
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13131
- gi No. 729814
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1805
- Ceres seq\_id 1501262
- Location of start within SEQ ID NO 1802: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13132

- gi No. 1082871
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13133
- gi No. 1352426
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13134
- gi No. 1352427
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13135
- gi No. 1794151
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1805: from 3 to 26
  
- Alignment No. 13136
- gi No. 2851524
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13137
- gi No. 3024017
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13138
- gi No. 3264536
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13139
- gi No. 3746340
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13140
- gi No. 3811355
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1805: from 1 to 29
  
- Alignment No. 13141
- gi No. 4503499
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13142
- gi No. 4587600

- % Identity 100
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13143
- gi No. 4758254
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13144
- gi No. 5690414
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13145
- gi No. 626041
- % Identity 96
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1805: from 2 to 26
  
- Alignment No. 13146
- gi No. 627817
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1805: from 2 to 26

Maximum Length Sequence corresponding to clone ID 283950

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1806
- Ceres seq\_id 1501268

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1807
- Ceres seq\_id 1501269
- Location of start within SEQ ID NO 1806: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13147
- gi No. 419789
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1807: from 146 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1808
- Ceres seq\_id 1501270
- Location of start within SEQ ID NO 1806: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13148
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1808: from 29 to 109 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284027

(A) Polynucleotide Sequence



- Pat. Appln. SEQ ID NO 1809
- Ceres seq\_id 1501280
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1810
  - Ceres seq\_id 1501281
  - Location of start within SEQ ID NO 1809: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13149
    - gi No. 100931
    - % Identity 72.7
    - Alignment Length 22
    - Location of Alignment in SEQ ID NO 1810: from 44 to 64
  - Alignment No. 13150
    - gi No. 1045052
    - % Identity 71.8
    - Alignment Length 39
    - Location of Alignment in SEQ ID NO 1810: from 29 to 64
  - Alignment No. 13151
    - gi No. 1065516
    - % Identity 77.8
    - Alignment Length 36
    - Location of Alignment in SEQ ID NO 1810: from 29 to 64
  - Alignment No. 13152
    - gi No. 1078809
    - % Identity 76
    - Alignment Length 25
    - Location of Alignment in SEQ ID NO 1810: from 38 to 62
  - Alignment No. 13153
    - gi No. 1078810
    - % Identity 76
    - Alignment Length 25
    - Location of Alignment in SEQ ID NO 1810: from 38 to 62
  - Alignment No. 13154
    - gi No. 1101025
    - % Identity 86.1
    - Alignment Length 36
    - Location of Alignment in SEQ ID NO 1810: from 29 to 64
  - Alignment No. 13155
    - gi No. 1136120
    - % Identity 78.4
    - Alignment Length 37
    - Location of Alignment in SEQ ID NO 1810: from 29 to 64
  - Alignment No. 13156
    - gi No. 1136122
    - % Identity 86.5
    - Alignment Length 37
    - Location of Alignment in SEQ ID NO 1810: from 29 to 64
  - Alignment No. 13157
    - gi No. 1174592
    - % Identity 83.9

- Alignment Length 31
- Location of Alignment in SEQ ID NO 1810: from 29 to 59
  
- Alignment No. 13158
- gi No. 1174593
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13159
- gi No. 1223784
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13160
- gi No. 1223786
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13161
- gi No. 1245776
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13162
- gi No. 1279206
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13163
- gi No. 1334748
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13164
- gi No. 1351200
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13165
- gi No. 135391
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13166
- gi No. 135392
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13167
- gi No. 135393
- % Identity 70.3
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13168
- gi No. 135394
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13169
- gi No. 135395
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13170
- gi No. 135396
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13171
- gi No. 135398
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13172
- gi No. 135399
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13173
- gi No. 135400
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13174
- gi No. 135401
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13175
- gi No. 135402
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13176
- gi No. 135404
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13177
- gi No. 135406
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13178
- gi No. 135407
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13179
- gi No. 135409
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13180
- gi No. 135411
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13181
- gi No. 135412
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13182
- gi No. 135413
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55
  
- Alignment No. 13183
- gi No. 135414
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13184
- gi No. 135415
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55
  
- Alignment No. 13185
- gi No. 135416
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13186
- gi No. 135417
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13187
- gi No. 135418
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13188
- gi No. 135419
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13189
- gi No. 135420
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13190
- gi No. 135422
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13191
- gi No. 135423
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13192
- gi No. 135424
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13193
- gi No. 135425
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13194
- gi No. 135426
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13195
- gi No. 135427
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13196
- gi No. 135428
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13197
- gi No. 135430
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13198

- gi No. 135431
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13199
- gi No. 135431
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13200
- gi No. 135432
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13201
- gi No. 135433
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13202
- gi No. 135434
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13203
- gi No. 135435
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13204
- gi No. 135436
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13205
- gi No. 135437
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13206
- gi No. 135438
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13207
- gi No. 135439
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13208
- gi No. 135440

- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13209
- gi No. 135441
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13210
- gi No. 1362559
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13211
- gi No. 1460090
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13212
- gi No. 1460092
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13213
- gi No. 1477428
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13214
- gi No. 1527170
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13215
- gi No. 1527172
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13216
- gi No. 1556446
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13217
- gi No. 1619297
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13218
- gi No. 1729834
- % Identity 79.3

- Alignment Length 29
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13219
- gi No. 1729835
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13220
- gi No. 1729837
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13221
- gi No. 1729838
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13222
- gi No. 1729839
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13223
- gi No. 1729841
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13224
- gi No. 1729842
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13225
- gi No. 173058
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13226
- gi No. 1854669
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13227
- gi No. 202223
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13228
- gi No. 202225
- % Identity 70.3
- Alignment Length 37



- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13229
- gi No. 2088848
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13230
- gi No. 2098751
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13231
- gi No. 2098753
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13232
- gi No. 2098757
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13233
- gi No. 2119263
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13234
- gi No. 2119268
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13235
- gi No. 2119269
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13236
- gi No. 212836
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13237
- gi No. 223280
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13238
- gi No. 223556
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13239
- gi No. 225587
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13240
- gi No. 226261
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13241
- gi No. 2401255
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13242
- gi No. 2511531
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13243
- gi No. 2511533
- % Identity 81.3
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13244
- gi No. 2511535
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13245
- gi No. 2522334
- % Identity 77.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13246
- gi No. 2522336
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13247
- gi No. 2599500
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13248
- gi No. 2613143
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13249
- gi No. 2625154
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13250
- gi No. 2625156
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13251
- gi No. 267069
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13252
- gi No. 267070
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13253
- gi No. 283503
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13254
- gi No. 2842514
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13255
- gi No. 2843123
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13256
- gi No. 3024695
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13257
- gi No. 306451
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13258
- gi No. 3163946
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13259

- gi No. 32015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13260
- gi No. 320182
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13261
- gi No. 320192
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13262
- gi No. 320960
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13263
- gi No. 3334365
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13264
- gi No. 3334366
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13265
- gi No. 3334366
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13266
- gi No. 3348122
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13267
- gi No. 3745821
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1810: from 29 to 52
  
- Alignment No. 13268
- gi No. 3876026
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13269
- gi No. 3876416

- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13270
- gi No. 3880320
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13271
- gi No. 3915082
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13272
- gi No. 3915086
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13273
- gi No. 3915092
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13274
- gi No. 3915094
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13275
- gi No. 401161
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13276
- gi No. 4050007
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13277
- gi No. 4090251
- % Identity 72.7
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13278
- gi No. 4090271
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13279
- gi No. 4098272
- % Identity 83.8

- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13280
- gi No. 416222
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13281
- gi No. 4165488
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13282
- gi No. 4206112
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13283
- gi No. 421757
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13284
- gi No. 4416179
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13285
- gi No. 4583673
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55
  
- Alignment No. 13286
- gi No. 464840
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13287
- gi No. 464841
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13288
- gi No. 464846
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13289
- gi No. 464847
- % Identity 81.1
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13290
- gi No. 464849
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13291
- gi No. 4741827
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13292
- gi No. 477233
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13293
- gi No. 477265
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13294
- gi No. 4929136
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13295
- gi No. 5174477
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13296
- gi No. 5174733
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13297
- gi No. 539933
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13298
- gi No. 542179
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13299
- gi No. 549051
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13300
- gi No. 549052
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13301
- gi No. 55775
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13302
- gi No. 586073
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13303
- gi No. 586074
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13304
- gi No. 606648
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13305
- gi No. 630460
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13306
- gi No. 630460
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13307
- gi No. 65165
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13308
- gi No. 71575
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13309
- gi No. 71577
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63



- Alignment No. 13310
- gi No. 730899
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13311
- gi No. 84169
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13312
- gi No. 84373
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13313
- gi No. 90217
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13314
- gi No. 942596
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1811
- Ceres seq\_id 1501282
- Location of start within SEQ ID NO 1809: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284113

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1812
- Ceres seq\_id 1501306

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1813
- Ceres seq\_id 1501307
- Location of start within SEQ ID NO 1812: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1814
- Ceres seq\_id 1501308
- Location of start within SEQ ID NO 1812: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1815
- Ceres seq\_id 1501309
- Location of start within SEQ ID NO 1812: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13315
- gi No. 3935169
- % Identity 80.9
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1815: from 1 to 68
- Alignment No. 13316
- gi No. 3935171
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1815: from 1 to 53

Maximum Length Sequence corresponding to clone ID 284115

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1816
- Ceres seq\_id 1501310

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1817
- Ceres seq\_id 1501311
- Location of start within SEQ ID NO 1816: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13317
- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1817: from 69 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1818
- Ceres seq\_id 1501312
- Location of start within SEQ ID NO 1816: at 16 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13318
- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1818: from 64 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1819
- Ceres seq\_id 1501313
- Location of start within SEQ ID NO 1816: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13319

- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1819: from 49 to 70

Maximum Length Sequence corresponding to clone ID 284319

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1820
- Ceres seq\_id 1501318

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1821
- Ceres seq\_id 1501319
- Location of start within SEQ ID NO 1820: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13320
- gi No. 1743354
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1821: from 28 to 55

Maximum Length Sequence corresponding to clone ID 284342

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1822
- Ceres seq\_id 1501324

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1823
- Ceres seq\_id 1501325
- Location of start within SEQ ID NO 1822: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13321
- gi No. 2385410
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1823: from 144 to 179
- Alignment No. 13322
- gi No. 586324
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1823: from 142 to 179

Maximum Length Sequence corresponding to clone ID 284346

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1824
- Ceres seq\_id 1501326

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1825
- Ceres seq\_id 1501327
- Location of start within SEQ ID NO 1824: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13323
- Initiation factor 2 subunit
- Location within SEQ ID NO 1825: from 92 to 177 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13324
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1825: from 70 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1826
- Ceres seq\_id 1501328
- Location of start within SEQ ID NO 1824: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13325
- Initiation factor 2 subunit
- Location within SEQ ID NO 1826: from 72 to 157 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13326
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1826: from 50 to 60

Maximum Length Sequence corresponding to clone ID 284539

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1827
- Ceres seq\_id 1501329

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1828
- Ceres seq\_id 1501330
- Location of start within SEQ ID NO 1827: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1829
- Ceres seq\_id 1501331
- Location of start within SEQ ID NO 1827: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13327
- Glycosyl hydrolase family 1
- Location within SEQ ID NO 1829: from 48 to 162 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1830
- Ceres seq\_id 1501339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1831
- Ceres seq\_id 1501340
- Location of start within SEQ ID NO 1830: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13328
- Purine/pyrimidine phosphoribosyl transferases
- Location within SEQ ID NO 1831: from 51 to 135 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1832
- Ceres seq\_id 1501341
- Location of start within SEQ ID NO 1830: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1833
- Ceres seq\_id 1501342
- Location of start within SEQ ID NO 1830: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13329
- Purine/pyrimidine phosphoribosyl transferases
- Location within SEQ ID NO 1833: from 27 to 111 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284741

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1834
- Ceres seq\_id 1501345

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1835
- Ceres seq\_id 1501346
- Location of start within SEQ ID NO 1834: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13330
- gi No. 1644232
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1835: from 43 to 53

- Alignment No. 13331
- gi No. 4505323
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1835: from 43 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1836
- Ceres seq\_id 1501347
- Location of start within SEQ ID NO 1834: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1837
- Ceres seq\_id 1501348
- Location of start within SEQ ID NO 1834: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284789

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1838
- Ceres seq\_id 1501364

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1839
- Ceres seq\_id 1501365
- Location of start within SEQ ID NO 1838: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1840
- Ceres seq\_id 1501366
- Location of start within SEQ ID NO 1838: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13332
- Aldo/keto reductase family
- Location within SEQ ID NO 1840: from 13 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13333
- gi No. 1935911
- % Identity 90.4
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1840: from 76 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1841
- Ceres seq\_id 1501367
- Location of start within SEQ ID NO 1838: at 212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13334
- Aldo/keto reductase family
- Location within SEQ ID NO 1841: from 1 to 99 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13335
- gi No. 1935911
- % Identity 90.4
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1841: from 49 to 99

Maximum Length Sequence corresponding to clone ID 285304

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1842
- Ceres seq\_id 1501400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1843
- Ceres seq\_id 1501401
- Location of start within SEQ ID NO 1842: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1844
- Ceres seq\_id 1501402
- Location of start within SEQ ID NO 1842: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13336
- gi No. 2997589
- % Identity 100
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1844: from 1 to 61

Maximum Length Sequence corresponding to clone ID 285353

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1845
- Ceres seq\_id 1501416

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1846
- Ceres seq\_id 1501417
- Location of start within SEQ ID NO 1845: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13337
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1846: from 65 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1847
- Ceres seq\_id 1501418
- Location of start within SEQ ID NO 1845: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13338
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1847: from 64 to 112 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285545

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1848
- Ceres seq\_id 1501439

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1849
- Ceres seq\_id 1501440
- Location of start within SEQ ID NO 1848: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13339
- Pyruvate kinase
- Location within SEQ ID NO 1849: from 25 to 143 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1850
- Ceres seq\_id 1501441
- Location of start within SEQ ID NO 1848: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13340
- Pyruvate kinase
- Location within SEQ ID NO 1850: from 1 to 95 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1851
- Ceres seq\_id 1501442
- Location of start within SEQ ID NO 1848: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13341
- Pyruvate kinase
- Location within SEQ ID NO 1851: from 1 to 85 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285623

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1852
- Ceres seq\_id 1501471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1853
- Ceres seq\_id 1501472
- Location of start within SEQ ID NO 1852: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13342
- DNA topoisomerase II (N-terminal region)
- Location within SEQ ID NO 1853: from 1 to 117 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285664

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1854
- Ceres seq\_id 1501485

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1855



- Ceres seq\_id 1501486
- Location of start within SEQ ID NO 1854: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13343
  - gi No. 2134209
  - % Identity 70.4
  - Alignment Length 27
  - Location of Alignment in SEQ ID NO 1855: from 64 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1856
- Ceres seq\_id 1501487
- Location of start within SEQ ID NO 1854: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13344
- Aspartate/ornithine carbamoyltransferase
- Location within SEQ ID NO 1856: from 70 to 141 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1857
- Ceres seq\_id 1501488
- Location of start within SEQ ID NO 1854: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13345
- Aspartate/ornithine carbamoyltransferase
- Location within SEQ ID NO 1857: from 69 to 140 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285671

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1858
- Ceres seq\_id 1501489

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1859
- Ceres seq\_id 1501490
- Location of start within SEQ ID NO 1858: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13346
  - gi No. 2507155
  - % Identity 81.8
  - Alignment Length 12
  - Location of Alignment in SEQ ID NO 1859: from 1 to 11
- 
- Alignment No. 13347
  - gi No. 3122386
  - % Identity 85.5
  - Alignment Length 145
  - Location of Alignment in SEQ ID NO 1859: from 48 to 191

- Alignment No. 13348
- gi No. 3122387
- % Identity 84.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 1859: from 48 to 191
  
- Alignment No. 13349
- gi No. 439289
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11
  
- Alignment No. 13350
- gi No. 465445
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1859: from 5 to 15
  
- Alignment No. 13351
- gi No. 871535
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1860
- Ceres seq\_id 1501491
- Location of start within SEQ ID NO 1858: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285805

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1861
- Ceres seq\_id 1501515

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1862
- Ceres seq\_id 1501516
- Location of start within SEQ ID NO 1861: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13352
- Elongation factor 1 (beta/delta chain)
- Location within SEQ ID NO 1862: from 126 to 251 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13353
- gi No. 232031
- % Identity 85.2
- Alignment Length 225
- Location of Alignment in SEQ ID NO 1862: from 33 to 251
  
- Alignment No. 13354
- gi No. 232033
- % Identity 82.6
- Alignment Length 223
- Location of Alignment in SEQ ID NO 1862: from 33 to 251

- Alignment No. 13355
- gi No. 461073
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1862: from 180 to 209

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1863
- Ceres seq\_id 1501517
- Location of start within SEQ ID NO 1861: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13356
- Elongation factor 1 (beta/delta chain)
- Location within SEQ ID NO 1863: from 94 to 219 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13357
- gi No. 232031
- % Identity 85.2
- Alignment Length 225
- Location of Alignment in SEQ ID NO 1863: from 1 to 219
  
- Alignment No. 13358
- gi No. 232033
- % Identity 82.6
- Alignment Length 223
- Location of Alignment in SEQ ID NO 1863: from 1 to 219
  
- Alignment No. 13359
- gi No. 461073
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1863: from 148 to 177

Maximum Length Sequence corresponding to clone ID 285925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1864
- Ceres seq\_id 1501543

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1865
- Ceres seq\_id 1501544
- Location of start within SEQ ID NO 1864: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13360
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1865: from 44 to 193
  
- Alignment No. 13361
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193

- Alignment No. 13362
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1865: from 142 to 193
  
- Alignment No. 13363
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1865: from 51 to 193
  
- Alignment No. 13364
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1865: from 44 to 193
  
- Alignment No. 13365
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1865: from 46 to 193
  
- Alignment No. 13366
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1865: from 51 to 193
  
- Alignment No. 13367
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193
  
- Alignment No. 13368
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1865: from 46 to 193
  
- Alignment No. 13369
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1865: from 44 to 193
  
- Alignment No. 13370
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1865: from 46 to 193
  
- Alignment No. 13371
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1866
- Ceres seq\_id 1501545
- Location of start within SEQ ID NO 1864: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13372
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13373
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150
- Alignment No. 13374
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1866: from 99 to 150
- Alignment No. 13375
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1866: from 8 to 150
- Alignment No. 13376
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13377
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150
- Alignment No. 13378
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1866: from 8 to 150
- Alignment No. 13379
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150
- Alignment No. 13380
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150

- Alignment No. 13381
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
  
- Alignment No. 13382
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150
  
- Alignment No. 13383
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1867
- Ceres seq\_id 1501546
- Location of start within SEQ ID NO 1864: at 227 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13384
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13385
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13386
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1867: from 67 to 118
  
- Alignment No. 13387
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13388
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13389
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13390
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13391
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13392
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13393
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13394
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
  
- Alignment No. 13395
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

Maximum Length Sequence corresponding to clone ID 286066

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1868
- Ceres seq\_id 1501547

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1869
- Ceres seq\_id 1501548
- Location of start within SEQ ID NO 1868: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13396
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1869: from 94 to 241 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13397
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1869: from 91 to 114
  
- Alignment No. 13398
- gi No. 1304478

- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130
  
- Alignment No. 13399
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130
  
- Alignment No. 13400
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1869: from 91 to 243
  
- Alignment No. 13401
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1869: from 15 to 243
  
- Alignment No. 13402
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1869: from 15 to 243

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1870
- Ceres seq\_id 1501549
- Location of start within SEQ ID NO 1868: at 17 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13403
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1870: from 89 to 236 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13404
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1870: from 86 to 109
  
- Alignment No. 13405
- gi No. 1304478
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1870: from 86 to 125
  
- Alignment No. 13406
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1870: from 86 to 125
  
- Alignment No. 13407
- gi No. 2129487
- % Identity 81



- Alignment Length 153
- Location of Alignment in SEQ ID NO 1870: from 86 to 238
- Alignment No. 13408
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1870: from 10 to 238
- Alignment No. 13409
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1870: from 10 to 238

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1871
- Ceres seq\_id 1501550
- Location of start within SEQ ID NO 1868: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13410
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1871: from 13 to 160 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13411
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1871: from 10 to 33
- Alignment No. 13412
- gi No. 1304478
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1871: from 10 to 49
- Alignment No. 13413
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1871: from 10 to 49
- Alignment No. 13414
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1871: from 10 to 162
- Alignment No. 13415
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1871: from 1 to 162
- Alignment No. 13416
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229

- Location of Alignment in SEQ ID NO 1871: from 1 to 162

Maximum Length Sequence corresponding to clone ID 286096

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1872
- Ceres seq\_id 1501565

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1873
- Ceres seq\_id 1501566
- Location of start within SEQ ID NO 1872: at 457 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13417
- gi No. 1002689
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1873: from 7 to 31
  
- Alignment No. 13418
- gi No. 1172600
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13419
- gi No. 130847
- % Identity 78.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1873: from 1 to 33
  
- Alignment No. 13420
- gi No. 130860
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13421
- gi No. 2621771
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1873: from 7 to 31
  
- Alignment No. 13422
- gi No. 2650136
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1873: from 7 to 31
  
- Alignment No. 13423
- gi No. 3080509
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13424
- gi No. 3114275
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1873: from 5 to 33

- Alignment No. 13425
- gi No. 3421096
- % Identity 94.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13426
- gi No. 3914413
- % Identity 93.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1873: from 3 to 34
  
- Alignment No. 13427
- gi No. 3914424
- % Identity 91.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13428
- gi No. 3914431
- % Identity 94.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13429
- gi No. 3914438
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13430
- gi No. 3914440
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13431
- gi No. 4506183
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13432
- gi No. 542655
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
  
- Alignment No. 13433
- gi No. 585729
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1873: from 8 to 31

Maximum Length Sequence corresponding to clone ID 286125

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1874
- Ceres seq\_id 1501567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1875

- Ceres seq\_id 1501568
- Location of start within SEQ ID NO 1874: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1876
- Ceres seq\_id 1501569
- Location of start within SEQ ID NO 1874: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13434
- Ribosomal protein S11
- Location within SEQ ID NO 1876: from 29 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13435
- gi No. 1173200
- % Identity 95.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1876: from 67 to 129
  
- Alignment No. 13436
- gi No. 1173201
- % Identity 86.5
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1876: from 5 to 129
  
- Alignment No. 13437
- gi No. 131772
- % Identity 96.9
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13438
- gi No. 131773
- % Identity 94.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1876: from 3 to 129
  
- Alignment No. 13439
- gi No. 133771
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13440
- gi No. 133777
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
  
- Alignment No. 13441
- gi No. 133782
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13442
- gi No. 133785
- % Identity 84
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13443
- gi No. 133789
- % Identity 70.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1876: from 10 to 129
  
- Alignment No. 13444
- gi No. 1346941
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
  
- Alignment No. 13445
- gi No. 1350935
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13446
- gi No. 1350937
- % Identity 77.9
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13447
- gi No. 2350992
- % Identity 76
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1876: from 27 to 129
  
- Alignment No. 13448
- gi No. 2414647
- % Identity 80.9
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1876: from 16 to 129
  
- Alignment No. 13449
- gi No. 2500443
- % Identity 97.8
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1876: from 85 to 129
  
- Alignment No. 13450
- gi No. 3097244
- % Identity 85.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13451
- gi No. 3122785
- % Identity 90
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13452

- gi No. 4574240
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
  
- Alignment No. 13453
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13454
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13455
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13456
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13457
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1876: from 72 to 129
  
- Alignment No. 13458
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
  
- Alignment No. 13459
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
  
- Alignment No. 13460
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
  
- Alignment No. 13461
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
  
- Alignment No. 13462
- gi No. 83794

- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1877
- Ceres seq\_id 1501570
- Location of start within SEQ ID NO 1874: at 350 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13463
- Ribosomal protein S11
- Location within SEQ ID NO 1877: from 1 to 71 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13464
- gi No. 1173200
- % Identity 95.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1877: from 9 to 71
- Alignment No. 13465
- gi No. 1173201
- % Identity 86.5
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13466
- gi No. 131772
- % Identity 96.9
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13467
- gi No. 131773
- % Identity 94.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13468
- gi No. 133771
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13469
- gi No. 133777
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13470
- gi No. 133782
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13471
- gi No. 133785
- % Identity 84

- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13472
- gi No. 133789
- % Identity 70.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13473
- gi No. 1346941
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13474
- gi No. 1350935
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13475
- gi No. 1350937
- % Identity 77.9
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13476
- gi No. 2350992
- % Identity 76
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13477
- gi No. 2414647
- % Identity 80.9
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13478
- gi No. 2500443
- % Identity 97.8
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1877: from 27 to 71
  
- Alignment No. 13479
- gi No. 3097244
- % Identity 85.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13480
- gi No. 3122785
- % Identity 90
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
  
- Alignment No. 13481
- gi No. 4574240
- % Identity 84.5
- Alignment Length 110



- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13482
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13483
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13484
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13485
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13486
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1877: from 14 to 71
- Alignment No. 13487
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13488
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13489
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13490
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13491
- gi No. 83794
- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

Maximum Length Sequence corresponding to clone ID 286127

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1878
- Ceres seq\_id 1501571

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1879
- Ceres seq\_id 1501572
- Location of start within SEQ ID NO 1878: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13492
- gi No. 4506093
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1879: from 27 to 37

- Alignment No. 13493
- gi No. 973307
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1879: from 27 to 37

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1880
- Ceres seq\_id 1501573
- Location of start within SEQ ID NO 1878: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13494
- gi No. 2493240
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1880: from 145 to 158

- Alignment No. 13495
- gi No. 4808162
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157

- Alignment No. 13496
- gi No. 4808164
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157

- Alignment No. 13497
- gi No. 4808166
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157

- Alignment No. 13498
- gi No. 4808177
- % Identity 76.9
- Alignment Length 13

- Location of Alignment in SEQ ID NO 1880: from 145 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1881
- Ceres seq\_id 1501574
- Location of start within SEQ ID NO 1878: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13499
- gi No. 2493240
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1881: from 104 to 117
- Alignment No. 13500
- gi No. 4808162
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116
- Alignment No. 13501
- gi No. 4808164
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116
- Alignment No. 13502
- gi No. 4808166
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116
- Alignment No. 13503
- gi No. 4808177
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116

Maximum Length Sequence corresponding to clone ID 286161

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1882
- Ceres seq\_id 1501582

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1883
- Ceres seq\_id 1501583
- Location of start within SEQ ID NO 1882: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13504
- gi No. 2655291
- % Identity 84.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1883: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1884
- Ceres seq\_id 1501584

- Location of start within SEQ ID NO 1882: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13505
- gi No. 2655291
- % Identity 84.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1884: from 1 to 48

Maximum Length Sequence corresponding to clone ID 286175

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1885
- Ceres seq\_id 1501589

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1886
- Ceres seq\_id 1501590
- Location of start within SEQ ID NO 1885: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1887
- Ceres seq\_id 1501591
- Location of start within SEQ ID NO 1885: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13506
- Lysyl oxidase
- Location within SEQ ID NO 1887: from 53 to 170 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1888
- Ceres seq\_id 1501592
- Location of start within SEQ ID NO 1885: at 108 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13507
- Lysyl oxidase
- Location within SEQ ID NO 1888: from 18 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286275

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1889
- Ceres seq\_id 1501609

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1890
- Ceres seq\_id 1501610
- Location of start within SEQ ID NO 1889: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1891
- Ceres seq\_id 1501611
- Location of start within SEQ ID NO 1889: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1892
- Ceres seq\_id 1501612
- Location of start within SEQ ID NO 1889: at 324 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13508
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1892: from 3 to 42 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13509
- gi No. 2765531
- % Identity 76.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1892: from 1 to 15

Maximum Length Sequence corresponding to clone ID 286426

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1893
- Ceres seq\_id 1501624

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1894
- Ceres seq\_id 1501625
- Location of start within SEQ ID NO 1893: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13510
- gi No. 2135765
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1894: from 53 to 64

- Alignment No. 13511
- gi No. 4505285
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1894: from 53 to 64

- Alignment No. 13512
- gi No. 542994
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1894: from 21 to 34

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1895

- Ceres seq\_id 1501626
- Location of start within SEQ ID NO 1893: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13513
- gi No. 2224619
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1895: from 58 to 68
  
- Alignment No. 13514
- gi No. 418612
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1895: from 57 to 68

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1896
- Ceres seq\_id 1501627
- Location of start within SEQ ID NO 1893: at 82 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13515
- gi No. 2135765
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1896: from 26 to 37
  
- Alignment No. 13516
- gi No. 4505285
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1896: from 26 to 37

Maximum Length Sequence corresponding to clone ID 286438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1897
- Ceres seq\_id 1501632

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1898
- Ceres seq\_id 1501633
- Location of start within SEQ ID NO 1897: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13517
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1898: from 67 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1899
- Ceres seq\_id 1501634
- Location of start within SEQ ID NO 1897: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13518
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1899: from 28 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1900
- Ceres seq\_id 1501635
- Location of start within SEQ ID NO 1897: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13519
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1900: from 19 to 32

Maximum Length Sequence corresponding to clone ID 286538

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1901
- Ceres seq\_id 1501639

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1902
- Ceres seq\_id 1501640
- Location of start within SEQ ID NO 1901: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1903
- Ceres seq\_id 1501641
- Location of start within SEQ ID NO 1901: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1904
- Ceres seq\_id 1501642
- Location of start within SEQ ID NO 1901: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13520
- gi No. 2894559
- % Identity 89.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45
- Alignment No. 13521
- gi No. 4115936

- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45

Maximum Length Sequence corresponding to clone ID 286545

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1905
- Ceres seq\_id 1501643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1906
- Ceres seq\_id 1501644
- Location of start within SEQ ID NO 1905: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13522
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1906: from 1 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1907
- Ceres seq\_id 1501645
- Location of start within SEQ ID NO 1905: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13523
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1907: from 1 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1908
- Ceres seq\_id 1501646
- Location of start within SEQ ID NO 1905: at 399 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286676

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1909
- Ceres seq\_id 1501689

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1910
- Ceres seq\_id 1501690
- Location of start within SEQ ID NO 1909: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13524
- Ubiquitin family
- Location within SEQ ID NO 1910: from 1 to 74 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence



- Pat. Appln. SEQ ID NO 1911
- Ceres seq\_id 1501691
- Location of start within SEQ ID NO 1909: at 284 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1912
- Ceres seq\_id 1501692
- Location of start within SEQ ID NO 1909: at 368 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286738

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1913
- Ceres seq\_id 1501701

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1914
- Ceres seq\_id 1501702
- Location of start within SEQ ID NO 1913: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1915
- Ceres seq\_id 1501703
- Location of start within SEQ ID NO 1913: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13525
- gi No. 2244980
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1915: from 31 to 53
  
- Alignment No. 13526
- gi No. 4587539
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1915: from 31 to 50
  
- Alignment No. 13527
- gi No. 4914386
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1915: from 31 to 53

Maximum Length Sequence corresponding to clone ID 286767

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1916
- Ceres seq\_id 1501710

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1917
- Ceres seq\_id 1501711
- Location of start within SEQ ID NO 1916: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13528
- Protein phosphatase 2C
- Location within SEQ ID NO 1917: from 32 to 84 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1918
- Ceres seq\_id 1501712
- Location of start within SEQ ID NO 1916: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13529
- Protein phosphatase 2C
- Location within SEQ ID NO 1918: from 20 to 85 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1919
- Ceres seq\_id 1501713
- Location of start within SEQ ID NO 1916: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13530
- Protein phosphatase 2C
- Location within SEQ ID NO 1919: from 3 to 68 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286773

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1920
- Ceres seq\_id 1501718

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1921
- Ceres seq\_id 1501719
- Location of start within SEQ ID NO 1920: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13531
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13532
- gi No. 1340178
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1921: from 147 to 168

- Alignment No. 13533
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
  
- Alignment No. 13534
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
  
- Alignment No. 13535
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
  
- Alignment No. 13536
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
  
- Alignment No. 13537
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
  
- Alignment No. 13538
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166
  
- Alignment No. 13539
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1922
- Ceres seq\_id 1501720
- Location of start within SEQ ID NO 1920: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13540
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
  
- Alignment No. 13541
- gi No. 1340178
- % Identity 73.9
- Alignment Length 23

- Location of Alignment in SEQ ID NO 1922: from 131 to 152
- Alignment No. 13542
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13543
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13544
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13545
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13546
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13547
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150
- Alignment No. 13548
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1923
- Ceres seq\_id 1501721
- Location of start within SEQ ID NO 1920: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13549
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13550
- gi No. 1340178
- % Identity 73.9

- Alignment Length 23
- Location of Alignment in SEQ ID NO 1923: from 73 to 94
  
- Alignment No. 13551
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
  
- Alignment No. 13552
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
  
- Alignment No. 13553
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
  
- Alignment No. 13554
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
  
- Alignment No. 13555
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
  
- Alignment No. 13556
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92
  
- Alignment No. 13557
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92

Maximum Length Sequence corresponding to clone ID 286777

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1924
- Ceres seq\_id 1501722

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1925
- Ceres seq\_id 1501723
- Location of start within SEQ ID NO 1924: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1926
- Ceres seq\_id 1501724

- Location of start within SEQ ID NO 1924: at 41 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1927
- Ceres seq\_id 1501725
- Location of start within SEQ ID NO 1924: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13558
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1927: from 1 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286992

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1928
- Ceres seq\_id 1501730

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1929
- Ceres seq\_id 1501731
- Location of start within SEQ ID NO 1928: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13559
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 33 to 96 aa.
- Alignment No. 13560
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 45 to 102 aa.
- Alignment No. 13561
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 45 to 106 aa.
- Alignment No. 13562
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 62 to 108 aa.
- Alignment No. 13563
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 100 aa.
- Alignment No. 13564
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 106 aa.
- Alignment No. 13565
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 108 aa.
- Alignment No. 13566
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 94 aa.

- Alignment No. 13567
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 106 aa.
  
- Alignment No. 13568
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1930
- Ceres seq\_id 1501732
- Location of start within SEQ ID NO 1928: at 347 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1931
- Ceres seq\_id 1501733
- Location of start within SEQ ID NO 1928: at 389 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287753

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1932
- Ceres seq\_id 1501737

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1933
- Ceres seq\_id 1501738
- Location of start within SEQ ID NO 1932: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1934
- Ceres seq\_id 1501739
- Location of start within SEQ ID NO 1932: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13569
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1934: from 34 to 83 aa.
  
- Alignment No. 13570
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1934: from 5 to 83 aa.
  
- Alignment No. 13571
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1934: from 21 to 83 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13572
- gi No. 3327046
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1934: from 67 to 83
  
- Alignment No. 13573
- gi No. 3745837
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1934: from 65 to 83
  
- Alignment No. 13574
- gi No. 4028930
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1934: from 67 to 83
  
- Alignment No. 13575
- gi No. 4775349
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13576
- gi No. 4775349
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13577
- gi No. 4996894
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13578
- gi No. 4996894
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13579
- gi No. 688080
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1934: from 65 to 78

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1935
- Ceres seq\_id 1501740
- Location of start within SEQ ID NO 1932: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287760

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1936



- Ceres seq\_id 1501741
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1937
  - Ceres seq\_id 1501742
  - Location of start within SEQ ID NO 1936: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13580
- DnaJ domain
- Location within SEQ ID NO 1937: from 36 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13581
- gi No. 1125691
- % Identity 84.5
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13582
- gi No. 1169382
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13583
- gi No. 1169383
- % Identity 76.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13584
- gi No. 1169384
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13585
- gi No. 2129577
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13586
- gi No. 2370312
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13587
- gi No. 2641638
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13588
- gi No. 2984709
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13589
- gi No. 39890
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1937: from 37 to 55
  
- Alignment No. 13590
- gi No. 4008159
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13591
- gi No. 4097575
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13592
- gi No. 4097577
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13593
- gi No. 4210948
- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13594
- gi No. 421809
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13595
- gi No. 4589726
- % Identity 81
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13596
- gi No. 461942
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1937: from 45 to 81
  
- Alignment No. 13597
- gi No. 461944
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1938
- Ceres seq\_id 1501743
- Location of start within SEQ ID NO 1936: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1939
- Ceres seq\_id 1501744
- Location of start within SEQ ID NO 1936: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13598
- DnaJ domain
- Location within SEQ ID NO 1939: from 13 to 58 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13599
- gi No. 1125691
- % Identity 84.5
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13600
- gi No. 1169382
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13601
- gi No. 1169383
- % Identity 76.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13602
- gi No. 1169384
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13603
- gi No. 2129577
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13604
- gi No. 2370312
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13605
- gi No. 2641638
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13606
- gi No. 2984709
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13607
- gi No. 39890
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1939: from 14 to 32
  
- Alignment No. 13608
- gi No. 4008159
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
  
- Alignment No. 13609
- gi No. 4097575
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
  
- Alignment No. 13610
- gi No. 4097577
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
  
- Alignment No. 13611
- gi No. 4210948
- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
  
- Alignment No. 13612
- gi No. 421809
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
  
- Alignment No. 13613
- gi No. 4589726
- % Identity 81
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
  
- Alignment No. 13614
- gi No. 461942
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1939: from 22 to 58
  
- Alignment No. 13615
- gi No. 461944
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

Maximum Length Sequence corresponding to clone ID 288024

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1940
- Ceres seq\_id 1501755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1941

- Ceres seq\_id 1501756
- Location of start within SEQ ID NO 1940: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1942
- Ceres seq\_id 1501757
- Location of start within SEQ ID NO 1940: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1943
- Ceres seq\_id 1501758
- Location of start within SEQ ID NO 1940: at 207 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13616
- gi No. 2342735
- % Identity 81.8
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1943: from 37 to 91

Maximum Length Sequence corresponding to clone ID 288145

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1944
- Ceres seq\_id 1501763

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1945
- Ceres seq\_id 1501764
- Location of start within SEQ ID NO 1944: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13617
- Ribosomal protein L14
- Location within SEQ ID NO 1945: from 28 to 149 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13618
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
  
- Alignment No. 13619
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1945: from 17 to 149
  
- Alignment No. 13620
- gi No. 1350671
- % Identity 74.8

- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
  
- Alignment No. 13621
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
  
- Alignment No. 13622
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1945: from 10 to 96
  
- Alignment No. 13623
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1945: from 10 to 57
  
- Alignment No. 13624
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1945: from 14 to 149
  
- Alignment No. 13625
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
  
- Alignment No. 13626
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
  
- Alignment No. 13627
- gi No. 2706454
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1945: from 13 to 149
  
- Alignment No. 13628
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
  
- Alignment No. 13629
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1945: from 17 to 149
  
- Alignment No. 13630
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130

- Location of Alignment in SEQ ID NO 1945: from 20 to 149
- Alignment No. 13631
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1945: from 14 to 138
- Alignment No. 13632
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13633
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
- Alignment No. 13634
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13635
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13636
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1945: from 10 to 58
- Alignment No. 13637
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1946
- Ceres seq\_id 1501765
- Location of start within SEQ ID NO 1944: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13638
- Ribosomal protein L14
- Location within SEQ ID NO 1946: from 19 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13639
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13640
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1946: from 8 to 140
  
- Alignment No. 13641
- gi No. 1350671
- % Identity 74.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13642
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13643
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1946: from 1 to 87
  
- Alignment No. 13644
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1946: from 1 to 48
  
- Alignment No. 13645
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1946: from 5 to 140
  
- Alignment No. 13646
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140
  
- Alignment No. 13647
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13648
- gi No. 2706454
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1946: from 4 to 140
  
- Alignment No. 13649
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139



- Alignment No. 13650
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1946: from 8 to 140
  
- Alignment No. 13651
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1946: from 11 to 140
  
- Alignment No. 13652
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1946: from 5 to 129
  
- Alignment No. 13653
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13654
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140
  
- Alignment No. 13655
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13656
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13657
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1946: from 1 to 49
  
- Alignment No. 13658
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1947
- Ceres seq\_id 1501766
- Location of start within SEQ ID NO 1944: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13659
- Ribosomal protein L14
- Location within SEQ ID NO 1947: from 4 to 125 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13660
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13661
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13662
- gi No. 1350671
- % Identity 74.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13663
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13664
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1947: from 1 to 72
- Alignment No. 13665
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1947: from 1 to 33
- Alignment No. 13666
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13667
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13668
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13669
- gi No. 2706454

- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
  
- Alignment No. 13670
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
  
- Alignment No. 13671
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
  
- Alignment No. 13672
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
  
- Alignment No. 13673
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1947: from 1 to 114
  
- Alignment No. 13674
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
  
- Alignment No. 13675
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
  
- Alignment No. 13676
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
  
- Alignment No. 13677
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
  
- Alignment No. 13678
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1947: from 1 to 34
  
- Alignment No. 13679
- gi No. 730536
- % Identity 96.4

- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

Maximum Length Sequence corresponding to clone ID 288149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1948
- Ceres seq\_id 1501771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1949
- Ceres seq\_id 1501772
- Location of start within SEQ ID NO 1948: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1949: from 88 to 176 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1950
- Ceres seq\_id 1501773
- Location of start within SEQ ID NO 1948: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13681
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1950: from 43 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1951
- Ceres seq\_id 1501774
- Location of start within SEQ ID NO 1948: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13682
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1951: from 8 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 288431

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1952
- Ceres seq\_id 1501786

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1953
- Ceres seq\_id 1501787
- Location of start within SEQ ID NO 1952: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13683
- gi No. 1184100
- % Identity 90.9

- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50
- Alignment No. 13684
- gi No. 1914851
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 41 to 51
- Alignment No. 13685
- gi No. 688080
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1954
- Ceres seq\_id 1501788
- Location of start within SEQ ID NO 1952: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13686
- gi No. 19917
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1954: from 30 to 40
- Alignment No. 13687
- gi No. 322760
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1954: from 30 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1955
- Ceres seq\_id 1501789
- Location of start within SEQ ID NO 1952: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13688
- gi No. 19917
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1955: from 22 to 32
- Alignment No. 13689
- gi No. 322760
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1955: from 22 to 32

Maximum Length Sequence corresponding to clone ID 288440

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1956
- Ceres seq\_id 1501794

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1957

- Ceres seq\_id 1501795
- Location of start within SEQ ID NO 1956: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1958
- Ceres seq\_id 1501796
- Location of start within SEQ ID NO 1956: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13690
- gi No. 4521249
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

- Alignment No. 13691
- gi No. 4587311
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

- Alignment No. 13692
- gi No. 4929561
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1959
- Ceres seq\_id 1501797
- Location of start within SEQ ID NO 1956: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13693
- gi No. 4521249
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

- Alignment No. 13694
- gi No. 4587311
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

- Alignment No. 13695
- gi No. 4929561
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

Maximum Length Sequence corresponding to clone ID 288752

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1960
- Ceres seq\_id 1501804
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1961
  - Ceres seq\_id 1501805
  - Location of start within SEQ ID NO 1960: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13696
  - gi No. 1076501
  - % Identity 75
  - Alignment Length 12
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13697
  - gi No. 1076501
  - % Identity 76.9
  - Alignment Length 13
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13698
  - gi No. 1155068
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13699
  - gi No. 1155068
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13700
  - gi No. 1155068
  - % Identity 70.6
  - Alignment Length 17
  - Location of Alignment in SEQ ID NO 1961: from 62 to 74
- Alignment No. 13701
  - gi No. 1155068
  - % Identity 70.6
  - Alignment Length 17
  - Location of Alignment in SEQ ID NO 1961: from 62 to 74
- Alignment No. 13702
  - gi No. 2226329
  - % Identity 84.7
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 1961: from 34 to 91
- Alignment No. 13703
  - gi No. 399204
  - % Identity 86.4
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 1961: from 34 to 91
- Alignment No. 13704
  - gi No. 688422
  - % Identity 71.4

- Alignment Length 14
- Location of Alignment in SEQ ID NO 1961: from 79 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1962
- Ceres seq\_id 1501806
- Location of start within SEQ ID NO 1960: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13705
- Plant lipid transfer protein family
- Location within SEQ ID NO 1962: from 81 to 137 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13706
- gi No. 1092083
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1962: from 112 to 128
- Alignment No. 13707
- gi No. 2226329
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1962: from 89 to 136
- Alignment No. 13708
- gi No. 399204
- % Identity 81.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1962: from 89 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1963
- Ceres seq\_id 1501807
- Location of start within SEQ ID NO 1960: at 158 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 288760

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1964
- Ceres seq\_id 1501810

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1965
- Ceres seq\_id 1501811
- Location of start within SEQ ID NO 1964: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13709
- gi No. 1076418
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13710



- gi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 9 to 109
  
- Alignment No. 13711
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
  
- Alignment No. 13712
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 10 to 109
  
- Alignment No. 13713
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1965: from 12 to 105
  
- Alignment No. 13714
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
  
- Alignment No. 13715
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1965: from 34 to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1966
- Ceres seq\_id 1501812
- Location of start within SEQ ID NO 1964: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13716
- gi No. 1076418
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
  
- Alignment No. 13717
- gi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
  
- Alignment No. 13718
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

- Alignment No. 13719
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
  
- Alignment No. 13720
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1966: from 1 to 63
  
- Alignment No. 13721
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
  
- Alignment No. 13722
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

Maximum Length Sequence corresponding to clone ID 288771

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1967
- Ceres seq\_id 1501813

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1968
- Ceres seq\_id 1501814
- Location of start within SEQ ID NO 1967: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13723
- gi No. 3128181
- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1968: from 42 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1969
- Ceres seq\_id 1501815
- Location of start within SEQ ID NO 1967: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1970
- Ceres seq\_id 1501816
- Location of start within SEQ ID NO 1967: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13724
- gi No. 3128181

- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1970: from 1 to 59

Maximum Length Sequence corresponding to clone ID 289873

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1971
- Ceres seq\_id 1501824

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1972
- Ceres seq\_id 1501825
- Location of start within SEQ ID NO 1971: at 304 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13725
- GDP dissociation inhibitor
- Location within SEQ ID NO 1972: from 1 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13726
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1972: from 1 to 100
  
- Alignment No. 13727
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1972: from 1 to 100
  
- Alignment No. 13728
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1972: from 1 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1973
- Ceres seq\_id 1501826
- Location of start within SEQ ID NO 1971: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13729
- GDP dissociation inhibitor
- Location within SEQ ID NO 1973: from 1 to 95 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13730
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1973: from 1 to 95
  
- Alignment No. 13731
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

- Alignment No. 13732
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1974
- Ceres seq\_id 1501827
- Location of start within SEQ ID NO 1971: at 322 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13733
- GDP dissociation inhibitor
- Location within SEQ ID NO 1974: from 1 to 94 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13734
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1974: from 1 to 94
  
- Alignment No. 13735
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1974: from 1 to 94
  
- Alignment No. 13736
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

Maximum Length Sequence corresponding to clone ID 289892

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1975
- Ceres seq\_id 1501828

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1976
- Ceres seq\_id 1501829
- Location of start within SEQ ID NO 1975: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13737
- gi No. 3860272
- % Identity 85.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1976: from 62 to 163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1977
- Ceres seq\_id 1501830
- Location of start within SEQ ID NO 1975: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13738
- gi No. 3860272
- % Identity 85.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1977: from 1 to 102

Maximum Length Sequence corresponding to clone ID 291908

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1978
- Ceres seq\_id 1501850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1979
- Ceres seq\_id 1501851
- Location of start within SEQ ID NO 1978: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1980
- Ceres seq\_id 1501852
- Location of start within SEQ ID NO 1978: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1981
- Ceres seq\_id 1501853
- Location of start within SEQ ID NO 1978: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13739
- Thioredoxin
- Location within SEQ ID NO 1981: from 31 to 139 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13740
- gi No. 1848212
- % Identity 75.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1981: from 7 to 143

- Alignment No. 13741

- gi No. 2529680

- % Identity 74.6

- Alignment Length 138

- Location of Alignment in SEQ ID NO 1981: from 7 to 143

- Alignment No. 13742

- gi No. 729442

- % Identity 74.3

- Alignment Length 140

- Location of Alignment in SEQ ID NO 1981: from 5 to 143

- Alignment No. 13743
- gi No. 99991
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1981: from 52 to 70
  
- Alignment No. 13744
- gi No. 99991
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1981: from 51 to 70

Maximum Length Sequence corresponding to clone ID 292482

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1982
- Ceres seq\_id 1501862

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1983
- Ceres seq\_id 1501863
- Location of start within SEQ ID NO 1982: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1984
- Ceres seq\_id 1501864
- Location of start within SEQ ID NO 1982: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13745
- Ribosomal protein L13e
- Location within SEQ ID NO 1984: from 6 to 82 aa.

- Alignment No. 13746
- Fatty acid desaturase
- Location within SEQ ID NO 1984: from 77 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13747
- gi No. 1350664
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1984: from 10 to 82

- Alignment No. 13748
- gi No. 2662188
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1984: from 1 to 84

- Alignment No. 13749
- gi No. 730449
- % Identity 86.9
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1984: from 2 to 84

- Alignment No. 13750
- gi No. 730450

- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82
  
- Alignment No. 13751
- gi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1985
- Ceres seq\_id 1501865
- Location of start within SEQ ID NO 1982: at 274 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13752
- Fatty acid desaturase
- Location within SEQ ID NO 1985: from 11 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13753
- gi No. 1350664
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1985: from 1 to 16
  
- Alignment No. 13754
- gi No. 2662188
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1985: from 1 to 18
  
- Alignment No. 13755
- gi No. 730449
- % Identity 86.9
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1985: from 1 to 18
  
- Alignment No. 13756
- gi No. 730450
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1985: from 1 to 16
  
- Alignment No. 13757
- gi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1985: from 1 to 16

Maximum Length Sequence corresponding to clone ID 293228

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1986
- Ceres seq\_id 1501872

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1987
- Ceres seq\_id 1501873
- Location of start within SEQ ID NO 1986: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1988
- Ceres seq\_id 1501874
- Location of start within SEQ ID NO 1986: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13758
- Oleosin
- Location within SEQ ID NO 1988: from 1 to 78 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1989
- Ceres seq\_id 1501875
- Location of start within SEQ ID NO 1986: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13759
- Oleosin
- Location within SEQ ID NO 1989: from 1 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293659

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1990
- Ceres seq\_id 1501884

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1991
- Ceres seq\_id 1501885
- Location of start within SEQ ID NO 1990: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1992
- Ceres seq\_id 1501886
- Location of start within SEQ ID NO 1990: at 217 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13760
- gi No. 166410
- % Identity 78.8
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1992: from 1 to 112
- Alignment No. 13761
- gi No. 3894178
- % Identity 81.4
- Alignment Length 102



- Location of Alignment in SEQ ID NO 1992: from 12 to 112
- Alignment No. 13762
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13763
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13764
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1992: from 3 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1993
- Ceres seq\_id 1501887
- Location of start within SEQ ID NO 1990: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13765
- gi No. 166410
- % Identity 78.8
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13766
- gi No. 3894178
- % Identity 81.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13767
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13768
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13769
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1993: from 1 to 69

Maximum Length Sequence corresponding to clone ID 293683

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1994

- Ceres seq\_id 1501888
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1995
  - Ceres seq\_id 1501889
  - Location of start within SEQ ID NO 1994: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13770
- Aminotransferases class-I
- Location within SEQ ID NO 1995: from 16 to 109 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1996
  - Ceres seq\_id 1501890
  - Location of start within SEQ ID NO 1994: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13771
- Aminotransferases class-I
- Location within SEQ ID NO 1996: from 1 to 91 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1997
  - Ceres seq\_id 1501891
  - Location of start within SEQ ID NO 1994: at 299 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13772
- Aminotransferases class-I
- Location within SEQ ID NO 1997: from 1 to 77 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293689

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1998
  - Ceres seq\_id 1501895
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1999
  - Ceres seq\_id 1501896
  - Location of start within SEQ ID NO 1998: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13773
- DnaJ domain
- Location within SEQ ID NO 1999: from 5 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13774
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1999: from 13 to 47

- Alignment No. 13775
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1999: from 24 to 47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2000
- Ceres seq\_id 1501897
- Location of start within SEQ ID NO 1998: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13776
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2000: from 4 to 38
  
- Alignment No. 13777
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2000: from 15 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2001
- Ceres seq\_id 1501898
- Location of start within SEQ ID NO 1998: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13778
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2001: from 1 to 19
  
- Alignment No. 13779
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2001: from 1 to 19

Maximum Length Sequence corresponding to clone ID 293692

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2002
- Ceres seq\_id 1501899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2003
- Ceres seq\_id 1501900
- Location of start within SEQ ID NO 2002: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13780
- Pyruvate kinase
- Location within SEQ ID NO 2003: from 110 to 143 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13781
- gi No. 125606
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143
  
- Alignment No. 13782
- gi No. 2497538
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143
  
- Alignment No. 13783
- gi No. 2497543
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2003: from 109 to 143
  
- Alignment No. 13784
- gi No. 322787
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143
  
- Alignment No. 13785
- gi No. 4033431
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2003: from 109 to 143

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2004
- Ceres seq\_id 1501901
- Location of start within SEQ ID NO 2002: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13786
- gi No. 2134206
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2004: from 53 to 63

Maximum Length Sequence corresponding to clone ID 293697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2005
- Ceres seq\_id 1501902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2006
- Ceres seq\_id 1501903
- Location of start within SEQ ID NO 2005: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13787
- gi No. 1947160
- % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34
- Alignment No. 13788
- gi No. 3858883
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 18 to 28
- Alignment No. 13789
- gi No. 4996894
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2007
- Ceres seq\_id 1501904
- Location of start within SEQ ID NO 2005: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13790
- Syndecan domain
- Location within SEQ ID NO 2007: from 39 to 141 aa.
- Alignment No. 13791
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2007: from 24 to 139 aa.
- Alignment No. 13792
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 35 to 140 aa.
- Alignment No. 13793
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 35 to 141 aa.
- Alignment No. 13794
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 41 to 139 aa.
- Alignment No. 13795
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 59 to 139 aa.
- Alignment No. 13796
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 76 to 139 aa.
- Alignment No. 13797
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2007: from 21 to 137 aa.
- Alignment No. 13798
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2007: from 21 to 141 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13799
- gi No. 585527

- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2007: from 128 to 141

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2008
- Ceres seq\_id 1501905
- Location of start within SEQ ID NO 2005: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13800
- gi No. 113928
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2008: from 7 to 18
  
- Alignment No. 13801
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2008: from 18 to 28
  
- Alignment No. 13802
- gi No. 2077900
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2008: from 17 to 27
  
- Alignment No. 13803
- gi No. 280655
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2008: from 7 to 18

Maximum Length Sequence corresponding to clone ID 293718

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2009
- Ceres seq\_id 1501906

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2010
- Ceres seq\_id 1501907
- Location of start within SEQ ID NO 2009: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13804
- gi No. 2909522
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2010: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2011
- Ceres seq\_id 1501908
- Location of start within SEQ ID NO 2009: at 388 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2012
- Ceres seq\_id 1501909
- Location of start within SEQ ID NO 2009: at 407 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2013
- Ceres seq\_id 1501922

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2014
- Ceres seq\_id 1501923
- Location of start within SEQ ID NO 2013: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13805
- Peroxidase
- Location within SEQ ID NO 2014: from 48 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2015
- Ceres seq\_id 1501924
- Location of start within SEQ ID NO 2013: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13806
- Peroxidase
- Location within SEQ ID NO 2015: from 43 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2016
- Ceres seq\_id 1501925
- Location of start within SEQ ID NO 2013: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13807
- Peroxidase
- Location within SEQ ID NO 2016: from 42 to 107 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293858

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2017
- Ceres seq\_id 1501926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2018
- Ceres seq\_id 1501927

- Location of start within SEQ ID NO 2017: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13808
- Synaptobrevin
- Location within SEQ ID NO 2018: from 62 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13809
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2018: from 62 to 121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2019
- Ceres seq\_id 1501928
- Location of start within SEQ ID NO 2017: at 205 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13810
- Synaptobrevin
- Location within SEQ ID NO 2019: from 57 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13811
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2019: from 57 to 116

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2020
- Ceres seq\_id 1501929
- Location of start within SEQ ID NO 2017: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13812
- Synaptobrevin
- Location within SEQ ID NO 2020: from 10 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13813
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2020: from 10 to 69

Maximum Length Sequence corresponding to clone ID 293863

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2021
- Ceres seq\_id 1501930

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2022
- Ceres seq\_id 1501931
- Location of start within SEQ ID NO 2021: at 2 nt.



(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2023
- Ceres seq\_id 1501932
- Location of start within SEQ ID NO 2021: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13814
- gi No. 2213626
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2023: from 9 to 27

- Alignment No. 13815
- gi No. 4850408
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2023: from 13 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2024
- Ceres seq\_id 1501933
- Location of start within SEQ ID NO 2021: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293882

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2025
- Ceres seq\_id 1501949

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2026
- Ceres seq\_id 1501950
- Location of start within SEQ ID NO 2025: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2027
- Ceres seq\_id 1501951
- Location of start within SEQ ID NO 2025: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2028
- Ceres seq\_id 1501952
- Location of start within SEQ ID NO 2025: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13816
- ABC transporter
- Location within SEQ ID NO 2028: from 83 to 147 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297023

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2029
- Ceres seq\_id 1501976

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2030
- Ceres seq\_id 1501977
- Location of start within SEQ ID NO 2029: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2031
- Ceres seq\_id 1501978
- Location of start within SEQ ID NO 2029: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13817
- gi No. 4678325
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2031: from 41 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2032
- Ceres seq\_id 1501979
- Location of start within SEQ ID NO 2029: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13818
- gi No. 4678325
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2032: from 17 to 86

Maximum Length Sequence corresponding to clone ID 297685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2033
- Ceres seq\_id 1502003

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2034
- Ceres seq\_id 1502004
- Location of start within SEQ ID NO 2033: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2035
- Ceres seq\_id 1502005
- Location of start within SEQ ID NO 2033: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13819
- Gag polyprotein, inner coat protein p12
- Location within SEQ ID NO 2035: from 35 to 89 aa.
- Alignment No. 13820
- Mucin-like glycoprotein
- Location within SEQ ID NO 2035: from 12 to 130 aa.
- Alignment No. 13821
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 27 to 85 aa.
- Alignment No. 13822
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 27 to 93 aa.
- Alignment No. 13823
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 33 to 116 aa.
- Alignment No. 13824
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 34 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13825
- gi No. 2134206
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13826
- gi No. 2134208
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13827
- gi No. 2134209
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13828
- gi No. 2507155
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13829
- gi No. 439289
- % Identity 72.7
- Alignment Length 11

- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13830
- gi No. 871535
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13831
- gi No. 93144
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2035: from 32 to 52
- Alignment No. 13832
- gi No. 93144
- % Identity 73.9
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2035: from 32 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2036
- Ceres seq\_id 1502006
- Location of start within SEQ ID NO 2033: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297707

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2037
- Ceres seq\_id 1502011

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2038
- Ceres seq\_id 1502012
- Location of start within SEQ ID NO 2037: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13833
- gi No. 3915131
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2038: from 24 to 61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2039
- Ceres seq\_id 1502013
- Location of start within SEQ ID NO 2037: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13834
- GMC oxidoreductases
- Location within SEQ ID NO 2039: from 1 to 55 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13835
- gi No. 4903006

- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63
- Alignment No. 13836
- gi No. 4903018
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2040
- Ceres seq\_id 1502014
- Location of start within SEQ ID NO 2037: at 575 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297709

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2041
- Ceres seq\_id 1502015

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2042
- Ceres seq\_id 1502016
- Location of start within SEQ ID NO 2041: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2043
- Ceres seq\_id 1502017
- Location of start within SEQ ID NO 2041: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13837
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2043: from 41 to 54

- Alignment No. 13838
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2043: from 41 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2044
- Ceres seq\_id 1502018
- Location of start within SEQ ID NO 2041: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13839

- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29
  
- Alignment No. 13840
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29

Maximum Length Sequence corresponding to clone ID 297786

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2045
- Ceres seq\_id 1502023

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2046
- Ceres seq\_id 1502024
- Location of start within SEQ ID NO 2045: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13841
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2046: from 78 to 129 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2047
- Ceres seq\_id 1502025
- Location of start within SEQ ID NO 2045: at 289 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2048
- Ceres seq\_id 1502026
- Location of start within SEQ ID NO 2045: at 298 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297797

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2049
- Ceres seq\_id 1502027

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2050
- Ceres seq\_id 1502028
- Location of start within SEQ ID NO 2049: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2051

- Ceres seq\_id 1502029
- Location of start within SEQ ID NO 2049: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2052
- Ceres seq\_id 1502030
- Location of start within SEQ ID NO 2049: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13842
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2052: from 1 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13843
- gi No. 1174852
- % Identity 78.9
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2052: from 7 to 81
  
- Alignment No. 13844
- gi No. 136647
- % Identity 86.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2052: from 23 to 81
  
- Alignment No. 13845
- gi No. 2129758
- % Identity 83.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2052: from 6 to 81
  
- Alignment No. 13846
- gi No. 2624417
- % Identity 98.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2052: from 1 to 81
  
- Alignment No. 13847
- gi No. 2641619
- % Identity 89
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2052: from 1 to 81
  
- Alignment No. 13848
- gi No. 992706
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2052: from 6 to 81

Maximum Length Sequence corresponding to clone ID 297802

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2053
- Ceres seq\_id 1502031

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2054

- Ceres seq\_id 1502032
- Location of start within SEQ ID NO 2053: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13849
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2054: from 110 to 174 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13850
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2054: from 35 to 174
- Alignment No. 13851
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2054: from 22 to 174
- Alignment No. 13852
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2054: from 29 to 174
- Alignment No. 13853
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174
- Alignment No. 13854
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2054: from 84 to 174
- Alignment No. 13855
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2054: from 53 to 174
- Alignment No. 13856
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174
- Alignment No. 13857
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2054: from 53 to 174
- Alignment No. 13858
- gi No. 97570
- % Identity 75



- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2055
- Ceres seq\_id 1502033
- Location of start within SEQ ID NO 2053: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13859
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2055: from 89 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13860
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2055: from 14 to 153
  
- Alignment No. 13861
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2055: from 1 to 153
  
- Alignment No. 13862
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2055: from 8 to 153
  
- Alignment No. 13863
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
  
- Alignment No. 13864
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2055: from 63 to 153
  
- Alignment No. 13865
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2055: from 32 to 153
  
- Alignment No. 13866
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
  
- Alignment No. 13867
- gi No. 399785
- % Identity 78
- Alignment Length 123

- Location of Alignment in SEQ ID NO 2055: from 32 to 153
- Alignment No. 13868
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2056
- Ceres seq\_id 1502034
- Location of start within SEQ ID NO 2053: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13869
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2056: from 69 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13870
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13871
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13872
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13873
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133
- Alignment No. 13874
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2056: from 43 to 133
- Alignment No. 13875
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133
- Alignment No. 13876
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

- Alignment No. 13877
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133
  
- Alignment No. 13878
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

Maximum Length Sequence corresponding to clone ID 297826

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2057
- Ceres seq\_id 1502035

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2058
- Ceres seq\_id 1502036
- Location of start within SEQ ID NO 2057: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13879
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2058: from 67 to 119 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2059
- Ceres seq\_id 1502037
- Location of start within SEQ ID NO 2057: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13880
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2059: from 65 to 117 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2060
- Ceres seq\_id 1502038
- Location of start within SEQ ID NO 2057: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13881
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2060: from 57 to 109 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298533

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2061
- Ceres seq\_id 1502048

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2062
- Ceres seq\_id 1502049
- Location of start within SEQ ID NO 2061: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2063
- Ceres seq\_id 1502050
- Location of start within SEQ ID NO 2061: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13882
- Sugar (and other) transporter
- Location within SEQ ID NO 2063: from 26 to 175 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2064
- Ceres seq\_id 1502056

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2065
- Ceres seq\_id 1502057
- Location of start within SEQ ID NO 2064: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2066
- Ceres seq\_id 1502058
- Location of start within SEQ ID NO 2064: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13883
- gi No. 3402683
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2066: from 22 to 48

- Alignment No. 13884
- gi No. 4678298
- % Identity 95.7
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2066: from 22 to 44

- Alignment No. 13885
- gi No. 4914404
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2066: from 24 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2067
- Ceres seq\_id 1502059
- Location of start within SEQ ID NO 2064: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13886
- gi No. 3402683
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2067: from 16 to 42
  
- Alignment No. 13887
- gi No. 4678298
- % Identity 95.7
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2067: from 16 to 38
  
- Alignment No. 13888
- gi No. 4914404
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2067: from 18 to 46

Maximum Length Sequence corresponding to clone ID 298567

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2068
- Ceres seq\_id 1502066

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2069
- Ceres seq\_id 1502067
- Location of start within SEQ ID NO 2068: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13889
- DnaJ domain
- Location within SEQ ID NO 2069: from 12 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298580

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2070
- Ceres seq\_id 1502074

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2071
- Ceres seq\_id 1502075
- Location of start within SEQ ID NO 2070: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13890
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2071: from 70 to 120 aa.
  
- Alignment No. 13891
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 34 to 153 aa.

- Alignment No. 13892
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 58 to 148 aa.
  
- Alignment No. 13893
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 58 to 151 aa.
  
- Alignment No. 13894
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 41 to 153 aa.
  
- Alignment No. 13895
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 48 to 153 aa.
  
- Alignment No. 13896
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 59 to 134 aa.
  
- Alignment No. 13897
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 116 aa.
  
- Alignment No. 13898
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 140 aa.
  
- Alignment No. 13899
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 147 aa.
  
- Alignment No. 13900
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 150 aa.
  
- Alignment No. 13901
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13902
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2071: from 32 to 153
  
- Alignment No. 13903
- gi No. 228937
- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
  
- Alignment No. 13904
- gi No. 228938
- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
  
- Alignment No. 13905
- gi No. 283032

- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
  
- Alignment No. 13906
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
  
- Alignment No. 13907
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 107 to 141
  
- Alignment No. 13908
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 118 to 153
  
- Alignment No. 13909
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2071: from 112 to 149
  
- Alignment No. 13910
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
  
- Alignment No. 13911
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
  
- Alignment No. 13912
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2071: from 107 to 148
  
- Alignment No. 13913
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2071: from 28 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2072
- Ceres seq\_id 1502076
- Location of start within SEQ ID NO 2070: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13914
- Collagen triple helix repeat (20 copies)

- Location within SEQ ID NO 2072: from 44 to 94 aa.
- Alignment No. 13915
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 8 to 127 aa.
- Alignment No. 13916
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 122 aa.
- Alignment No. 13917
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 125 aa.
- Alignment No. 13918
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 15 to 127 aa.
- Alignment No. 13919
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 22 to 127 aa.
- Alignment No. 13920
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 33 to 108 aa.
- Alignment No. 13921
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 90 aa.
- Alignment No. 13922
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 114 aa.
- Alignment No. 13923
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 121 aa.
- Alignment No. 13924
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 124 aa.
- Alignment No. 13925
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13926
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2072: from 6 to 127
- Alignment No. 13927
- gi No. 228937
- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- Alignment No. 13928
- gi No. 228938



- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
  
- Alignment No. 13929
- gi No. 283032
- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
  
- Alignment No. 13930
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
  
- Alignment No. 13931
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2072: from 81 to 115
  
- Alignment No. 13932
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2072: from 92 to 127
  
- Alignment No. 13933
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2072: from 86 to 123
  
- Alignment No. 13934
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2072: from 86 to 125
  
- Alignment No. 13935
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2072: from 86 to 125
  
- Alignment No. 13936
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2072: from 81 to 122
  
- Alignment No. 13937
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2073
- Ceres seq\_id 1502077

- Location of start within SEQ ID NO 2070: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13938
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2073: from 43 to 93 aa.
  
- Alignment No. 13939
- Mucin-like glycoprotein
- Location within SEQ ID NO 2073: from 7 to 126 aa.
  
- Alignment No. 13940
- Mucin-like glycoprotein
- Location within SEQ ID NO 2073: from 31 to 121 aa.
  
- Alignment No. 13941
- Mucin-like glycoprotein
- Location within SEQ ID NO 2073: from 31 to 124 aa.
  
- Alignment No. 13942
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 14 to 126 aa.
  
- Alignment No. 13943
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 21 to 126 aa.
  
- Alignment No. 13944
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 32 to 107 aa.
  
- Alignment No. 13945
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 89 aa.
  
- Alignment No. 13946
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 113 aa.
  
- Alignment No. 13947
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 120 aa.
  
- Alignment No. 13948
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 123 aa.
  
- Alignment No. 13949
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13950
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2073: from 5 to 126
  
- Alignment No. 13951
- gi No. 228937

- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
  
- Alignment No. 13952
- gi No. 228938
- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
  
- Alignment No. 13953
- gi No. 283032
- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
  
- Alignment No. 13954
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
  
- Alignment No. 13955
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2073: from 80 to 114
  
- Alignment No. 13956
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2073: from 91 to 126
  
- Alignment No. 13957
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2073: from 85 to 122
  
- Alignment No. 13958
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2073: from 85 to 124
  
- Alignment No. 13959
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2073: from 85 to 124
  
- Alignment No. 13960
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2073: from 80 to 121
  
- Alignment No. 13961
- gi No. 82698
- % Identity 91.6

- Alignment Length 137
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

Maximum Length Sequence corresponding to clone ID 300006

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2074
- Ceres seq\_id 1502086

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2075
- Ceres seq\_id 1502087
- Location of start within SEQ ID NO 2074: at 222 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13962
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2075: from 35 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13963
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112
- Alignment No. 13964
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112
- Alignment No. 13965
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112
- Alignment No. 13966
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2076
- Ceres seq\_id 1502088
- Location of start within SEQ ID NO 2074: at 294 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13967
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2076: from 11 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13968
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

- Alignment No. 13969
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
  
- Alignment No. 13970
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
  
- Alignment No. 13971
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2077
- Ceres seq\_id 1502089
- Location of start within SEQ ID NO 2074: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13972
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2077: from 5 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13973
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82
  
- Alignment No. 13974
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82
  
- Alignment No. 13975
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82
  
- Alignment No. 13976
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82

Maximum Length Sequence corresponding to clone ID 300011

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2078
- Ceres seq\_id 1502090

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2079
- Ceres seq\_id 1502091

- Location of start within SEQ ID NO 2078: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13977
- gi No. 2134207
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13978
- gi No. 2134208
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13979
- gi No. 2134209
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13980
- gi No. 2134210
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13981
- gi No. 2134211
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2080
- Ceres seq\_id 1502092
- Location of start within SEQ ID NO 2078: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2081
- Ceres seq\_id 1502093
- Location of start within SEQ ID NO 2078: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300014

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2082
- Ceres seq\_id 1502094

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2083
- Ceres seq\_id 1502095
- Location of start within SEQ ID NO 2082: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13982
- Glutathione S-transferases.
- Location within SEQ ID NO 2083: from 32 to 211 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2084
- Ceres seq\_id 1502096
- Location of start within SEQ ID NO 2082: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13983
- Glutathione S-transferases.
- Location within SEQ ID NO 2084: from 26 to 205 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2085
- Ceres seq\_id 1502097
- Location of start within SEQ ID NO 2082: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13984
- Glutathione S-transferases.
- Location within SEQ ID NO 2085: from 16 to 195 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300700

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2086
- Ceres seq\_id 1502100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2087
- Ceres seq\_id 1502101
- Location of start within SEQ ID NO 2086: at 53 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2088
- Ceres seq\_id 1502102
- Location of start within SEQ ID NO 2086: at 171 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13985
- Pentapeptide repeats (8 copies)
- Location within SEQ ID NO 2088: from 101 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2089
- Ceres seq\_id 1502130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2090
- Ceres seq\_id 1502131
- Location of start within SEQ ID NO 2089: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13986
- gi No. 1352442
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155
- Alignment No. 13987
- gi No. 170753
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155
- Alignment No. 13988
- gi No. 3342823
- % Identity 84.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2090: from 58 to 155
- Alignment No. 13989
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2091
- Ceres seq\_id 1502132
- Location of start within SEQ ID NO 2089: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13990
- gi No. 1352442
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101
- Alignment No. 13991
- gi No. 170753
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101
- Alignment No. 13992
- gi No. 3342823
- % Identity 84.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2091: from 4 to 101



- Alignment No. 13993
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101

Maximum Length Sequence corresponding to clone ID 302718

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2092
- Ceres seq\_id 1502133

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2093
- Ceres seq\_id 1502134
- Location of start within SEQ ID NO 2092: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2094
- Ceres seq\_id 1502135
- Location of start within SEQ ID NO 2092: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13994
- Protamine P1
- Location within SEQ ID NO 2094: from 22 to 94 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2095
- Ceres seq\_id 1502136
- Location of start within SEQ ID NO 2092: at 247 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13995
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2095: from 23 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13996
- gi No. 266410
- % Identity 82.9
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2095: from 7 to 88

Maximum Length Sequence corresponding to clone ID 302744

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2096
- Ceres seq\_id 1502153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2097
- Ceres seq\_id 1502154
- Location of start within SEQ ID NO 2096: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13997
- Cytochrome P450
- Location within SEQ ID NO 2097: from 66 to 173 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13998
- gi No. 1870203
- % Identity 99.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 2097: from 10 to 173
- Alignment No. 13999
- gi No. 5420116
- % Identity 99.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 2097: from 11 to 173

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2098
- Ceres seq\_id 1502155
- Location of start within SEQ ID NO 2096: at 28 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14000
- Cytochrome P450
- Location within SEQ ID NO 2098: from 57 to 164 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14001
- gi No. 1870203
- % Identity 99.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 2098: from 1 to 164
- Alignment No. 14002
- gi No. 5420116
- % Identity 99.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 2098: from 2 to 164

Maximum Length Sequence corresponding to clone ID 303152

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2099
- Ceres seq\_id 1502165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2100
- Ceres seq\_id 1502166
- Location of start within SEQ ID NO 2099: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2101
- Ceres seq\_id 1502167
- Location of start within SEQ ID NO 2099: at 177 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14003
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2101: from 60 to 126 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 303165

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2102
- Ceres seq\_id 1502168

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2103
- Ceres seq\_id 1502169
- Location of start within SEQ ID NO 2102: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14004
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 2103: from 18 to 153 aa.
- Alignment No. 14005
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 2103: from 21 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14006
- gi No. 3269286
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2103: from 19 to 52
- Alignment No. 14007
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2103: from 20 to 50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2104
- Ceres seq\_id 1502170
- Location of start within SEQ ID NO 2102: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14008
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 2104: from 5 to 140 aa.
- Alignment No. 14009
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 2104: from 8 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14010
- gi No. 3269286
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2104: from 6 to 39

- Alignment No. 14011
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2104: from 7 to 37

Maximum Length Sequence corresponding to clone ID 303456

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2105
- Ceres seq\_id 1502189

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2106
- Ceres seq\_id 1502190
- Location of start within SEQ ID NO 2105: at 192 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14012
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2106: from 14 to 165 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14013
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2106: from 14 to 165
  
- Alignment No. 14014
- gi No. 2529670
- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2106: from 14 to 165
  
- Alignment No. 14015
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2106: from 14 to 165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2107
- Ceres seq\_id 1502191
- Location of start within SEQ ID NO 2105: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14016
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2107: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14017
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
  
- Alignment No. 14018
- gi No. 2529670

- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
- Alignment No. 14019
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2108
- Ceres seq\_id 1502192
- Location of start within SEQ ID NO 2105: at 315 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14020
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2108: from 1 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14021
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2108: from 1 to 124
- Alignment No. 14022
- gi No. 2529670
- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2108: from 1 to 124
- Alignment No. 14023
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2108: from 1 to 124

Maximum Length Sequence corresponding to clone ID 303464

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2109
- Ceres seq\_id 1502193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2110
- Ceres seq\_id 1502194
- Location of start within SEQ ID NO 2109: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14024
- gi No. 100219
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2110: from 7 to 24
- Alignment No. 14025
- gi No. 100219
- % Identity 73.7

- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25
- Alignment No. 14026
- gi No. 100219
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25

Maximum Length Sequence corresponding to clone ID 303902

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2111
- Ceres seq\_id 1502205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2112
- Ceres seq\_id 1502206
- Location of start within SEQ ID NO 2111: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14027
- Glutathione peroxidases
- Location within SEQ ID NO 2112: from 9 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14028
- gi No. 1362150
- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2112: from 53 to 98
- Alignment No. 14029
- gi No. 1708062
- % Identity 71.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14030
- gi No. 2274857
- % Identity 71.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14031
- gi No. 232190
- % Identity 74.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14032
- gi No. 2388885
- % Identity 76.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2112: from 4 to 98
- Alignment No. 14033
- gi No. 2388887
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2112: from 70 to 98

- Alignment No. 14034
- gi No. 2392021
- % Identity 75
- Alignment Length 100
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
  
- Alignment No. 14035
- gi No. 2632109
- % Identity 71.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 2112: from 9 to 98
  
- Alignment No. 14036
- gi No. 2746232
- % Identity 74
- Alignment Length 100
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
  
- Alignment No. 14037
- gi No. 2760606
- % Identity 86.7
- Alignment Length 98
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
  
- Alignment No. 14038
- gi No. 3023912
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2112: from 59 to 75
  
- Alignment No. 14039
- gi No. 3913793
- % Identity 81.4
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2112: from 13 to 98
  
- Alignment No. 14040
- gi No. 3913794
- % Identity 71.4
- Alignment Length 98
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
  
- Alignment No. 14041
- gi No. 4138608
- % Identity 91.7
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2112: from 1 to 72
  
- Alignment No. 14042
- gi No. 4584526
- % Identity 73.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
  
- Alignment No. 14043
- gi No. 485512
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98
  
- Alignment No. 14044

- gi No. 544437
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98

Maximum Length Sequence corresponding to clone ID 304670

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2113
- Ceres seq\_id 1502220

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2114
- Ceres seq\_id 1502221
- Location of start within SEQ ID NO 2113: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14045
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14046
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2114: from 95 to 173
  
- Alignment No. 14047
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14048
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14049
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14050
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14051
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14052
- gi No. 687927



- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2114: from 106 to 125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2115
- Ceres seq\_id 1502222
- Location of start within SEQ ID NO 2113: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14053
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14054
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2115: from 92 to 170
  
- Alignment No. 14055
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14056
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14057
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14058
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14059
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14060
- gi No. 687927
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2115: from 103 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2116
- Ceres seq\_id 1502223
- Location of start within SEQ ID NO 2113: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14061
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14062
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2116: from 38 to 116
- Alignment No. 14063
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14064
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14065
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14066
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14067
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14068
- gi No. 687927
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2116: from 49 to 68

Maximum Length Sequence corresponding to clone ID 304673

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2117
- Ceres seq\_id 1502224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2118

- Ceres seq\_id 1502225
- Location of start within SEQ ID NO 2117: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14069
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2118: from 110 to 183 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2119
- Ceres seq\_id 1502226
- Location of start within SEQ ID NO 2117: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14070
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2119: from 96 to 169 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2120
- Ceres seq\_id 1502227
- Location of start within SEQ ID NO 2117: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14071
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2120: from 75 to 148 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304677

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2121
- Ceres seq\_id 1502228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2122
- Ceres seq\_id 1502229
- Location of start within SEQ ID NO 2121: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2123
- Ceres seq\_id 1502230
- Location of start within SEQ ID NO 2121: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14072
- Pollen allergen
- Location within SEQ ID NO 2123: from 28 to 105 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2124
- Ceres seq\_id 1502231
- Location of start within SEQ ID NO 2121: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14073
- Pollen allergen
- Location within SEQ ID NO 2124: from 16 to 93 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311105

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2125
- Ceres seq\_id 1502270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2126
- Ceres seq\_id 1502271
- Location of start within SEQ ID NO 2125: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14074
- Ras family
- Location within SEQ ID NO 2126: from 31 to 158 aa.
- Alignment No. 14075
- ADP-ribosylation factor family
- Location within SEQ ID NO 2126: from 31 to 148 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14076
- gi No. 1370172
- % Identity 72.9
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2126: from 20 to 158
- Alignment No. 14077
- gi No. 2723477
- % Identity 75.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2126: from 19 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2127
- Ceres seq\_id 1502272
- Location of start within SEQ ID NO 2125: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14078
- Ras family
- Location within SEQ ID NO 2127: from 14 to 141 aa.
- Alignment No. 14079
- ADP-ribosylation factor family
- Location within SEQ ID NO 2127: from 14 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14080
- gi No. 1370172
- % Identity 72.9
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2127: from 3 to 141
  
- Alignment No. 14081
- gi No. 2723477
- % Identity 75.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2127: from 2 to 141

Maximum Length Sequence corresponding to clone ID 311199

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2128
- Ceres seq\_id 1502285

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2129
- Ceres seq\_id 1502286
- Location of start within SEQ ID NO 2128: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14082
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2129: from 94 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2130
- Ceres seq\_id 1502287
- Location of start within SEQ ID NO 2128: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14083
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2130: from 77 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2131
- Ceres seq\_id 1502288
- Location of start within SEQ ID NO 2128: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14084
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2131: from 73 to 91

Maximum Length Sequence corresponding to clone ID 311212

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2132
- Ceres seq\_id 1502297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2133
- Ceres seq\_id 1502298
- Location of start within SEQ ID NO 2132: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2134
- Ceres seq\_id 1502299
- Location of start within SEQ ID NO 2132: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14085
- gi No. 102706
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2134: from 81 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2135
- Ceres seq\_id 1502300
- Location of start within SEQ ID NO 2132: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14086
- gi No. 102706
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2135: from 66 to 81

Maximum Length Sequence corresponding to clone ID 311293

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2136
- Ceres seq\_id 1502315

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2137
- Ceres seq\_id 1502316
- Location of start within SEQ ID NO 2136: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14087
- gi No. 2739368
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2137: from 56 to 130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2138
- Ceres seq\_id 1502317

- Location of start within SEQ ID NO 2136: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14088
- gi No. 2739368
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2138: from 1 to 75

Maximum Length Sequence corresponding to clone ID 311422

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2139
- Ceres seq\_id 1502363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2140
- Ceres seq\_id 1502364
- Location of start within SEQ ID NO 2139: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14089
- gi No. 396749
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2140: from 84 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2141
- Ceres seq\_id 1502365
- Location of start within SEQ ID NO 2139: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2142
- Ceres seq\_id 1502366
- Location of start within SEQ ID NO 2139: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14090
- gi No. 2828285
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2142: from 138 to 157

- Alignment No. 14091

- gi No. 2832638

- % Identity 76.2

- Alignment Length 21

- Location of Alignment in SEQ ID NO 2142: from 138 to 157

Maximum Length Sequence corresponding to clone ID 311431

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2143

- Ceres seq\_id 1502367
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2144
  - Ceres seq\_id 1502368
  - Location of start within SEQ ID NO 2143: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14092
- Kinesin motor domain
- Location within SEQ ID NO 2144: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14093
- gi No. 1170619
- % Identity 89.7
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78
  
- Alignment No. 14094
- gi No. 1170620
- % Identity 88.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78
  
- Alignment No. 14095
- gi No. 1170621
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78
  
- Alignment No. 14096
- gi No. 125477
- % Identity 70.9
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2144: from 1 to 77
  
- Alignment No. 14097
- gi No. 2826849
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15
  
- Alignment No. 14098
- gi No. 3023586
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2144: from 1 to 77
  
- Alignment No. 14099
- gi No. 3913957
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15
  
- Alignment No. 14100
- gi No. 4490714
- % Identity 88.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78



- Alignment No. 14101
- gi No. 4504869
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15

Maximum Length Sequence corresponding to clone ID 311460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2145
- Ceres seq\_id 1502373

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2146
- Ceres seq\_id 1502374
- Location of start within SEQ ID NO 2145: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2147
- Ceres seq\_id 1502375
- Location of start within SEQ ID NO 2145: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14102
- gi No. 2655291
- % Identity 82.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2147: from 1 to 66
  
- Alignment No. 14103
- gi No. 2979494
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2147: from 22 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2148
- Ceres seq\_id 1502376
- Location of start within SEQ ID NO 2145: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14104
- gi No. 2655291
- % Identity 82.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2148: from 1 to 38
  
- Alignment No. 14105
- gi No. 2979494
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2148: from 1 to 30

Maximum Length Sequence corresponding to clone ID 311474

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2149
- Ceres seq\_id 1502381
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2150
  - Ceres seq\_id 1502382
  - Location of start within SEQ ID NO 2149: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14106
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2150: from 1 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14107
- gi No. 1066501
- % Identity 70.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
  
- Alignment No. 14108
- gi No. 1168470
- % Identity 73.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2150: from 1 to 131
  
- Alignment No. 14109
- gi No. 1168471
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2150: from 42 to 131
  
- Alignment No. 14110
- gi No. 1778444
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2150: from 88 to 131
  
- Alignment No. 14111
- gi No. 2852447
- % Identity 72
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2150: from 1 to 131
  
- Alignment No. 14112
- gi No. 2852449
- % Identity 71.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2150: from 1 to 131
  
- Alignment No. 14113
- gi No. 3075390
- % Identity 76.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
  
- Alignment No. 14114
- gi No. 3461835
- % Identity 73.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14115
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
  
- Alignment No. 14116
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
  
- Alignment No. 14117
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2150: from 42 to 131
  
- Alignment No. 14118
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
  
- Alignment No. 14119
- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2150: from 69 to 130
  
- Alignment No. 14120
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2151
- Ceres seq\_id 1502383
- Location of start within SEQ ID NO 2149: at 160 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14121
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2151: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14122
- gi No. 1066501
- % Identity 70.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14123
- gi No. 1168470
- % Identity 73.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14124
- gi No. 1168471
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14125
- gi No. 1778444
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2151: from 35 to 78
  
- Alignment No. 14126
- gi No. 2852447
- % Identity 72
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14127
- gi No. 2852449
- % Identity 71.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14128
- gi No. 3075390
- % Identity 76.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14129
- gi No. 3461835
- % Identity 73.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14130
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14131
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14132
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14133
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
  
- Alignment No. 14134

- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2151: from 16 to 77
  
- Alignment No. 14135
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

Maximum Length Sequence corresponding to clone ID 311490

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2152
- Ceres seq\_id 1502387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2153
- Ceres seq\_id 1502388
- Location of start within SEQ ID NO 2152: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14136
- Ribosomal protein L5
- Location within SEQ ID NO 2153: from 65 to 100 aa.
  
- Alignment No. 14137
- ribosomal L5P family C-terminus
- Location within SEQ ID NO 2153: from 104 to 158 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14138
- gi No. 1125808
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14139
- gi No. 1172816
- % Identity 96.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14140
- gi No. 1172817
- % Identity 97.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14141
- gi No. 1172952
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14142
- gi No. 1172954
- % Identity 78.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14143
- gi No. 1172969
- % Identity 97.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14144
- gi No. 1173055
- % Identity 100
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14145
- gi No. 1246369
- % Identity 74.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14146
- gi No. 132649
- % Identity 85.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14147
- gi No. 132777
- % Identity 74.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14148
- gi No. 132951
- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14149
- gi No. 132992
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2153: from 65 to 127
  
- Alignment No. 14150
- gi No. 1350658
- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14151
- gi No. 1350659
- % Identity 77.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14152
- gi No. 1710480
- % Identity 75.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14153

- gi No. 1710494
- % Identity 87.4
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14154
- gi No. 2500240
- % Identity 84
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14155
- gi No. 2500241
- % Identity 81.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2153: from 65 to 155
  
- Alignment No. 14156
- gi No. 2570507
- % Identity 89.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14157
- gi No. 3914659
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14158
- gi No. 4322
- % Identity 82.1
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14159
- gi No. 4432750
- % Identity 96
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2153: from 65 to 89
  
- Alignment No. 14160
- gi No. 4506595
- % Identity 81.1
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14161
- gi No. 4512679
- % Identity 88.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14162
- gi No. 4586222
- % Identity 85.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
  
- Alignment No. 14163
- gi No. 71107

- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2154
- Ceres seq\_id 1502389
- Location of start within SEQ ID NO 2152: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14164
- gi No. 1172816
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28
  
- Alignment No. 14165
- gi No. 1172817
- % Identity 85.2
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2154: from 2 to 28
  
- Alignment No. 14166
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28
  
- Alignment No. 14167
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28
  
- Alignment No. 14168
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2155
- Ceres seq\_id 1502390
- Location of start within SEQ ID NO 2152: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14169
- gi No. 1172816
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
  
- Alignment No. 14170
- gi No. 1172817
- % Identity 85.2
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2155: from 1 to 18



- Alignment No. 14171
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
  
- Alignment No. 14172
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
  
- Alignment No. 14173
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

Maximum Length Sequence corresponding to clone ID 311538

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2156
- Ceres seq\_id 1502407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2157
- Ceres seq\_id 1502408
- Location of start within SEQ ID NO 2156: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14174
- Peroxidase
- Location within SEQ ID NO 2157: from 61 to 134 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2158
- Ceres seq\_id 1502409
- Location of start within SEQ ID NO 2156: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14175
- Peroxidase
- Location within SEQ ID NO 2158: from 15 to 88 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311554

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2159
- Ceres seq\_id 1502420

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2160
- Ceres seq\_id 1502421
- Location of start within SEQ ID NO 2159: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14176

- Ribosomal protein S12
- Location within SEQ ID NO 2160: from 58 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14177
- gi No. 1173187
- % Identity 97.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14178
- gi No. 1350965
- % Identity 97.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2160: from 58 to 143
- Alignment No. 14179
- gi No. 1850766
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14180
- gi No. 2500455
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14181
- gi No. 2829742
- % Identity 81.8
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14182
- gi No. 2833303
- % Identity 79.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14183
- gi No. 3088342
- % Identity 92.9
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2160: from 118 to 144
- Alignment No. 14184
- gi No. 417716
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14185
- gi No. 4493905
- % Identity 75.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2160: from 54 to 144
- Alignment No. 14186
- gi No. 4506701
- % Identity 81.8

- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144

Maximum Length Sequence corresponding to clone ID 311571

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2161
- Ceres seq\_id 1502422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2162
- Ceres seq\_id 1502423
- Location of start within SEQ ID NO 2161: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14187
- AhpC/TSA family
- Location within SEQ ID NO 2162: from 11 to 67 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14188
- gi No. 5441879
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2162: from 28 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2163
- Ceres seq\_id 1502424
- Location of start within SEQ ID NO 2161: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14189
- AhpC/TSA family
- Location within SEQ ID NO 2163: from 66 to 142 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14190
- gi No. 5441879
- % Identity 72.2
- Alignment Length 97
- Location of Alignment in SEQ ID NO 2163: from 65 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2164
- Ceres seq\_id 1502425
- Location of start within SEQ ID NO 2161: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311596

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2165
- Ceres seq\_id 1502429

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2166
- Ceres seq\_id 1502430
- Location of start within SEQ ID NO 2165: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14191
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2166: from 1 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2167
- Ceres seq\_id 1502431
- Location of start within SEQ ID NO 2165: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14192
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2167: from 1 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2168
- Ceres seq\_id 1502432
- Location of start within SEQ ID NO 2165: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14193
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2168: from 1 to 68

Maximum Length Sequence corresponding to clone ID 311614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2169
- Ceres seq\_id 1502441

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2170
- Ceres seq\_id 1502442
- Location of start within SEQ ID NO 2169: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14194
- gi No. 3335351
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2170: from 41 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2171
- Ceres seq\_id 1502443
- Location of start within SEQ ID NO 2169: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14195
- gi No. 2924785
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2171: from 12 to 29

Maximum Length Sequence corresponding to clone ID 311726

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2172
- Ceres seq\_id 1502461

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2173
- Ceres seq\_id 1502462
- Location of start within SEQ ID NO 2172: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14196
- gi No. 4028260
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2173: from 38 to 48

Maximum Length Sequence corresponding to clone ID 311791

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2174
- Ceres seq\_id 1502479

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2175
- Ceres seq\_id 1502480
- Location of start within SEQ ID NO 2174: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2176
- Ceres seq\_id 1502481
- Location of start within SEQ ID NO 2174: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14197
- Elongation factor 1 gamma, conserved domain.
- Location within SEQ ID NO 2176: from 29 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14198
- gi No. 2160158
- % Identity 75.9
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2176: from 1 to 73
- Alignment No. 14199
- gi No. 3868758
- % Identity 87.8

- Alignment Length 74
- Location of Alignment in SEQ ID NO 2176: from 1 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2177
- Ceres seq\_id 1502482
- Location of start within SEQ ID NO 2174: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311814

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2178
- Ceres seq\_id 1502487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2179
- Ceres seq\_id 1502488
- Location of start within SEQ ID NO 2178: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14200
- G-protein alpha subunit
- Location within SEQ ID NO 2179: from 46 to 112 aa.

- Alignment No. 14201
- ADP-ribosylation factor family
- Location within SEQ ID NO 2179: from 1 to 117 aa.

- Alignment No. 14202
- Ras family
- Location within SEQ ID NO 2179: from 18 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14203
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2179: from 1 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2180
- Ceres seq\_id 1502489
- Location of start within SEQ ID NO 2178: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14204
- G-protein alpha subunit
- Location within SEQ ID NO 2180: from 30 to 96 aa.

- Alignment No. 14205
- ADP-ribosylation factor family
- Location within SEQ ID NO 2180: from 1 to 101 aa.

- Alignment No. 14206
- Ras family
- Location within SEQ ID NO 2180: from 2 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14207
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2180: from 1 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2181
- Ceres seq\_id 1502490
- Location of start within SEQ ID NO 2178: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14208
- G-protein alpha subunit
- Location within SEQ ID NO 2181: from 26 to 92 aa.
- Alignment No. 14209
- ADP-ribosylation factor family
- Location within SEQ ID NO 2181: from 1 to 97 aa.
- Alignment No. 14210
- Ras family
- Location within SEQ ID NO 2181: from 1 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14211
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2181: from 1 to 97

Maximum Length Sequence corresponding to clone ID 311865

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2182
- Ceres seq\_id 1502514

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2183
- Ceres seq\_id 1502515
- Location of start within SEQ ID NO 2182: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2184
- Ceres seq\_id 1502516
- Location of start within SEQ ID NO 2182: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14212
- Ribosomal L29 protein
- Location within SEQ ID NO 2184: from 6 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14213
- gi No. 3355468
- % Identity 85.2

- Alignment Length 122
- Location of Alignment in SEQ ID NO 2184: from 1 to 122

Maximum Length Sequence corresponding to clone ID 311870

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2185
- Ceres seq\_id 1502517

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2186
- Ceres seq\_id 1502518
- Location of start within SEQ ID NO 2185: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14214
- Protein-tyrosine phosphatase
- Location within SEQ ID NO 2186: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14215
- gi No. 3413473
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2186: from 1 to 60
  
- Alignment No. 14216
- gi No. 3413500
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2186: from 1 to 60
  
- Alignment No. 14217
- gi No. 348540
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2186: from 1 to 14
  
- Alignment No. 14218
- gi No. 464498
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2186: from 1 to 14

Maximum Length Sequence corresponding to clone ID 311889

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2187
- Ceres seq\_id 1502519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2188
- Ceres seq\_id 1502520
- Location of start within SEQ ID NO 2187: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2189
- Ceres seq\_id 1502521
- Location of start within SEQ ID NO 2187: at 197 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14219
- gi No. 1769895
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2189: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2190
- Ceres seq\_id 1502522
- Location of start within SEQ ID NO 2187: at 218 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14220
- gi No. 1769895
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2190: from 1 to 69

Maximum Length Sequence corresponding to clone ID 311911

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2191
- Ceres seq\_id 1502527

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2192
- Ceres seq\_id 1502528
- Location of start within SEQ ID NO 2191: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14221
- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 2192: from 1 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14222
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14223
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14224
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14225
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14226
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14227
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14228
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2192: from 1 to 91
- Alignment No. 14229
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14230
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14231
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14232
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14233
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14234
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14235
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14236
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
  
- Alignment No. 14237
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
  
- Alignment No. 14238
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
  
- Alignment No. 14239
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2193
- Ceres seq\_id 1502529
- Location of start within SEQ ID NO 2191: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14240
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
  
- Alignment No. 14241
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
  
- Alignment No. 14242
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
  
- Alignment No. 14243
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
  
- Alignment No. 14244
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14245
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14246
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2193: from 1 to 66
- Alignment No. 14247
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14248
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14249
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14250
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14251
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14252
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14253
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14254
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14255
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
  
- Alignment No. 14256
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
  
- Alignment No. 14257
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2194
- Ceres seq\_id 1502530
- Location of start within SEQ ID NO 2191: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14258
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
  
- Alignment No. 14259
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
  
- Alignment No. 14260
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
  
- Alignment No. 14261
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
  
- Alignment No. 14262
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
  
- Alignment No. 14263
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14264
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2194: from 1 to 63
- Alignment No. 14265
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14266
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14267
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14268
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14269
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14270
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14271
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14272
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14273
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14274
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
  
- Alignment No. 14275
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Maximum Length Sequence corresponding to clone ID 311937

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2195
- Ceres seq\_id 1502542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2196
- Ceres seq\_id 1502543
- Location of start within SEQ ID NO 2195: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14276
- Ras family
- Location within SEQ ID NO 2196: from 69 to 147 aa.
  
- Alignment No. 14277
- ADP-ribosylation factor family
- Location within SEQ ID NO 2196: from 52 to 169 aa.
  
- Alignment No. 14278
- G-protein alpha subunit
- Location within SEQ ID NO 2196: from 94 to 169 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14279
- gi No. 1065361
- % Identity 90.8
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 52 to 169
  
- Alignment No. 14280
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14281
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14282
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14283
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
  
- Alignment No. 14284
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14285
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14286
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14287
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14288
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14289
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14290
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14291
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14292
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14293



- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14294
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
  
- Alignment No. 14295
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14296
- gi No. 2129946
- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2196: from 51 to 137
  
- Alignment No. 14297
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14298
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2196: from 51 to 92
  
- Alignment No. 14299
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14300
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14301
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14302
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14303
- gi No. 2854182

- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14304
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14305
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14306
- gi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14307
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14308
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2196: from 68 to 160
  
- Alignment No. 14309
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169
  
- Alignment No. 14310
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169
  
- Alignment No. 14311
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14312
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2196: from 51 to 116
  
- Alignment No. 14313
- gi No. 4324967
- % Identity 98.3

- Alignment Length 117
- Location of Alignment in SEQ ID NO 2196: from 54 to 169
  
- Alignment No. 14314
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14315
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14316
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14317
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14318
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
  
- Alignment No. 14319
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14320
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14321
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14322
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
  
- Alignment No. 14323
- gi No. 543842
- % Identity 90
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14324
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14325
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14326
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2196: from 48 to 169
- Alignment No. 14327
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14328
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14329
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2197
- Ceres seq\_id 1502544
- Location of start within SEQ ID NO 2195: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14330
- Ras family
- Location within SEQ ID NO 2197: from 19 to 97 aa.
- Alignment No. 14331
- ADP-ribosylation factor family
- Location within SEQ ID NO 2197: from 2 to 119 aa.
- Alignment No. 14332
- G-protein alpha subunit
- Location within SEQ ID NO 2197: from 44 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14333
- gi No. 1065361
- % Identity 90.8

- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 2 to 119
  
- Alignment No. 14334
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14335
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14336
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14337
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
  
- Alignment No. 14338
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14339
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14340
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14341
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14342
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14343
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14344
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14345
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14346
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14347
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14348
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14349
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14350
- gi No. 2129946
- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2197: from 1 to 87
- Alignment No. 14351
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14352
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2197: from 1 to 42
- Alignment No. 14353
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14354
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14355
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14356
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14357
- gi No. 2854182
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14358
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14359
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14360
- gi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14361
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14362
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2197: from 18 to 110
  
- Alignment No. 14363
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2197: from 19 to 119

- Alignment No. 14364
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2197: from 19 to 119
  
- Alignment No. 14365
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14366
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2197: from 1 to 66
  
- Alignment No. 14367
- gi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2197: from 4 to 119
  
- Alignment No. 14368
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14369
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14370
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14371
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14372
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
  
- Alignment No. 14373
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14374



- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14375
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14376
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14377
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14378
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14379
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14380
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14381
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
  
- Alignment No. 14382
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
  
- Alignment No. 14383
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2198

- Ceres seq\_id 1502545
- Location of start within SEQ ID NO 2195: at 202 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14384
- Ras family
- Location within SEQ ID NO 2198: from 2 to 80 aa.
- Alignment No. 14385
- ADP-ribosylation factor family
- Location within SEQ ID NO 2198: from 1 to 102 aa.
- Alignment No. 14386
- G-protein alpha subunit
- Location within SEQ ID NO 2198: from 27 to 102 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14387
- gi No. 1065361
- % Identity 90.8
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14388
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14389
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14390
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14391
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14392
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14393
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14394

- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14395
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14396
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14397
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14398
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14399
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14400
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14401
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14402
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14403
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14404
- gi No. 2129946

- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2198: from 1 to 70
  
- Alignment No. 14405
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14406
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2198: from 1 to 25
  
- Alignment No. 14407
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14408
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14409
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14410
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14411
- gi No. 2854182
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14412
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14413
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14414
- gi No. 3182917
- % Identity 90.8

- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14415
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14416
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2198: from 1 to 93
  
- Alignment No. 14417
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
  
- Alignment No. 14418
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
  
- Alignment No. 14419
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14420
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2198: from 1 to 49
  
- Alignment No. 14421
- gi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14422
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14423
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14424
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14425
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14426
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14427
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14428
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14429
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14430
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14431
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14432
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14433
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14434
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14435
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14436
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14437
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

Maximum Length Sequence corresponding to clone ID 312050

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2199
- Ceres seq\_id 1502573

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2200
- Ceres seq\_id 1502574
- Location of start within SEQ ID NO 2199: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14438
- gi No. 3935181
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2200: from 9 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2201
- Ceres seq\_id 1502575
- Location of start within SEQ ID NO 2199: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2202
- Ceres seq\_id 1502576
- Location of start within SEQ ID NO 2199: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14439
- gi No. 3935181
- % Identity 71.7
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2202: from 50 to 161

Maximum Length Sequence corresponding to clone ID 312126

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2203
- Ceres seq\_id 1502613

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2204
- Ceres seq\_id 1502614
- Location of start within SEQ ID NO 2203: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2205
- Ceres seq\_id 1502615
- Location of start within SEQ ID NO 2203: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14440
- gi No. 3023243
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2205: from 48 to 61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2206
- Ceres seq\_id 1502616
- Location of start within SEQ ID NO 2203: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14441
- gi No. 3023243
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2206: from 26 to 39

Maximum Length Sequence corresponding to clone ID 312149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2207
- Ceres seq\_id 1502621

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2208
- Ceres seq\_id 1502622
- Location of start within SEQ ID NO 2207: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14442
- gi No. 330442
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15
  
- Alignment No. 14443
- gi No. 3925252
- % Identity 72.7



- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 35 to 45
  
- Alignment No. 14444
- gi No. 423830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15
  
- Alignment No. 14445
- gi No. 4504731
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
  
- Alignment No. 14446
- gi No. 4511969
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
  
- Alignment No. 14447
- gi No. 4838513
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
  
- Alignment No. 14448
- gi No. 4838515
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
  
- Alignment No. 14449
- gi No. 5305335
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 34 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2209
- Ceres seq\_id 1502623
- Location of start within SEQ ID NO 2207: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14450
- gi No. 1722778
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2209: from 19 to 30
  
- Alignment No. 14451
- gi No. 5257260
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2209: from 21 to 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2210

- Ceres seq\_id 1502624
- Location of start within SEQ ID NO 2207: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14452
- gi No. 102425
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14453
- gi No. 102426
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 43
- Alignment No. 14454
- gi No. 1161370
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 26 to 36
- Alignment No. 14455
- gi No. 134950
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2210: from 23 to 35
- Alignment No. 14456
- gi No. 1353462
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 26 to 36
- Alignment No. 14457
- gi No. 1644455
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14458
- gi No. 1644457
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14459
- gi No. 1644459
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14460
- gi No. 1644461
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14461

- gi No. 2108256
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2210: from 28 to 43
  
- Alignment No. 14462
- gi No. 2143272
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 40
  
- Alignment No. 14463
- gi No. 2257986
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 26 to 37
  
- Alignment No. 14464
- gi No. 2384847
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 22 to 33
  
- Alignment No. 14465
- gi No. 2384847
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 23 to 34
  
- Alignment No. 14466
- gi No. 2501953
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2210: from 28 to 40
  
- Alignment No. 14467
- gi No. 2950355
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2210: from 21 to 35
  
- Alignment No. 14468
- gi No. 310574
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37
  
- Alignment No. 14469
- gi No. 310574
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37
  
- Alignment No. 14470
- gi No. 3874146
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37
  
- Alignment No. 14471
- gi No. 4885040

- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
  
- Alignment No. 14472
- gi No. 539033
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 42
  
- Alignment No. 14473
- gi No. 5689489
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 28 to 38
  
- Alignment No. 14474
- gi No. 871830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
  
- Alignment No. 14475
- gi No. 91094
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 21 to 34

Maximum Length Sequence corresponding to clone ID 312179

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2211
- Ceres seq\_id 1502635

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2212
- Ceres seq\_id 1502636
- Location of start within SEQ ID NO 2211: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14476
- Ribosomal protein S28e
- Location within SEQ ID NO 2212: from 1 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14477
- gi No. 1173237
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
  
- Alignment No. 14478
- gi No. 1313916
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2212: from 6 to 65
  
- Alignment No. 14479
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14480
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
  
- Alignment No. 14481
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
  
- Alignment No. 14482
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
  
- Alignment No. 14483
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
  
- Alignment No. 14484
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2212: from 3 to 65
  
- Alignment No. 14485
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2213
- Ceres seq\_id 1502637
- Location of start within SEQ ID NO 2211: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14486
- Ribosomal protein S28e
- Location within SEQ ID NO 2213: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14487
- gi No. 1173237
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14488
- gi No. 1313916
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14489
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14490
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14491
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14492
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14493
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14494
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14495
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2214
- Ceres seq\_id 1502638
- Location of start within SEQ ID NO 2211: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312184

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2215
- Ceres seq\_id 1502643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2216
- Ceres seq\_id 1502644
- Location of start within SEQ ID NO 2215: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14496
- Zinc finger, C2H2 type
- Location within SEQ ID NO 2216: from 60 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14497
- gi No. 1362015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2216: from 57 to 91
- Alignment No. 14498
- gi No. 1362020
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91
- Alignment No. 14499
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2216: from 57 to 91
- Alignment No. 14500
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91
- Alignment No. 14501
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2217
- Ceres seq\_id 1502645
- Location of start within SEQ ID NO 2215: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14502
- Zinc finger, C2H2 type
- Location within SEQ ID NO 2217: from 24 to 46 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14503
- gi No. 1362015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55
- Alignment No. 14504
- gi No. 1362020
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55

- Alignment No. 14505
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55
  
- Alignment No. 14506
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55
  
- Alignment No. 14507
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55

Maximum Length Sequence corresponding to clone ID 312187

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2218
- Ceres seq\_id 1502649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2219
- Ceres seq\_id 1502650
- Location of start within SEQ ID NO 2218: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14508
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14509
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14510
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14511
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14512
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14513



- gi No. 2947081
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2219: from 69 to 79
  
- Alignment No. 14514
- gi No. 2947081
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 68 to 81
  
- Alignment No. 14515
- gi No. 4097820
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14516
- gi No. 4097820
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 68 to 81
  
- Alignment No. 14517
- gi No. 4097820
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 67 to 80
  
- Alignment No. 14518
- gi No. 539415
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2219: from 68 to 78
  
- Alignment No. 14519
- gi No. 539415
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14520
- gi No. 539415
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14521
- gi No. 539415
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2220
- Ceres seq\_id 1502651
- Location of start within SEQ ID NO 2218: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2221
  - Ceres seq\_id 1502652
  - Location of start within SEQ ID NO 2218: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312195

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2222
  - Ceres seq\_id 1502653
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2223
  - Ceres seq\_id 1502654
  - Location of start within SEQ ID NO 2222: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 14522
    - gi No. 2894228
    - % Identity 73.3
    - Alignment Length 15
    - Location of Alignment in SEQ ID NO 2223: from 9 to 23
  - Alignment No. 14523
    - gi No. 3378540
    - % Identity 71.4
    - Alignment Length 21
    - Location of Alignment in SEQ ID NO 2223: from 4 to 24
  - Alignment No. 14524
    - gi No. 3660471
    - % Identity 87.5
    - Alignment Length 24
    - Location of Alignment in SEQ ID NO 2223: from 1 to 24
  - Alignment No. 14525
    - gi No. 4309723
    - % Identity 79.2
    - Alignment Length 24
    - Location of Alignment in SEQ ID NO 2223: from 1 to 24

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2224
  - Ceres seq\_id 1502655
  - Location of start within SEQ ID NO 2222: at 250 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 14526
    - gi No. 3660471
    - % Identity 72.2
    - Alignment Length 18
    - Location of Alignment in SEQ ID NO 2224: from 29 to 46
  - Alignment No. 14527

- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2224: from 29 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2225
- Ceres seq\_id 1502656
- Location of start within SEQ ID NO 2222: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14528
- gi No. 3660471
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2225: from 27 to 44
  
- Alignment No. 14529
- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2225: from 27 to 44

Maximum Length Sequence corresponding to clone ID 312268

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2226
- Ceres seq\_id 1502682

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2227
- Ceres seq\_id 1502683
- Location of start within SEQ ID NO 2226: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2228
- Ceres seq\_id 1502684
- Location of start within SEQ ID NO 2226: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14530
- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2228: from 65 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2229
- Ceres seq\_id 1502685
- Location of start within SEQ ID NO 2226: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14531

- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2229: from 51 to 61

Maximum Length Sequence corresponding to clone ID 312393

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2230
- Ceres seq\_id 1502713

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2231
- Ceres seq\_id 1502714
- Location of start within SEQ ID NO 2230: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14532
- Asparagine synthase
- Location within SEQ ID NO 2231: from 1 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14533
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2231: from 1 to 145
  
- Alignment No. 14534
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
  
- Alignment No. 14535
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2231: from 1 to 134
  
- Alignment No. 14536
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2231: from 1 to 121
  
- Alignment No. 14537
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
  
- Alignment No. 14538
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
  
- Alignment No. 14539
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122

- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14540
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2231: from 1 to 132
- Alignment No. 14541
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14542
- gi No. 1771880
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2231: from 1 to 145
- Alignment No. 14543
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14544
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2231: from 1 to 121
- Alignment No. 14545
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14546
- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2231: from 1 to 134
- Alignment No. 14547
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14548
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 146
- Alignment No. 14549
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14550
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 144
  
- Alignment No. 14551
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2231: from 1 to 139
  
- Alignment No. 14552
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2231: from 1 to 75
  
- Alignment No. 14553
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
  
- Alignment No. 14554
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2232
- Ceres seq\_id 1502715
- Location of start within SEQ ID NO 2230: at 132 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14555
- Asparagine synthase
- Location within SEQ ID NO 2232: from 1 to 61 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14556
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2232: from 1 to 102
  
- Alignment No. 14557
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14558
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91

- Alignment No. 14559
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2232: from 1 to 78
  
- Alignment No. 14560
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14561
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14562
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
  
- Alignment No. 14563
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2232: from 1 to 89
  
- Alignment No. 14564
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
  
- Alignment No. 14565
- gi No. 1771880
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2232: from 1 to 102
  
- Alignment No. 14566
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14567
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2232: from 1 to 78
  
- Alignment No. 14568
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14569

- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91
  
- Alignment No. 14570
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14571
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 103
  
- Alignment No. 14572
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
  
- Alignment No. 14573
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 101
  
- Alignment No. 14574
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2232: from 1 to 96
  
- Alignment No. 14575
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2232: from 1 to 32
  
- Alignment No. 14576
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
  
- Alignment No. 14577
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2233
- Ceres seq\_id 1502716
- Location of start within SEQ ID NO 2230: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14578



- Asparagine synthase
- Location within SEQ ID NO 2233: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14579
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2233: from 1 to 101
- Alignment No. 14580
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14581
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2233: from 1 to 90
- Alignment No. 14582
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2233: from 1 to 77
- Alignment No. 14583
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14584
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14585
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14586
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2233: from 1 to 88
- Alignment No. 14587
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14588
- gi No. 1771880
- % Identity 70.3

- Alignment Length 145
- Location of Alignment in SEQ ID NO 2233: from 1 to 101
  
- Alignment No. 14589
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
  
- Alignment No. 14590
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2233: from 1 to 77
  
- Alignment No. 14591
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
  
- Alignment No. 14592
- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2233: from 1 to 90
  
- Alignment No. 14593
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
  
- Alignment No. 14594
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2233: from 1 to 102
  
- Alignment No. 14595
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
  
- Alignment No. 14596
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2233: from 1 to 100
  
- Alignment No. 14597
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2233: from 1 to 95
  
- Alignment No. 14598
- gi No. 3913098
- % Identity 80
- Alignment Length 75

- Location of Alignment in SEQ ID NO 2233: from 1 to 31
- Alignment No. 14599
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14600
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78

Maximum Length Sequence corresponding to clone ID 312402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2234
- Ceres seq\_id 1502717

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2235
- Ceres seq\_id 1502718
- Location of start within SEQ ID NO 2234: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14601
- gi No. 1778093
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2235: from 1 to 19
- Alignment No. 14602
- gi No. 1778095
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2235: from 1 to 19
- Alignment No. 14603
- gi No. 4678208
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2235: from 1 to 19

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2236
- Ceres seq\_id 1502719
- Location of start within SEQ ID NO 2234: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2237
- Ceres seq\_id 1502720
- Location of start within SEQ ID NO 2234: at 194 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312407

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2238
- Ceres seq\_id 1502721

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2239
- Ceres seq\_id 1502722
- Location of start within SEQ ID NO 2238: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14604
- gi No. 1705677
- % Identity 76.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2239: from 1 to 108
- Alignment No. 14605
- gi No. 1705678
- % Identity 75.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2239: from 1 to 108
- Alignment No. 14606
- gi No. 2492504
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2239: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2240
- Ceres seq\_id 1502723
- Location of start within SEQ ID NO 2238: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14607
- gi No. 1705677
- % Identity 76.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2240: from 1 to 85
- Alignment No. 14608
- gi No. 1705678
- % Identity 75.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2240: from 1 to 85
- Alignment No. 14609
- gi No. 2492504
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2240: from 1 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2241
- Ceres seq\_id 1502724
- Location of start within SEQ ID NO 2238: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312409

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2242
  - Ceres seq\_id 1502726
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2243
  - Ceres seq\_id 1502727
  - Location of start within SEQ ID NO 2242: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2244
  - Ceres seq\_id 1502728
  - Location of start within SEQ ID NO 2242: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14610
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2244: from 21 to 78 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2245
  - Ceres seq\_id 1502729
  - Location of start within SEQ ID NO 2242: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312432

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2246
  - Ceres seq\_id 1502730
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2247
  - Ceres seq\_id 1502731
  - Location of start within SEQ ID NO 2246: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 14611
  - gi No. 2500047
  - % Identity 87.5
  - Alignment Length 40
  - Location of Alignment in SEQ ID NO 2247: from 15 to 54
- 
- Alignment No. 14612
  - gi No. 3510259
  - % Identity 73.2

- Alignment Length 56
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14613
- gi No. 4033417
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14614
- gi No. 4033424
- % Identity 100
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2247: from 1 to 54

Maximum Length Sequence corresponding to clone ID 312476

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2248
- Ceres seq\_id 1502755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2249
- Ceres seq\_id 1502756
- Location of start within SEQ ID NO 2248: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2250
- Ceres seq\_id 1502757
- Location of start within SEQ ID NO 2248: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14615
- gi No. 2129800
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14616
- gi No. 2129804
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14617
- gi No. 2129805
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14618
- gi No. 2317758
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14619

- gi No. 2317758
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2250: from 65 to 87
- Alignment No. 14620
- gi No. 5391446
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2251
- Ceres seq\_id 1502758
- Location of start within SEQ ID NO 2248: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312486

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2252
- Ceres seq\_id 1502759

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2253
- Ceres seq\_id 1502760
- Location of start within SEQ ID NO 2252: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2254
- Ceres seq\_id 1502761
- Location of start within SEQ ID NO 2252: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14621
- gi No. 2781345
- % Identity 79.3
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2254: from 1 to 58
- Alignment No. 14622
- gi No. 3157933
- % Identity 76.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 2254: from 1 to 71

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2255
- Ceres seq\_id 1502762
- Location of start within SEQ ID NO 2252: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312499

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2256
- Ceres seq\_id 1502763

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2257
- Ceres seq\_id 1502764
- Location of start within SEQ ID NO 2256: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14623
- gi No. 4512216
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2257: from 114 to 154
  
- Alignment No. 14624
- gi No. 5689236
- % Identity 75.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2257: from 114 to 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2258
- Ceres seq\_id 1502765
- Location of start within SEQ ID NO 2256: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2259
- Ceres seq\_id 1502766
- Location of start within SEQ ID NO 2256: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312502

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2260
- Ceres seq\_id 1502767

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2261
- Ceres seq\_id 1502768
- Location of start within SEQ ID NO 2260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2262
- Ceres seq\_id 1502769
- Location of start within SEQ ID NO 2260: at 135 nt.



(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2263
- Ceres seq\_id 1502770
- Location of start within SEQ ID NO 2260: at 250 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14625
- gi No. 5262791
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2263: from 57 to 69

Maximum Length Sequence corresponding to clone ID 312503

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2264
- Ceres seq\_id 1502771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2265
- Ceres seq\_id 1502772
- Location of start within SEQ ID NO 2264: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14626
- gi No. 2149640
- % Identity 81.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99

- Alignment No. 14627
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99

- Alignment No. 14628
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2266
- Ceres seq\_id 1502773
- Location of start within SEQ ID NO 2264: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14629
- gi No. 2149640
- % Identity 81.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

- Alignment No. 14630
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51
  
- Alignment No. 14631
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

Maximum Length Sequence corresponding to clone ID 312523

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2267
- Ceres seq\_id 1502781

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2268
- Ceres seq\_id 1502782
- Location of start within SEQ ID NO 2267: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2269
- Ceres seq\_id 1502783
- Location of start within SEQ ID NO 2267: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14632
- gi No. 3264598
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2269: from 19 to 39

Maximum Length Sequence corresponding to clone ID 312525

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2270
- Ceres seq\_id 1502784

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2271
- Ceres seq\_id 1502785
- Location of start within SEQ ID NO 2270: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2272
- Ceres seq\_id 1502786
- Location of start within SEQ ID NO 2270: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2273
- Ceres seq\_id 1502787
- Location of start within SEQ ID NO 2270: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14633
- gi No. 102706
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
  
- Alignment No. 14634
- gi No. 1042189
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19
  
- Alignment No. 14635
- gi No. 1168711
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2273: from 5 to 18
  
- Alignment No. 14636
- gi No. 131044
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
  
- Alignment No. 14637
- gi No. 1362586
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
  
- Alignment No. 14638
- gi No. 1362587
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19
  
- Alignment No. 14639
- gi No. 1362587
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19

Maximum Length Sequence corresponding to clone ID 312595

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2274
- Ceres seq\_id 1502805

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2275
- Ceres seq\_id 1502806
- Location of start within SEQ ID NO 2274: at 123 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14640
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2275: from 2 to 104 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2276
- Ceres seq\_id 1502807
- Location of start within SEQ ID NO 2274: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14641
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2276: from 1 to 65 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2277
- Ceres seq\_id 1502808
- Location of start within SEQ ID NO 2274: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14642
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2277: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312598

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2278
- Ceres seq\_id 1502809

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2279
- Ceres seq\_id 1502810
- Location of start within SEQ ID NO 2278: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2280
- Ceres seq\_id 1502811
- Location of start within SEQ ID NO 2278: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14643
- gi No. 4115377
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2280: from 58 to 115

Maximum Length Sequence corresponding to clone ID 312622

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2281
- Ceres seq\_id 1502820

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2282
- Ceres seq\_id 1502821
- Location of start within SEQ ID NO 2281: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2283
- Ceres seq\_id 1502822
- Location of start within SEQ ID NO 2281: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14644
- Ribosomal protein S11
- Location within SEQ ID NO 2283: from 28 to 105 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14645
- gi No. 1173200
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2283: from 67 to 105
- Alignment No. 14646
- gi No. 1173201
- % Identity 82.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2283: from 5 to 105
- Alignment No. 14647
- gi No. 131772
- % Identity 92.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14648
- gi No. 131773
- % Identity 89.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 2283: from 3 to 105
- Alignment No. 14649
- gi No. 133771
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14650
- gi No. 133777
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14651
- gi No. 133782
- % Identity 72.9
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14652
- gi No. 133785
- % Identity 78.3
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14653
- gi No. 1346941
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
  
- Alignment No. 14654
- gi No. 1350935
- % Identity 74.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14655
- gi No. 2350992
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2283: from 27 to 100
  
- Alignment No. 14656
- gi No. 2414647
- % Identity 80.5
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2283: from 16 to 102
  
- Alignment No. 14657
- gi No. 2500442
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2283: from 4 to 80
  
- Alignment No. 14658
- gi No. 2500443
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2283: from 85 to 105
  
- Alignment No. 14659
- gi No. 3097244
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14660
- gi No. 3122785
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14661

- gi No. 4574240
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
  
- Alignment No. 14662
- gi No. 4588920
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14663
- gi No. 4678226
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14664
- gi No. 4886269
- % Identity 85.7
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14665
- gi No. 5032051
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14666
- gi No. 5441523
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2283: from 72 to 105
  
- Alignment No. 14667
- gi No. 547604
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
  
- Alignment No. 14668
- gi No. 70946
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
  
- Alignment No. 14669
- gi No. 730453
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
  
- Alignment No. 14670
- gi No. 730633
- % Identity 76.4
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
  
- Alignment No. 14671
- gi No. 83794

- % Identity 74.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

Maximum Length Sequence corresponding to clone ID 312649

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2284
- Ceres seq\_id 1502834

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2285
- Ceres seq\_id 1502835
- Location of start within SEQ ID NO 2284: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14672
- Forkhead-associated (FHA) domain
- Location within SEQ ID NO 2285: from 92 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2286
- Ceres seq\_id 1502836
- Location of start within SEQ ID NO 2284: at 57 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14673
- Forkhead-associated (FHA) domain
- Location within SEQ ID NO 2286: from 74 to 127 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312672

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2287
- Ceres seq\_id 1502844

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2288
- Ceres seq\_id 1502845
- Location of start within SEQ ID NO 2287: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14674
- DnaJ domain
- Location within SEQ ID NO 2288: from 1 to 29 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2289
- Ceres seq\_id 1502850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2290
- Ceres seq\_id 1502851
- Location of start within SEQ ID NO 2289: at 2 nt.



(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2291
- Ceres seq\_id 1502852
- Location of start within SEQ ID NO 2289: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2292
- Ceres seq\_id 1502853
- Location of start within SEQ ID NO 2289: at 217 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14675
- gi No. 4220472
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2292: from 1 to 19

Maximum Length Sequence corresponding to clone ID 312744

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2293
- Ceres seq\_id 1502860

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2294
- Ceres seq\_id 1502861
- Location of start within SEQ ID NO 2293: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2295
- Ceres seq\_id 1502862
- Location of start within SEQ ID NO 2293: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14676
- Plant lipid transfer protein family
- Location within SEQ ID NO 2295: from 75 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14677
- gi No. 1084462
- % Identity 70
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2295: from 75 to 152
- Alignment No. 14678
- gi No. 2226329
- % Identity 93.8

- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154
- Alignment No. 14679
- gi No. 399204
- % Identity 92.5
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154

Maximum Length Sequence corresponding to clone ID 312842

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2296
- Ceres seq\_id 1502896

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2297
- Ceres seq\_id 1502897
- Location of start within SEQ ID NO 2296: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2297: from 1 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14681
- gi No. 100610
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14682
- gi No. 100611
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14683
- gi No. 1076633
- % Identity 88.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14684
- gi No. 1082205
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14685
- gi No. 1216280
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14686
- gi No. 1216285
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14687
- gi No. 134588
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
  
- Alignment No. 14688
- gi No. 1362153
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14689
- gi No. 1362154
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14690
- gi No. 1362155
- % Identity 96.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14691
- gi No. 1477684
- % Identity 94.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14692
- gi No. 1703034
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
  
- Alignment No. 14693
- gi No. 1729444
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14694
- gi No. 1742967
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14695
- gi No. 1743009
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14696
- gi No. 1935916
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14697

- gi No. 2130048
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14698
- gi No. 2136044
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2297: from 3 to 34
  
- Alignment No. 14699
- gi No. 2137442
- % Identity 94.1
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2297: from 1 to 34
  
- Alignment No. 14700
- gi No. 2146759
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14701
- gi No. 2146812
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14702
- gi No. 2274869
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2297: from 5 to 40
  
- Alignment No. 14703
- gi No. 2499626
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
  
- Alignment No. 14704
- gi No. 2507201
- % Identity 71.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
  
- Alignment No. 14705
- gi No. 3023235
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2297: from 2 to 31
  
- Alignment No. 14706
- gi No. 322596
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14707
- gi No. 3341452

- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14708
- gi No. 400982
- % Identity 82.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14709
- gi No. 4091885
- % Identity 93.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14710
- gi No. 4099088
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14711
- gi No. 4107001
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14712
- gi No. 4107003
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14713
- gi No. 4107005
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14714
- gi No. 4107009
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14715
- gi No. 4432983
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2297: from 8 to 47
  
- Alignment No. 14716
- gi No. 4520332
- % Identity 74.3
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
  
- Alignment No. 14717
- gi No. 4567091
- % Identity 92.8

- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14718
- gi No. 4982468
- % Identity 75.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 2 to 110
  
- Alignment No. 14719
- gi No. 5410312
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
  
- Alignment No. 14720
- gi No. 5442424
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
  
- Alignment No. 14721
- gi No. 5453964
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
  
- Alignment No. 14722
- gi No. 5453966
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
  
- Alignment No. 14723
- gi No. 575292
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14724
- gi No. 728758
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
  
- Alignment No. 14725
- gi No. 862473
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2298
- Ceres seq\_id 1502898
- Location of start within SEQ ID NO 2296: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312860

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2299
- Ceres seq\_id 1502902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2300
- Ceres seq\_id 1502903
- Location of start within SEQ ID NO 2299: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14726
- gi No. 2160438
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
  
- Alignment No. 14727
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
  
- Alignment No. 14728
- gi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
  
- Alignment No. 14729
- gi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2301
- Ceres seq\_id 1502904
- Location of start within SEQ ID NO 2299: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14730
- gi No. 3413810
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2301: from 26 to 37

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2302
- Ceres seq\_id 1502905
- Location of start within SEQ ID NO 2299: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14731
- gi No. 2160438
- % Identity 72.7
- Alignment Length 11

- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14732
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14733
- gi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14734
- gi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61

Maximum Length Sequence corresponding to clone ID 312920

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2303
- Ceres seq\_id 1502937

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2304
- Ceres seq\_id 1502938
- Location of start within SEQ ID NO 2303: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14735
- gi No. 3367741
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2304: from 85 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2305
- Ceres seq\_id 1502939
- Location of start within SEQ ID NO 2303: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14736
- Nuclear transition protein 2
- Location within SEQ ID NO 2305: from 7 to 72 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2306
- Ceres seq\_id 1502940
- Location of start within SEQ ID NO 2303: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313030



(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2307
- Ceres seq\_id 1502981

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2308
- Ceres seq\_id 1502982
- Location of start within SEQ ID NO 2307: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14737
- gi No. 465445
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2308: from 107 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2309
- Ceres seq\_id 1502983
- Location of start within SEQ ID NO 2307: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2310
- Ceres seq\_id 1502984
- Location of start within SEQ ID NO 2307: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14738
- gi No. 102706
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118

- Alignment No. 14739

- gi No. 102706
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14740

- gi No. 102706
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14741

- gi No. 102706
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14742

- gi No. 102707
- % Identity 92.3

- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
  
- Alignment No. 14743
- gi No. 1170389
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14744
- gi No. 1170392
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14745
- gi No. 1170396
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14746
- gi No. 1170397
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14747
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14748
- gi No. 1170401
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 108 to 119
  
- Alignment No. 14749
- gi No. 1170405
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14750
- gi No. 1170406
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14751
- gi No. 123689
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14752
- gi No. 123689
- % Identity 82.4
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2310: from 106 to 122
- Alignment No. 14753
- gi No. 123695
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
- Alignment No. 14754
- gi No. 131040
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 107 to 117
- Alignment No. 14755
- gi No. 131040
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118
- Alignment No. 14756
- gi No. 131044
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118
- Alignment No. 14757
- gi No. 131044
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14758
- gi No. 131044
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14759
- gi No. 131044
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14760
- gi No. 163635
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14761
- gi No. 163635
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14762
- gi No. 163635
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 122

- Alignment No. 14763
- gi No. 2134213
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
  
- Alignment No. 14764
- gi No. 2134213
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14765
- gi No. 225057
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
  
- Alignment No. 14766
- gi No. 225057
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 122
  
- Alignment No. 14767
- gi No. 357984
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118
  
- Alignment No. 14768
- gi No. 5456964
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118
  
- Alignment No. 14769
- gi No. 85630
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 107 to 117
  
- Alignment No. 14770
- gi No. 85630
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118

Maximum Length Sequence corresponding to clone ID 313054

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2311
- Ceres seq\_id 1502985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2312
- Ceres seq\_id 1502986
- Location of start within SEQ ID NO 2311: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14771

- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2312: from 21 to 102 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2313
- Ceres seq\_id 1502987
- Location of start within SEQ ID NO 2311: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313104

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2314
- Ceres seq\_id 1503000

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2315
- Ceres seq\_id 1503001
- Location of start within SEQ ID NO 2314: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2316
- Ceres seq\_id 1503002
- Location of start within SEQ ID NO 2314: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14772
- CRAL/TRIO domain.
- Location within SEQ ID NO 2316: from 7 to 80 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2317
- Ceres seq\_id 1503010

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2318
- Ceres seq\_id 1503011
- Location of start within SEQ ID NO 2317: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14773
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2318: from 58 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2319
- Ceres seq\_id 1503012
- Location of start within SEQ ID NO 2317: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14774
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2319: from 33 to 81 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313273

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2320
- Ceres seq\_id 1503042

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2321
- Ceres seq\_id 1503043
- Location of start within SEQ ID NO 2320: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14775
- gi No. 2529670
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2321: from 24 to 39
- Alignment No. 14776
- gi No. 3021348
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2321: from 26 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2322
- Ceres seq\_id 1503044
- Location of start within SEQ ID NO 2320: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14777
- gi No. 2529670
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2322: from 2 to 17
- Alignment No. 14778
- gi No. 3021348
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2322: from 4 to 18

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2323
- Ceres seq\_id 1503045
- Location of start within SEQ ID NO 2320: at 225 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14779

- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2323: from 1 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14780
- gi No. 1172977
- % Identity 72.3
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2323: from 1 to 49
- Alignment No. 14781
- gi No. 2529670
- % Identity 73.1
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2323: from 1 to 44

Maximum Length Sequence corresponding to clone ID 313280

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2324
- Ceres seq\_id 1503048

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2325
- Ceres seq\_id 1503049
- Location of start within SEQ ID NO 2324: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14782
- gi No. 1171036
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14783
- gi No. 1480016
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14784
- gi No. 2407331
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14785
- gi No. 2497887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14786
- gi No. 2497888
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14787
- gi No. 2497890
- % Identity 77.8

- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
  
- Alignment No. 14788
- gi No. 2497892
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14789
- gi No. 2497893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14790
- gi No. 2497895
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14791
- gi No. 2497901
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14792
- gi No. 2497903
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14793
- gi No. 2497904
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14794
- gi No. 2507587
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14795
- gi No. 266579
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14796
- gi No. 3694984
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
  
- Alignment No. 14797
- gi No. 3900980
- % Identity 70
- Alignment Length 20



- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14798
- gi No. 3901014
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14799
- gi No. 4877893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14800
- gi No. 72178
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

Maximum Length Sequence corresponding to clone ID 313319

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2326
- Ceres seq\_id 1503064

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2327
- Ceres seq\_id 1503065
- Location of start within SEQ ID NO 2326: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14801
- Fatty acid desaturase
- Location within SEQ ID NO 2327: from 37 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14802
- gi No. 4104056
- % Identity 71.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 2327: from 5 to 169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2328
- Ceres seq\_id 1503066
- Location of start within SEQ ID NO 2326: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14803
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14804
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- Alignment No. 14805
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
  
- Alignment No. 14806
- gi No. 1185397
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15
  
- Alignment No. 14807
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
  
- Alignment No. 14808
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
  
- Alignment No. 14809
- gi No. 168237
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
  
- Alignment No. 14810
- gi No. 2429362
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2328: from 5 to 15
  
- Alignment No. 14811
- gi No. 4096360
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15
  
- Alignment No. 14812
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
  
- Alignment No. 14813
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
  
- Alignment No. 14814
- gi No. 5430752
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2329
  - Ceres seq\_id 1503067
  - Location of start within SEQ ID NO 2326: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14815
- Fatty acid desaturase
- Location within SEQ ID NO 2329: from 1 to 90 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14816
- gi No. 4104056
- % Identity 71.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 2329: from 1 to 131

Maximum Length Sequence corresponding to clone ID 313321

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2330
- Ceres seq\_id 1503071

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2331
- Ceres seq\_id 1503072
- Location of start within SEQ ID NO 2330: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14817
- gi No. 3850569
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2331: from 16 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2332
- Ceres seq\_id 1503073
- Location of start within SEQ ID NO 2330: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313406

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2333
- Ceres seq\_id 1503104

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2334
- Ceres seq\_id 1503105
- Location of start within SEQ ID NO 2333: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14818
- gi No. 2564066
- % Identity 78.5
- Alignment Length 65

- Location of Alignment in SEQ ID NO 2334: from 38 to 102
- Alignment No. 14819
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2334: from 38 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2335
- Ceres seq\_id 1503106
- Location of start within SEQ ID NO 2333: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14820
- gi No. 2564066
- % Identity 78.5
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2335: from 1 to 65
- Alignment No. 14821
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2335: from 1 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2336
- Ceres seq\_id 1503107
- Location of start within SEQ ID NO 2333: at 222 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14822
- gi No. 2464905
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2336: from 29 to 63
- Alignment No. 14823
- gi No. 2564066
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63
- Alignment No. 14824
- gi No. 3269288
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63
- Alignment No. 14825
- gi No. 5031275
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63

Maximum Length Sequence corresponding to clone ID 313421

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2337
- Ceres seq\_id 1503108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2338
- Ceres seq\_id 1503109
- Location of start within SEQ ID NO 2337: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14826
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2338: from 38 to 145 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14827
- gi No. 1161254
- % Identity 83.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14828
- gi No. 1168529
- % Identity 80.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14829
- gi No. 1168530
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14830
- gi No. 1362002
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14831
- gi No. 1362026
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14832
- gi No. 1362050
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14833
- gi No. 1362051
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14834
- gi No. 1669573
- % Identity 93.8
- Alignment Length 112

- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14835
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14836
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14837
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14838
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14839
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14840
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14841
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2338: from 36 to 148
- Alignment No. 14842
- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14843
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14844
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145

- Alignment No. 14845
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2338: from 45 to 145
  
- Alignment No. 14846
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
  
- Alignment No. 14847
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2339
- Ceres seq\_id 1503110
- Location of start within SEQ ID NO 2337: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14848
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2339: from 5 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14849
- gi No. 1161254
- % Identity 83.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14850
- gi No. 1168529
- % Identity 80.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14851
- gi No. 1168530
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14852
- gi No. 1362002
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14853
- gi No. 1362026
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14854
- gi No. 1362050
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14855
- gi No. 1362051
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14856
- gi No. 1669573
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14857
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14858
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14859
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14860
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14861
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14862
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14863
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2339: from 3 to 115
  
- Alignment No. 14864



- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14865
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14866
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
  
- Alignment No. 14867
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2339: from 12 to 112
  
- Alignment No. 14868
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
  
- Alignment No. 14869
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

Maximum Length Sequence corresponding to clone ID 313476

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2340
- Ceres seq\_id 1503132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2341
- Ceres seq\_id 1503133
- Location of start within SEQ ID NO 2340: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2342
- Ceres seq\_id 1503134
- Location of start within SEQ ID NO 2340: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14870
- gi No. 547305
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2342: from 32 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2343
- Ceres seq\_id 1503135
- Location of start within SEQ ID NO 2340: at 122 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14871
- gi No. 547305
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2343: from 18 to 37

Maximum Length Sequence corresponding to clone ID 313477

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2344
- Ceres seq\_id 1503136

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2345
- Ceres seq\_id 1503137
- Location of start within SEQ ID NO 2344: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14872
- gi No. 103026
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2345: from 4 to 14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2346
- Ceres seq\_id 1503138
- Location of start within SEQ ID NO 2344: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14873
- gi No. 1869859
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2346: from 64 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2347
- Ceres seq\_id 1503139
- Location of start within SEQ ID NO 2344: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14874
- gi No. 1869859
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2347: from 51 to 62

Maximum Length Sequence corresponding to clone ID 313513

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2348
- Ceres seq\_id 1503144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2349
- Ceres seq\_id 1503145
- Location of start within SEQ ID NO 2348: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14875
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2349: from 28 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2350
- Ceres seq\_id 1503146
- Location of start within SEQ ID NO 2348: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14876
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2350: from 22 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2351
- Ceres seq\_id 1503147
- Location of start within SEQ ID NO 2348: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14877
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2351: from 1 to 63

Maximum Length Sequence corresponding to clone ID 313560

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2352
- Ceres seq\_id 1503148

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2353
- Ceres seq\_id 1503149
- Location of start within SEQ ID NO 2352: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14878
- gi No. 1351999
- % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2353: from 1 to 21
  
- Alignment No. 14879
- gi No. 2129613
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2353: from 1 to 23
  
- Alignment No. 14880
- gi No. 3096930
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19
  
- Alignment No. 14881
- gi No. 4510417
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2353: from 1 to 22
  
- Alignment No. 14882
- gi No. 4544389
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19
  
- Alignment No. 14883
- gi No. 5678605
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2353: from 1 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2354
- Ceres seq\_id 1503150
- Location of start within SEQ ID NO 2352: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313561

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2355
- Ceres seq\_id 1503151

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2356
- Ceres seq\_id 1503152
- Location of start within SEQ ID NO 2355: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2357
- Ceres seq\_id 1503153
- Location of start within SEQ ID NO 2355: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2358
- Ceres seq\_id 1503154
- Location of start within SEQ ID NO 2355: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14884
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2358: from 5 to 95 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313590

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2359
- Ceres seq\_id 1503160

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2360
- Ceres seq\_id 1503161
- Location of start within SEQ ID NO 2359: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14885
- gi No. 5689238
- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2360: from 108 to 150

Maximum Length Sequence corresponding to clone ID 313616

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2361
- Ceres seq\_id 1503170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2362
- Ceres seq\_id 1503171
- Location of start within SEQ ID NO 2361: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14886
- Integrase
- Location within SEQ ID NO 2362: from 58 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2363
- Ceres seq\_id 1503172
- Location of start within SEQ ID NO 2361: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14887
- Integrase

- Location within SEQ ID NO 2363: from 58 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313650

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2364
- Ceres seq\_id 1503191

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2365
- Ceres seq\_id 1503192
- Location of start within SEQ ID NO 2364: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14888
- gi No. 102707
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2365: from 115 to 126
  
- Alignment No. 14889
- gi No. 3153821
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2365: from 13 to 26
  
- Alignment No. 14890
- gi No. 5032119
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2365: from 13 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2366
- Ceres seq\_id 1503193
- Location of start within SEQ ID NO 2364: at 134 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313677

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2367
- Ceres seq\_id 1503200

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2368
- Ceres seq\_id 1503201
- Location of start within SEQ ID NO 2367: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14891
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2368: from 73 to 151 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2369
- Ceres seq\_id 1503202
- Location of start within SEQ ID NO 2367: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14892
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2369: from 73 to 151 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2370
- Ceres seq\_id 1503203
- Location of start within SEQ ID NO 2367: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14893
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2370: from 38 to 116 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313754

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2371
- Ceres seq\_id 1503237

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2372
- Ceres seq\_id 1503238
- Location of start within SEQ ID NO 2371: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14894
- gi No. 1710490
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14895
- gi No. 2245098
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2372: from 24 to 40

- Alignment No. 14896
- gi No. 2982249
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14897
- gi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14898
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14899
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14900
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14901
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14902
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2373
- Ceres seq\_id 1503239
- Location of start within SEQ ID NO 2371: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2374
- Ceres seq\_id 1503240
- Location of start within SEQ ID NO 2371: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14903
- gi No. 1710490
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14904
- gi No. 2245098
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2374: from 3 to 19
  
- Alignment No. 14905
- gi No. 2982249



- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14906
- gi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14907
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14908
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14909
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14910
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14911
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

Maximum Length Sequence corresponding to clone ID 313846

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2375
- Ceres seq\_id 1503268

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2376
- Ceres seq\_id 1503269
- Location of start within SEQ ID NO 2375: at 197 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14912
- gi No. 2062167
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2376: from 24 to 62

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2377
- Ceres seq\_id 1503270

- Location of start within SEQ ID NO 2375: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14913
- gi No. 2062167
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2377: from 1 to 39

Maximum Length Sequence corresponding to clone ID 313854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2378
- Ceres seq\_id 1503275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2379
- Ceres seq\_id 1503276
- Location of start within SEQ ID NO 2378: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14914
- gi No. 1174492
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14915
- gi No. 2494300
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14916
- gi No. 2832707
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14917
- gi No. 3142294
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2379: from 39 to 83
- Alignment No. 14918
- gi No. 3790165
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83
- Alignment No. 14919
- gi No. 3790184
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83
- Alignment No. 14920
- gi No. 4185138

- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
  
- Alignment No. 14921
- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2380
- Ceres seq\_id 1503277
- Location of start within SEQ ID NO 2378: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14922
- gi No. 1174492
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
  
- Alignment No. 14923
- gi No. 2494300
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
  
- Alignment No. 14924
- gi No. 2832707
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
  
- Alignment No. 14925
- gi No. 3142294
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2380: from 1 to 45
  
- Alignment No. 14926
- gi No. 3790165
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
  
- Alignment No. 14927
- gi No. 3790184
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
  
- Alignment No. 14928
- gi No. 4185138
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
  
- Alignment No. 14929

- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2381
- Ceres seq\_id 1503278
- Location of start within SEQ ID NO 2378: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14930
- Elongation factor Tu family
- Location within SEQ ID NO 2381: from 4 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14931
- gi No. 1174492
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2381: from 4 to 42
- Alignment No. 14932
- gi No. 2494300
- % Identity 76.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2381: from 4 to 67
- Alignment No. 14933
- gi No. 2494301
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2381: from 4 to 69
- Alignment No. 14934
- gi No. 2832707
- % Identity 89.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14935
- gi No. 3142294
- % Identity 90.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14936
- gi No. 3790165
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14937
- gi No. 3790184
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71
- Alignment No. 14938
- gi No. 417179

- % Identity 73.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71
- Alignment No. 14939
- gi No. 4185138
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14940
- gi No. 4503507
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71

Maximum Length Sequence corresponding to clone ID 313864

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2382
- Ceres seq\_id 1503279

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2383
- Ceres seq\_id 1503280
- Location of start within SEQ ID NO 2382: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14941
- gi No. 4512664
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14942
- gi No. 4874278
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14943
- gi No. 4902470
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14944
- gi No. 4902877
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14945
- gi No. 4902879
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2384
- Ceres seq\_id 1503281

- Location of start within SEQ ID NO 2382: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2385
- Ceres seq\_id 1503282
- Location of start within SEQ ID NO 2382: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14946
- gi No. 4512664
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2385: from 1 to 49

Maximum Length Sequence corresponding to clone ID 313894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2386
- Ceres seq\_id 1503297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2387
- Ceres seq\_id 1503298
- Location of start within SEQ ID NO 2386: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14947
- C2 domain
- Location within SEQ ID NO 2387: from 27 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313912

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2388
- Ceres seq\_id 1503299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2389
- Ceres seq\_id 1503300
- Location of start within SEQ ID NO 2388: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14948
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2389: from 1 to 54 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14949
- gi No. 2191149
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14950
- gi No. 2505874

- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
  
- Alignment No. 14951
- gi No. 3482919
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54
  
- Alignment No. 14952
- gi No. 4204849
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
  
- Alignment No. 14953
- gi No. 4263791
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2389: from 1 to 79
  
- Alignment No. 14954
- gi No. 4512659
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54
  
- Alignment No. 14955
- gi No. 4836880
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56
  
- Alignment No. 14956
- gi No. 5042449
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56

Maximum Length Sequence corresponding to clone ID 313922

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2390
- Ceres seq\_id 1503305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2391
- Ceres seq\_id 1503306
- Location of start within SEQ ID NO 2390: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2392
- Ceres seq\_id 1503307
- Location of start within SEQ ID NO 2390: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14957

- Major intrinsic protein
- Location within SEQ ID NO 2392: from 35 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14958
- gi No. 1076687
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2392: from 30 to 135
- Alignment No. 14959
- gi No. 1212915
- % Identity 71.7
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14960
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14961
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14962
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14963
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14964
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14965
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14966
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14967
- gi No. 2245093
- % Identity 74.3



- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
  
- Alignment No. 14968
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
  
- Alignment No. 14969
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
  
- Alignment No. 14970
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
  
- Alignment No. 14971
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2392: from 103 to 137
  
- Alignment No. 14972
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
  
- Alignment No. 14973
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2392: from 69 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2393
- Ceres seq\_id 1503308
- Location of start within SEQ ID NO 2390: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14974
- Major intrinsic protein
- Location within SEQ ID NO 2393: from 11 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14975
- gi No. 1076687
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2393: from 6 to 111
  
- Alignment No. 14976
- gi No. 1212915
- % Identity 71.7
- Alignment Length 113

- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14977
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14978
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14979
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14980
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14981
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14982
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14983
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14984
- gi No. 2245093
- % Identity 74.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14985
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14986
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111

- Alignment No. 14987
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
  
- Alignment No. 14988
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2393: from 79 to 113
  
- Alignment No. 14989
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
  
- Alignment No. 14990
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2393: from 45 to 113

Maximum Length Sequence corresponding to clone ID 314003

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2394
- Ceres seq\_id 1503322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2395
- Ceres seq\_id 1503323
- Location of start within SEQ ID NO 2394: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2396
- Ceres seq\_id 1503324
- Location of start within SEQ ID NO 2394: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14991
- short chain dehydrogenase
- Location within SEQ ID NO 2396: from 7 to 102 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2397
- Ceres seq\_id 1503325
- Location of start within SEQ ID NO 2394: at 174 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14992
- short chain dehydrogenase
- Location within SEQ ID NO 2397: from 1 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314019

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2398
- Ceres seq\_id 1503330

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2399
- Ceres seq\_id 1503331
- Location of start within SEQ ID NO 2398: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14993
- gi No. 4680192
- % Identity 87.4
- Alignment Length 143
- Location of Alignment in SEQ ID NO 2399: from 6 to 148

Maximum Length Sequence corresponding to clone ID 314030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2400
- Ceres seq\_id 1503332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2401
- Ceres seq\_id 1503333
- Location of start within SEQ ID NO 2400: at 132 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14994
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14995
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14996
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14997
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2402
- Ceres seq\_id 1503334
- Location of start within SEQ ID NO 2400: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14998
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2402: from 1 to 97
  
- Alignment No. 14999
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97
  
- Alignment No. 15000
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97
  
- Alignment No. 15001
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2403
- Ceres seq\_id 1503335
- Location of start within SEQ ID NO 2400: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15002
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2403: from 1 to 88
  
- Alignment No. 15003
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88
  
- Alignment No. 15004
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88
  
- Alignment No. 15005
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88

Maximum Length Sequence corresponding to clone ID 314034

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2404  
- Ceres seq\_id 1503336

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2405  
- Ceres seq\_id 1503337  
- Location of start within SEQ ID NO 2404: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 15006  
- gi No. 4006906  
- % Identity 75  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2405: from 2 to 13

Maximum Length Sequence corresponding to clone ID 314077

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2406  
- Ceres seq\_id 1503342

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2407  
- Ceres seq\_id 1503343  
- Location of start within SEQ ID NO 2406: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 15007  
- gi No. 3786009  
- % Identity 87.3  
- Alignment Length 157  
- Location of Alignment in SEQ ID NO 2407: from 1 to 157

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2408  
- Ceres seq\_id 1503344  
- Location of start within SEQ ID NO 2406: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 15008  
- gi No. 3786009  
- % Identity 87.3  
- Alignment Length 157  
- Location of Alignment in SEQ ID NO 2408: from 1 to 98

Maximum Length Sequence corresponding to clone ID 314080

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2409  
- Ceres seq\_id 1503345

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2410  
- Ceres seq\_id 1503346  
- Location of start within SEQ ID NO 2409: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2411
  - Ceres seq\_id 1503347
  - Location of start within SEQ ID NO 2409: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15009
  - gi No. 2150000
  - % Identity 71.7
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2411: from 1 to 53

Maximum Length Sequence corresponding to clone ID 314106

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2412
  - Ceres seq\_id 1503351

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2413
  - Ceres seq\_id 1503352
  - Location of start within SEQ ID NO 2412: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15010
  - gi No. 1185397
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- 
- Alignment No. 15011
  - gi No. 1644455
  - % Identity 81.8
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- 
- Alignment No. 15012
  - gi No. 1644455
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- 
- Alignment No. 15013
  - gi No. 1644457
  - % Identity 81.8
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- 
- Alignment No. 15014
  - gi No. 1644457
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- 
- Alignment No. 15015
  - gi No. 1644457
  - % Identity 72.7
  - Alignment Length 11

- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15016
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15017
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15018
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15019
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15020
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15021
- gi No. 1644461
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15022
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15023
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15024
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15025
- gi No. 178014
- % Identity 75
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2413: from 13 to 24



- Alignment No. 15026
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
  
- Alignment No. 15027
- gi No. 19923
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
  
- Alignment No. 15028
- gi No. 2244878
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
  
- Alignment No. 15029
- gi No. 2462823
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
  
- Alignment No. 15030
- gi No. 322755
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 15 to 25
  
- Alignment No. 15031
- gi No. 322755
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 15 to 25
  
- Alignment No. 15032
- gi No. 322755
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2413: from 14 to 27
  
- Alignment No. 15033
- gi No. 322757
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
  
- Alignment No. 15034
- gi No. 3551531
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
  
- Alignment No. 15035
- gi No. 5306259
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2414
  - Ceres seq\_id 1503353
  - Location of start within SEQ ID NO 2412: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314122

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2415
  - Ceres seq\_id 1503354
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2416
  - Ceres seq\_id 1503355
  - Location of start within SEQ ID NO 2415: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2417
  - Ceres seq\_id 1503356
  - Location of start within SEQ ID NO 2415: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2418
  - Ceres seq\_id 1503357
  - Location of start within SEQ ID NO 2415: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15036
- DnaJ domain
- Location within SEQ ID NO 2418: from 24 to 75 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314197

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2419
  - Ceres seq\_id 1503378
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2420
  - Ceres seq\_id 1503379
  - Location of start within SEQ ID NO 2419: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15037
- Protein phosphatase 2C
- Location within SEQ ID NO 2420: from 3 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314305

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2421
- Ceres seq\_id 1503400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2422
- Ceres seq\_id 1503401
- Location of start within SEQ ID NO 2421: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15038
- gi No. 445612
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2422: from 39 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2423
- Ceres seq\_id 1503402
- Location of start within SEQ ID NO 2421: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2424
- Ceres seq\_id 1503403
- Location of start within SEQ ID NO 2421: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15039
- gi No. 445612
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2424: from 6 to 48

Maximum Length Sequence corresponding to clone ID 314409

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2425
- Ceres seq\_id 1503422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2426
- Ceres seq\_id 1503423
- Location of start within SEQ ID NO 2425: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15040
- gi No. 1743388
- % Identity 94.2
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2426: from 77 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2427

- Ceres seq\_id 1503424
- Location of start within SEQ ID NO 2425: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15041
  - gi No. 1743388
  - % Identity 94.2
  - Alignment Length 86
  - Location of Alignment in SEQ ID NO 2427: from 33 to 117

Maximum Length Sequence corresponding to clone ID 314420

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2428
- Ceres seq\_id 1503429

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2429
- Ceres seq\_id 1503430
- Location of start within SEQ ID NO 2428: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15042
  - gi No. 2914700
  - % Identity 86.7
  - Alignment Length 30
  - Location of Alignment in SEQ ID NO 2429: from 2 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2430
- Ceres seq\_id 1503431
- Location of start within SEQ ID NO 2428: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2431
- Ceres seq\_id 1503432
- Location of start within SEQ ID NO 2428: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314461

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2432
- Ceres seq\_id 1503443

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2433
- Ceres seq\_id 1503444
- Location of start within SEQ ID NO 2432: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2434
  - Ceres seq\_id 1503445
  - Location of start within SEQ ID NO 2432: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15043
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2434: from 38 to 51
- Alignment No. 15044
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2434: from 41 to 51
- Alignment No. 15045
- gi No. 4008584
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2434: from 37 to 51
- Alignment No. 15046
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2434: from 38 to 51
- Alignment No. 15047
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2434: from 38 to 51
- Alignment No. 15048
- gi No. 688080
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2434: from 42 to 52

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2435
  - Ceres seq\_id 1503446
  - Location of start within SEQ ID NO 2432: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15049
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
- Alignment No. 15050
- gi No. 4008584
- % Identity 75

- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 8 to 18
  
- Alignment No. 15051
- gi No. 4008584
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2435: from 4 to 18
  
- Alignment No. 15052
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
  
- Alignment No. 15053
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
  
- Alignment No. 15054
- gi No. 688080
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 9 to 19

Maximum Length Sequence corresponding to clone ID 314605

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2436
- Ceres seq\_id 1503476

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2437
- Ceres seq\_id 1503477
- Location of start within SEQ ID NO 2436: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2438
- Ceres seq\_id 1503478
- Location of start within SEQ ID NO 2436: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15055
- Chitin recognition protein
- Location within SEQ ID NO 2438: from 44 to 77 aa.

- Alignment No. 15056
- Chitinases class I
- Location within SEQ ID NO 2438: from 90 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15057
- gi No. 299189
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69

- Alignment No. 15058
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69
  
- Alignment No. 15059
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2438: from 112 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2439
- Ceres seq\_id 1503479
- Location of start within SEQ ID NO 2436: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15060
- Chitin recognition protein
- Location within SEQ ID NO 2439: from 25 to 58 aa.
  
- Alignment No. 15061
- Chitinases class I
- Location within SEQ ID NO 2439: from 71 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15062
- gi No. 299189
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2439: from 30 to 50
  
- Alignment No. 15063
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2439: from 30 to 50
  
- Alignment No. 15064
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2439: from 93 to 125

Maximum Length Sequence corresponding to clone ID 314613

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2440
- Ceres seq\_id 1503480

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2441
- Ceres seq\_id 1503481
- Location of start within SEQ ID NO 2440: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15065
- chorismate binding enzyme
- Location within SEQ ID NO 2441: from 4 to 147 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15066
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15067
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2441: from 2 to 147
  
- Alignment No. 15068
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2441: from 2 to 155
  
- Alignment No. 15069
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15070
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2441: from 2 to 147
  
- Alignment No. 15071
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15072
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2441: from 1 to 147
  
- Alignment No. 15073
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15074
- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2441: from 1 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2442
- Ceres seq\_id 1503482
- Location of start within SEQ ID NO 2440: at 4 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15075
- chorismate binding enzyme
- Location within SEQ ID NO 2442: from 3 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15076
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15077
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15078
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2442: from 1 to 154
- Alignment No. 15079
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15080
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15081
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15082
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15083
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15084
- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2442: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2443
- Ceres seq\_id 1503483
- Location of start within SEQ ID NO 2440: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15085
- chorismate binding enzyme
- Location within SEQ ID NO 2443: from 1 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15086
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15087
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15088
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2443: from 1 to 137
- Alignment No. 15089
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15090
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15091
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15092
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15093
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15094

- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129

Maximum Length Sequence corresponding to clone ID 314618

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2444
- Ceres seq\_id 1503484

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2445
- Ceres seq\_id 1503485
- Location of start within SEQ ID NO 2444: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15095
- Thioredoxin
- Location within SEQ ID NO 2445: from 22 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15096
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2445: from 16 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2446
- Ceres seq\_id 1503486
- Location of start within SEQ ID NO 2444: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15097
- Thioredoxin
- Location within SEQ ID NO 2446: from 7 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15098
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2446: from 1 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2447
- Ceres seq\_id 1503487
- Location of start within SEQ ID NO 2444: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15099
- Thioredoxin
- Location within SEQ ID NO 2447: from 1 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15100
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123

- Location of Alignment in SEQ ID NO 2447: from 1 to 102

Maximum Length Sequence corresponding to clone ID 314637

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2448
- Ceres seq\_id 1503492

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2449
- Ceres seq\_id 1503493
- Location of start within SEQ ID NO 2448: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15101
- Chalcone and stilbene synthases
- Location within SEQ ID NO 2449: from 12 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15102
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2449: from 41 to 62

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2450
- Ceres seq\_id 1503494
- Location of start within SEQ ID NO 2448: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15103
- Chalcone and stilbene synthases
- Location within SEQ ID NO 2450: from 3 to 53 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15104
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2450: from 32 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2451
- Ceres seq\_id 1503495
- Location of start within SEQ ID NO 2448: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15105
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2451: from 21 to 42

Maximum Length Sequence corresponding to clone ID 314643

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2452
- Ceres seq\_id 1503496

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2453
- Ceres seq\_id 1503497
- Location of start within SEQ ID NO 2452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15106
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2453: from 9 to 136 aa.
- Alignment No. 15107
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2453: from 28 to 151 aa.
- Alignment No. 15108
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2453: from 23 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2454
- Ceres seq\_id 1503498
- Location of start within SEQ ID NO 2452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15109
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2454: from 9 to 136 aa.
- Alignment No. 15110
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2454: from 28 to 151 aa.
- Alignment No. 15111
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2454: from 23 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2455
- Ceres seq\_id 1503499
- Location of start within SEQ ID NO 2452: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314669

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2456
- Ceres seq\_id 1503507

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2457
- Ceres seq\_id 1503508
- Location of start within SEQ ID NO 2456: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15112
  - gi No. 2894378
  - % Identity 82.5
  - Alignment Length 114
  - Location of Alignment in SEQ ID NO 2457: from 1 to 114

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2458
  - Ceres seq\_id 1503509
  - Location of start within SEQ ID NO 2456: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15113
  - gi No. 2894378
  - % Identity 82.5
  - Alignment Length 114
  - Location of Alignment in SEQ ID NO 2458: from 1 to 38

Maximum Length Sequence corresponding to clone ID 314683

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2459
  - Ceres seq\_id 1503510

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2460
  - Ceres seq\_id 1503511
  - Location of start within SEQ ID NO 2459: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15114
  - gi No. 4091080
  - % Identity 70.7
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 2460: from 1 to 57

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2461
  - Ceres seq\_id 1503512
  - Location of start within SEQ ID NO 2459: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15115
  - gi No. 4091080
  - % Identity 70.7
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 2461: from 1 to 45

Maximum Length Sequence corresponding to clone ID 314729

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2462
  - Ceres seq\_id 1503522

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2463
  - Ceres seq\_id 1503523
  - Location of start within SEQ ID NO 2462: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15116
- gi No. 1173045
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15117
- gi No. 1346945
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15118
- gi No. 2281793
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2463: from 12 to 28
  
- Alignment No. 15119
- gi No. 2565332
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2463: from 3 to 28
  
- Alignment No. 15120
- gi No. 2996185
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15121
- gi No. 3098458
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28
  
- Alignment No. 15122
- gi No. 3845189
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15123
- gi No. 400996
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15124
- gi No. 4090257
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15125
- gi No. 4455775
- % Identity 71.4

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28
- Alignment No. 15126
- gi No. 4506643
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15127
- gi No. 4741896
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15128
- gi No. 5007072
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2463: from 9 to 23

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2464
- Ceres seq\_id 1503524
- Location of start within SEQ ID NO 2462: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2465
- Ceres seq\_id 1503525
- Location of start within SEQ ID NO 2462: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314734

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2466
- Ceres seq\_id 1503526

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2467
- Ceres seq\_id 1503527
- Location of start within SEQ ID NO 2466: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2468
- Ceres seq\_id 1503528
- Location of start within SEQ ID NO 2466: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15129
- Ribosomal protein L13



- Location within SEQ ID NO 2468: from 29 to 85 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2469
- Ceres seq\_id 1503529
- Location of start within SEQ ID NO 2466: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314824

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2470
- Ceres seq\_id 1503550

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2471
- Ceres seq\_id 1503551
- Location of start within SEQ ID NO 2470: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15130
- gi No. 3935157
- % Identity 71.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2471: from 28 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2472
- Ceres seq\_id 1503552
- Location of start within SEQ ID NO 2470: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2473
- Ceres seq\_id 1503553
- Location of start within SEQ ID NO 2470: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15131
- gi No. 3935157
- % Identity 71.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2473: from 4 to 126

Maximum Length Sequence corresponding to clone ID 314826

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2474
- Ceres seq\_id 1503554

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2475
- Ceres seq\_id 1503555

- Location of start within SEQ ID NO 2474: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15132
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2475: from 2 to 94 aa.
- Alignment No. 15133
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2475: from 9 to 133 aa.
- Alignment No. 15134
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2475: from 11 to 138 aa.
- Alignment No. 15135
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2475: from 3 to 114 aa.
- Alignment No. 15136
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2475: from 4 to 138 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15137
- gi No. 2281102
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2475: from 128 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2476
- Ceres seq\_id 1503556
- Location of start within SEQ ID NO 2474: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15138
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2476: from 1 to 75 aa.
- Alignment No. 15139
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2476: from 1 to 114 aa.
- Alignment No. 15140
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2476: from 1 to 119 aa.
- Alignment No. 15141
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2476: from 1 to 95 aa.
- Alignment No. 15142
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2476: from 1 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15143
- gi No. 2281102

- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2476: from 109 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2477
- Ceres seq\_id 1503557
- Location of start within SEQ ID NO 2474: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15144
- gi No. 109944
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15145
- gi No. 1350911
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15146
- gi No. 1350912
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15147
- gi No. 200880
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15148
- gi No. 2564955
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2477: from 76 to 86
  
- Alignment No. 15149
- gi No. 337720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15150
- gi No. 483195
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15151
- gi No. 542994
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

Maximum Length Sequence corresponding to clone ID 314875

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2478  
- Ceres seq\_id 1503569

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2479  
- Ceres seq\_id 1503570  
- Location of start within SEQ ID NO 2478: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 15152  
- gi No. 4455361  
- % Identity 72.2  
- Alignment Length 54  
- Location of Alignment in SEQ ID NO 2479: from 34 to 87

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2480  
- Ceres seq\_id 1503571  
- Location of start within SEQ ID NO 2478: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 15153  
- gi No. 4455361  
- % Identity 72.2  
- Alignment Length 54  
- Location of Alignment in SEQ ID NO 2480: from 1 to 54

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2481  
- Ceres seq\_id 1503572  
- Location of start within SEQ ID NO 2478: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 15154  
- gi No. 4455361  
- % Identity 72.2  
- Alignment Length 54  
- Location of Alignment in SEQ ID NO 2481: from 1 to 40

Maximum Length Sequence corresponding to clone ID 314917

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2482  
- Ceres seq\_id 1503585

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2483  
- Ceres seq\_id 1503586  
- Location of start within SEQ ID NO 2482: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15155  
- WD domain, G-beta repeat  
- Location within SEQ ID NO 2483: from 20 to 58 aa.

- (D) Related Amino Acid Sequences

- Alignment No. 15156
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15157
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15158
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15159
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15160
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15161
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15162
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15163
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15164
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15165
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
  
- Alignment No. 15166

- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2484
- Ceres seq\_id 1503587
- Location of start within SEQ ID NO 2482: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15167
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15168
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15169
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15170
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15171
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15172
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15173
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15174
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15175
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15176
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15177
- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

Maximum Length Sequence corresponding to clone ID 314924

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2485
- Ceres seq\_id 1503588

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2486
- Ceres seq\_id 1503589
- Location of start within SEQ ID NO 2485: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15178
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2486: from 1 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15179
- gi No. 1142614
- % Identity 85.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15180
- gi No. 1174848
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 98
  
- Alignment No. 15181
- gi No. 1174849
- % Identity 79.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15182
- gi No. 136643
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15183
- gi No. 136645
- % Identity 75.7

- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15184
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15185
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15186
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15187
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15188
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15189
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 1 to 74
  
- Alignment No. 15190
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15191
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2486: from 59 to 100
  
- Alignment No. 15192
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15193
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105



- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15194
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100
- Alignment No. 15195
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15196
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15197
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2486: from 32 to 100
- Alignment No. 15198
- gi No. 4507773
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15199
- gi No. 4507775
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15200
- gi No. 4507777
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15201
- gi No. 456568
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15202
- gi No. 4581117
- % Identity 85.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15203
- gi No. 4583656
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2486: from 1 to 98

- Alignment No. 15204
- gi No. 464979
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15205
- gi No. 464981
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15206
- gi No. 464985
- % Identity 87.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15207
- gi No. 464986
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15208
- gi No. 464987
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15209
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2486: from 2 to 100
  
- Alignment No. 15210
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15211
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
  
- Alignment No. 15212
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2487
- Ceres seq\_id 1503590
- Location of start within SEQ ID NO 2485: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15213
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2487: from 1 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15214
- gi No. 1142614
- % Identity 85.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15215
- gi No. 1174848
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 90
- Alignment No. 15216
- gi No. 1174849
- % Identity 79.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15217
- gi No. 136643
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15218
- gi No. 136645
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15219
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15220
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15221
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15222
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15223
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15224
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 1 to 66
  
- Alignment No. 15225
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15226
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2487: from 51 to 92
  
- Alignment No. 15227
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15228
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15229
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92
  
- Alignment No. 15230
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15231
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15232
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2487: from 24 to 92
  
- Alignment No. 15233

- gi No. 4507773
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15234
- gi No. 4507775
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15235
- gi No. 4507777
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15236
- gi No. 456568
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15237
- gi No. 4581117
- % Identity 85.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15238
- gi No. 4583656
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2487: from 1 to 90
  
- Alignment No. 15239
- gi No. 464979
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15240
- gi No. 464981
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15241
- gi No. 464985
- % Identity 87.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15242
- gi No. 464986
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15243
- gi No. 464987

- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15244
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15245
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15246
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
  
- Alignment No. 15247
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92

Maximum Length Sequence corresponding to clone ID 314967

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2488
- Ceres seq\_id 1503591

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2489
- Ceres seq\_id 1503592
- Location of start within SEQ ID NO 2488: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15248
- Glycosyl hydrolases family 16
- Location within SEQ ID NO 2489: from 1 to 115 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15249
- gi No. 2129770
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126
  
- Alignment No. 15250
- gi No. 2154609
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126
  
- Alignment No. 15251
- gi No. 5533313
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2490
  - Ceres seq\_id 1503593
  - Location of start within SEQ ID NO 2488: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15252
- Mucin-like glycoprotein
- Location within SEQ ID NO 2490: from 1 to 126 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314971

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2491
- Ceres seq\_id 1503594

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2492
- Ceres seq\_id 1503595
- Location of start within SEQ ID NO 2491: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15253
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2492: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15254
- gi No. 4006890
- % Identity 84.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2492: from 1 to 59
- Alignment No. 15255
- gi No. 4217999
- % Identity 84.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2492: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2493
- Ceres seq\_id 1503596
- Location of start within SEQ ID NO 2491: at 224 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2494
- Ceres seq\_id 1503597
- Location of start within SEQ ID NO 2491: at 246 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314996

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2495
- Ceres seq\_id 1503600

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2496
- Ceres seq\_id 1503601
- Location of start within SEQ ID NO 2495: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15256
- gi No. 1173018
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
  
- Alignment No. 15257
- gi No. 132849
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
  
- Alignment No. 15258
- gi No. 266944
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
  
- Alignment No. 15259
- gi No. 2961372
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
  
- Alignment No. 15260
- gi No. 3088346
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
  
- Alignment No. 15261
- gi No. 4406816
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2497
- Ceres seq\_id 1503602
- Location of start within SEQ ID NO 2495: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15262
- Ribosomal Proteins L2
- Location within SEQ ID NO 2497: from 25 to 110 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15263
- gi No. 132849



- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
  
- Alignment No. 15264
- gi No. 266944
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
  
- Alignment No. 15265
- gi No. 2961372
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
  
- Alignment No. 15266
- gi No. 4406816
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

Maximum Length Sequence corresponding to clone ID 315057

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2498
- Ceres seq\_id 1503615

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2499
- Ceres seq\_id 1503616
- Location of start within SEQ ID NO 2498: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15267
- gi No. 481728
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2499: from 76 to 86
  
- Alignment No. 15268
- gi No. 481728
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2499: from 76 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2500
- Ceres seq\_id 1503617
- Location of start within SEQ ID NO 2498: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15269
- gi No. 3941736
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
  
- Alignment No. 15270

- gi No. 4337109
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
  
- Alignment No. 15271
- gi No. 4758110
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
  
- Alignment No. 15272
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
  
- Alignment No. 15273
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 95 to 106

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2501
- Ceres seq\_id 1503618
- Location of start within SEQ ID NO 2498: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315079

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2502
- Ceres seq\_id 1503621

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2503
- Ceres seq\_id 1503622
- Location of start within SEQ ID NO 2502: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15274
- Putative GTP-ase activating protein for Arf
- Location within SEQ ID NO 2503: from 74 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15275
- gi No. 3236238
- % Identity 83.1
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2503: from 74 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2504
- Ceres seq\_id 1503623
- Location of start within SEQ ID NO 2502: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2505
- Ceres seq\_id 1503624
- Location of start within SEQ ID NO 2502: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2506
- Ceres seq\_id 1503662

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2507
- Ceres seq\_id 1503663
- Location of start within SEQ ID NO 2506: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15276
- gi No. 3123264
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2507: from 81 to 128

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2508
- Ceres seq\_id 1503664
- Location of start within SEQ ID NO 2506: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15277
- gi No. 3123264
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86

- Alignment No. 15278

- gi No. 498906

- % Identity 70.5

- Alignment Length 61

- Location of Alignment in SEQ ID NO 2508: from 26 to 86

- Alignment No. 15279

- gi No. 730547

- % Identity 75.4

- Alignment Length 61

- Location of Alignment in SEQ ID NO 2508: from 26 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2509
- Ceres seq\_id 1503665
- Location of start within SEQ ID NO 2506: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15280
- gi No. 3123264
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61
  
- Alignment No. 15281
- gi No. 498906
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61
  
- Alignment No. 15282
- gi No. 730547
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61

Maximum Length Sequence corresponding to clone ID 315227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2510
- Ceres seq\_id 1503670

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2511
- Ceres seq\_id 1503671
- Location of start within SEQ ID NO 2510: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15283
- gi No. 1170395
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
  
- Alignment No. 15284
- gi No. 1170396
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
  
- Alignment No. 15285
- gi No. 1170396
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45
  
- Alignment No. 15286
- gi No. 1170397
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
  
- Alignment No. 15287
- gi No. 1170397
- % Identity 70.6
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2511: from 29 to 45
- Alignment No. 15288
- gi No. 1170398
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
- Alignment No. 15289
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45

Maximum Length Sequence corresponding to clone ID 315373

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2512
- Ceres seq\_id 1503697

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2513
- Ceres seq\_id 1503698
- Location of start within SEQ ID NO 2512: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15290
- Copper amine oxidase
- Location within SEQ ID NO 2513: from 1 to 123 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15291
- gi No. 4559342
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122
- Alignment No. 15292
- gi No. 4567319
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122
- Alignment No. 15293
- gi No. 5230728
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122

Maximum Length Sequence corresponding to clone ID 315404

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2514
- Ceres seq\_id 1503703

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2515
- Ceres seq\_id 1503704
- Location of start within SEQ ID NO 2514: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2516
- Ceres seq\_id 1503705
- Location of start within SEQ ID NO 2514: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15294
- gi No. 4512664
- % Identity 77.8
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2516: from 35 to 79
- Alignment No. 15295
- gi No. 4874278
- % Identity 74
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15296
- gi No. 4902470
- % Identity 74
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15297
- gi No. 4902877
- % Identity 72.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15298
- gi No. 4902879
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2516: from 36 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2517
- Ceres seq\_id 1503706
- Location of start within SEQ ID NO 2514: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15299
- gi No. 4512664
- % Identity 77.8
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2517: from 12 to 56
- Alignment No. 15300
- gi No. 4874278
- % Identity 74
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15301
- gi No. 4902470
- % Identity 74

- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
  
- Alignment No. 15302
- gi No. 4902877
- % Identity 72.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
  
- Alignment No. 15303
- gi No. 4902879
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2517: from 13 to 56

Maximum Length Sequence corresponding to clone ID 315430

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2518
- Ceres seq\_id 1503714

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2519
- Ceres seq\_id 1503715
- Location of start within SEQ ID NO 2518: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15304
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2519: from 36 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15305
- gi No. 141279
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2519: from 46 to 62
  
- Alignment No. 15306
- gi No. 1914851
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2519: from 46 to 61
  
- Alignment No. 15307
- gi No. 2224619
- % Identity 70
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2519: from 49 to 68
  
- Alignment No. 15308
- gi No. 539033
- % Identity 72
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2519: from 46 to 70
  
- Alignment No. 15309
- gi No. 688080
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2519: from 48 to 60

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2520
  - Ceres seq\_id 1503716
  - Location of start within SEQ ID NO 2518: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2521
  - Ceres seq\_id 1503717
  - Location of start within SEQ ID NO 2518: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315437

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2522
  - Ceres seq\_id 1503718
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2523
  - Ceres seq\_id 1503719
  - Location of start within SEQ ID NO 2522: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15310
- Cystatin domain
- Location within SEQ ID NO 2523: from 77 to 132 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315445

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2524
  - Ceres seq\_id 1503720
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2525
  - Ceres seq\_id 1503721
  - Location of start within SEQ ID NO 2524: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2526
  - Ceres seq\_id 1503722
  - Location of start within SEQ ID NO 2524: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2527
  - Ceres seq\_id 1503723
  - Location of start within SEQ ID NO 2524: at 200 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15311
- Armadillo/beta-catenin-like repeats
- Location within SEQ ID NO 2527: from 21 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15312
- gi No. 2950210
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2527: from 21 to 93
- Alignment No. 15313
- gi No. 3091280
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2527: from 22 to 77
- Alignment No. 15314
- gi No. 3122278
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2527: from 22 to 77
- Alignment No. 15315
- gi No. 3273243
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2527: from 21 to 93

Maximum Length Sequence corresponding to clone ID 315466

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2528
- Ceres seq\_id 1503728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2529
- Ceres seq\_id 1503729
- Location of start within SEQ ID NO 2528: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15316
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2529: from 4 to 108 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315475

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2530
- Ceres seq\_id 1503734

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2531
- Ceres seq\_id 1503735
- Location of start within SEQ ID NO 2530: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15317

- Multicopper oxidase
- Location within SEQ ID NO 2531: from 22 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15318
- gi No. 4454012
- % Identity 71.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2531: from 23 to 110
- Alignment No. 15319
- gi No. 4725941
- % Identity 71.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2531: from 22 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2532
- Ceres seq\_id 1503736
- Location of start within SEQ ID NO 2530: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2533
- Ceres seq\_id 1503737
- Location of start within SEQ ID NO 2530: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15320
- Multicopper oxidase
- Location within SEQ ID NO 2533: from 6 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15321
- gi No. 4454012
- % Identity 71.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2533: from 7 to 94
- Alignment No. 15322
- gi No. 4725941
- % Identity 71.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2533: from 6 to 94

Maximum Length Sequence corresponding to clone ID 315510

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2534
- Ceres seq\_id 1503743

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2535
- Ceres seq\_id 1503744
- Location of start within SEQ ID NO 2534: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2536
- Ceres seq\_id 1503745
- Location of start within SEQ ID NO 2534: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15323
- gi No. 1076556
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2536: from 20 to 31
  
- Alignment No. 15324
- gi No. 1655699
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2536: from 18 to 29
  
- Alignment No. 15325
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
  
- Alignment No. 15326
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
  
- Alignment No. 15327
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
  
- Alignment No. 15328
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
  
- Alignment No. 15329
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
  
- Alignment No. 15330
- gi No. 1655699
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
  
- Alignment No. 15331
- gi No. 1655699
- % Identity 70.6
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15332
- gi No. 322747
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30
- Alignment No. 15333
- gi No. 322749
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30

Maximum Length Sequence corresponding to clone ID 315548

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2537
- Ceres seq\_id 1503746

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2538
- Ceres seq\_id 1503747
- Location of start within SEQ ID NO 2537: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2539
- Ceres seq\_id 1503748
- Location of start within SEQ ID NO 2537: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15334
- gi No. 112110
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2539: from 2 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2540
- Ceres seq\_id 1503749
- Location of start within SEQ ID NO 2537: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315587

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2541
- Ceres seq\_id 1503769

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2542
- Ceres seq\_id 1503770
- Location of start within SEQ ID NO 2541: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15335
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 2542: from 2 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15336
- gi No. 1076713
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2542: from 1 to 22
- Alignment No. 15337
- gi No. 1304478
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2542: from 2 to 38
- Alignment No. 15338
- gi No. 1729427
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2542: from 1 to 38
- Alignment No. 15339
- gi No. 2129487
- % Identity 80.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114
- Alignment No. 15340
- gi No. 2829275
- % Identity 88.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114
- Alignment No. 15341
- gi No. 4972094
- % Identity 90.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114

Maximum Length Sequence corresponding to clone ID 315593

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2543
- Ceres seq\_id 1503775

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2544
- Ceres seq\_id 1503776
- Location of start within SEQ ID NO 2543: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15342
- Elongation factor G C-terminus
- Location within SEQ ID NO 2544: from 21 to 152 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15343
- gi No. 4895248
- % Identity 83.3
- Alignment Length 156

- Location of Alignment in SEQ ID NO 2544: from 1 to 156

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2545
- Ceres seq\_id 1503777
- Location of start within SEQ ID NO 2543: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15344
- Elongation factor G C-terminus
- Location within SEQ ID NO 2545: from 1 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15345
- gi No. 4895248
- % Identity 83.3
- Alignment Length 156
- Location of Alignment in SEQ ID NO 2545: from 1 to 120

Maximum Length Sequence corresponding to clone ID 315595

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2546
- Ceres seq\_id 1503778

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2547
- Ceres seq\_id 1503779
- Location of start within SEQ ID NO 2546: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15346
- gi No. 3786005
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2547: from 1 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2548
- Ceres seq\_id 1503780
- Location of start within SEQ ID NO 2546: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2549
- Ceres seq\_id 1503781
- Location of start within SEQ ID NO 2546: at 324 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315627

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2550
- Ceres seq\_id 1503796

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2551
- Ceres seq\_id 1503797
- Location of start within SEQ ID NO 2550: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2552
- Ceres seq\_id 1503798
- Location of start within SEQ ID NO 2550: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15347
- gi No. 2352921
- % Identity 87.1
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38
  
- Alignment No. 15348
- gi No. 2352923
- % Identity 82.3
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38
  
- Alignment No. 15349
- gi No. 3021508
- % Identity 73.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
  
- Alignment No. 15350
- gi No. 3021510
- % Identity 76.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
  
- Alignment No. 15351
- gi No. 3023815
- % Identity 77.4
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38
  
- Alignment No. 15352
- gi No. 4206114
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
  
- Alignment No. 15353
- gi No. 5360754
- % Identity 87.5
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
  
- Alignment No. 15354
- gi No. 585165
- % Identity 76.1

- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2553
- Ceres seq\_id 1503799
- Location of start within SEQ ID NO 2550: at 262 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15355
- Glucose-6-phosphate dehydrogenase
- Location within SEQ ID NO 2553: from 1 to 42 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15356
- gi No. 1169799
- % Identity 70.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2553: from 3 to 43
- Alignment No. 15357
- gi No. 3021508
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2553: from 3 to 43
- Alignment No. 15358
- gi No. 585165
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2553: from 1 to 43

Maximum Length Sequence corresponding to clone ID 315647

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2554
- Ceres seq\_id 1503810

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2555
- Ceres seq\_id 1503811
- Location of start within SEQ ID NO 2554: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15359
- gi No. 1173201
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2555: from 37 to 73
- Alignment No. 15360
- gi No. 131772
- % Identity 97.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15361
- gi No. 131773
- % Identity 89.7
- Alignment Length 39



- Location of Alignment in SEQ ID NO 2555: from 35 to 73
- Alignment No. 15362
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2555: from 60 to 73
- Alignment No. 15363
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2555: from 59 to 73
- Alignment No. 15364
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2555: from 48 to 73
- Alignment No. 15365
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15366
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15367
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2555: from 53 to 73
- Alignment No. 15368
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15369
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2556
- Ceres seq\_id 1503812
- Location of start within SEQ ID NO 2554: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15370
- gi No. 1173201
- % Identity 75.7

- Alignment Length 37
- Location of Alignment in SEQ ID NO 2556: from 5 to 41
  
- Alignment No. 15371
- gi No. 131772
- % Identity 97.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
  
- Alignment No. 15372
- gi No. 131773
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2556: from 3 to 41
  
- Alignment No. 15373
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2556: from 28 to 41
  
- Alignment No. 15374
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2556: from 27 to 41
  
- Alignment No. 15375
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2556: from 16 to 41
  
- Alignment No. 15376
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
  
- Alignment No. 15377
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
  
- Alignment No. 15378
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2556: from 21 to 41
  
- Alignment No. 15379
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
  
- Alignment No. 15380
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41

- Location of Alignment in SEQ ID NO 2556: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2557
- Ceres seq\_id 1503813
- Location of start within SEQ ID NO 2554: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15381
- Ribosomal protein S11
- Location within SEQ ID NO 2557: from 3 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15382
- gi No. 1173200
- % Identity 90.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2557: from 28 to 68
  
- Alignment No. 15383
- gi No. 1173201
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15384
- gi No. 131772
- % Identity 97
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15385
- gi No. 131773
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15386
- gi No. 133771
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15387
- gi No. 133777
- % Identity 80.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15388
- gi No. 133782
- % Identity 82.4
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15389
- gi No. 133785
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15390
- gi No. 133789
- % Identity 75.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15391
- gi No. 1346941
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15392
- gi No. 1350935
- % Identity 83.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15393
- gi No. 1350937
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15394
- gi No. 2350992
- % Identity 72.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2557: from 3 to 69
  
- Alignment No. 15395
- gi No. 2414647
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15396
- gi No. 2500442
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2557: from 3 to 41
  
- Alignment No. 15397
- gi No. 2500443
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2557: from 46 to 68
  
- Alignment No. 15398
- gi No. 3097244
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15399
- gi No. 3122785
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15400
- gi No. 4574240
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15401
- gi No. 4588920
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15402
- gi No. 4678226
- % Identity 93.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15403
- gi No. 4886269
- % Identity 93.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15404
- gi No. 5032051
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15405
- gi No. 5441523
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2557: from 33 to 68
  
- Alignment No. 15406
- gi No. 547604
- % Identity 78.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15407
- gi No. 70946
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15408
- gi No. 730453
- % Identity 78.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15409
- gi No. 730633
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
  
- Alignment No. 15410

- gi No. 83794
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

Maximum Length Sequence corresponding to clone ID 315681

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2558
- Ceres seq\_id 1503822

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2559
- Ceres seq\_id 1503823
- Location of start within SEQ ID NO 2558: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15411
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2559: from 57 to 150 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2560
- Ceres seq\_id 1503824
- Location of start within SEQ ID NO 2558: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15412
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2560: from 30 to 123 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2561
- Ceres seq\_id 1503825
- Location of start within SEQ ID NO 2558: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15413
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2561: from 8 to 101 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2562
- Ceres seq\_id 1503826

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2563
- Ceres seq\_id 1503827
- Location of start within SEQ ID NO 2562: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15414

- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2563: from 99 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2564
- Ceres seq\_id 1503828
- Location of start within SEQ ID NO 2562: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15415
- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2564: from 92 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2565
- Ceres seq\_id 1503829
- Location of start within SEQ ID NO 2562: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15416
- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2565: from 79 to 97

Maximum Length Sequence corresponding to clone ID 315810

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2566
- Ceres seq\_id 1503869

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2567
- Ceres seq\_id 1503870
- Location of start within SEQ ID NO 2566: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2568
- Ceres seq\_id 1503871
- Location of start within SEQ ID NO 2566: at 219 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15417
- gi No. 2072023
- % Identity 82.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
- Alignment No. 15418

- gi No. 2245008
- % Identity 91.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2568: from 14 to 81
  
- Alignment No. 15419
- gi No. 2583137
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2568: from 32 to 81
  
- Alignment No. 15420
- gi No. 2961343
- % Identity 87.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2568: from 17 to 81
  
- Alignment No. 15421
- gi No. 3024687
- % Identity 82.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
  
- Alignment No. 15422
- gi No. 3367536
- % Identity 78.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2568: from 1 to 81
  
- Alignment No. 15423
- gi No. 3810848
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
  
- Alignment No. 15424
- gi No. 4581162
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2568: from 1 to 81
  
- Alignment No. 15425
- gi No. 4773906
- % Identity 76.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2568: from 1 to 81
  
- Alignment No. 15426
- gi No. 4895235
- % Identity 82.1
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2568: from 4 to 81
  
- Alignment No. 15427
- gi No. 586441
- % Identity 72.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

Maximum Length Sequence corresponding to clone ID 315827  
(A) Polynucleotide Sequence



- Pat. Appln. SEQ ID NO 2569
- Ceres seq\_id 1503873
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2570
  - Ceres seq\_id 1503874
  - Location of start within SEQ ID NO 2569: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2571
  - Ceres seq\_id 1503875
  - Location of start within SEQ ID NO 2569: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2572
  - Ceres seq\_id 1503876
  - Location of start within SEQ ID NO 2569: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15428
  - gi No. 4539333
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 2572: from 52 to 65

Maximum Length Sequence corresponding to clone ID 315859

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2573
  - Ceres seq\_id 1503886
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2574
  - Ceres seq\_id 1503887
  - Location of start within SEQ ID NO 2573: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2575
  - Ceres seq\_id 1503888
  - Location of start within SEQ ID NO 2573: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2576
  - Ceres seq\_id 1503889
  - Location of start within SEQ ID NO 2573: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15429
- gi No. 3387886
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2576: from 1 to 12
  
- Alignment No. 15430
- gi No. 3402680
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2576: from 3 to 14

Maximum Length Sequence corresponding to clone ID 315865

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2577
- Ceres seq\_id 1503890

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2578
- Ceres seq\_id 1503891
- Location of start within SEQ ID NO 2577: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15431
- Peroxidase
- Location within SEQ ID NO 2578: from 48 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15432
- gi No. 1076635
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2578: from 68 to 82
  
- Alignment No. 15433
- gi No. 5002334
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2578: from 74 to 111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2579
- Ceres seq\_id 1503892
- Location of start within SEQ ID NO 2577: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2580
- Ceres seq\_id 1503893
- Location of start within SEQ ID NO 2577: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15434
- Peroxidase

- Location within SEQ ID NO 2580: from 41 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15435
- gi No. 1076635
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2580: from 61 to 75
  
- Alignment No. 15436
- gi No. 5002334
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2580: from 67 to 104

Maximum Length Sequence corresponding to clone ID 315868

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2581
- Ceres seq\_id 1503894

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2582
- Ceres seq\_id 1503895
- Location of start within SEQ ID NO 2581: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15437
- gi No. 1142653
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2582: from 79 to 157
  
- Alignment No. 15438
- gi No. 128844
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2582: from 53 to 76
  
- Alignment No. 15439
- gi No. 4539408
- % Identity 70.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 2582: from 36 to 159
  
- Alignment No. 15440
- gi No. 5031931
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2582: from 79 to 157
  
- Alignment No. 15441
- gi No. 92559
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2582: from 53 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2583
- Ceres seq\_id 1503896
- Location of start within SEQ ID NO 2581: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15442
- gi No. 1142653
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2583: from 57 to 135
  
- Alignment No. 15443
- gi No. 128844
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2583: from 31 to 54
  
- Alignment No. 15444
- gi No. 4539408
- % Identity 70.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 2583: from 14 to 137
  
- Alignment No. 15445
- gi No. 5031931
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2583: from 57 to 135
  
- Alignment No. 15446
- gi No. 92559
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2583: from 31 to 54

Maximum Length Sequence corresponding to clone ID 315884

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2584
- Ceres seq\_id 1503899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2585
- Ceres seq\_id 1503900
- Location of start within SEQ ID NO 2584: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15447
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2585: from 69 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2586
- Ceres seq\_id 1503901
- Location of start within SEQ ID NO 2584: at 18 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15448
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2586: from 64 to 101 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2587
- Ceres seq\_id 1503902
- Location of start within SEQ ID NO 2584: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15449
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2587: from 21 to 58 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316031

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2588
- Ceres seq\_id 1503924

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2589
- Ceres seq\_id 1503925
- Location of start within SEQ ID NO 2588: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15450
- gi No. 3004565
- % Identity 80
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2589: from 1 to 80

Maximum Length Sequence corresponding to clone ID 316062

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2590
- Ceres seq\_id 1503926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2591
- Ceres seq\_id 1503927
- Location of start within SEQ ID NO 2590: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15451
- Protein phosphatase 2C
- Location within SEQ ID NO 2591: from 24 to 163 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15452
- gi No. 3927836
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2591: from 3 to 13

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2592
- Ceres seq\_id 1503928
- Location of start within SEQ ID NO 2590: at 17 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15453
- Protein phosphatase 2C
- Location within SEQ ID NO 2592: from 19 to 158 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2593
- Ceres seq\_id 1503929
- Location of start within SEQ ID NO 2590: at 47 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15454
- Protein phosphatase 2C
- Location within SEQ ID NO 2593: from 9 to 148 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316101

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2594
- Ceres seq\_id 1503934

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2595
- Ceres seq\_id 1503935
- Location of start within SEQ ID NO 2594: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2596
- Ceres seq\_id 1503936
- Location of start within SEQ ID NO 2594: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15455
- gi No. 3822340
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2596: from 37 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2597
- Ceres seq\_id 1503937
- Location of start within SEQ ID NO 2594: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316143

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2598
- Ceres seq\_id 1503942

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2599
  - Ceres seq\_id 1503943
  - Location of start within SEQ ID NO 2598: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15456
  - gi No. 5441235
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2599: from 74 to 84

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2600
  - Ceres seq\_id 1503944
  - Location of start within SEQ ID NO 2598: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15457
- Sperm histone P2
- Location within SEQ ID NO 2600: from 38 to 118 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2601
  - Ceres seq\_id 1503945
  - Location of start within SEQ ID NO 2598: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 15458
  - gi No. 5441235
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2601: from 33 to 43

Maximum Length Sequence corresponding to clone ID 316146

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2602
  - Ceres seq\_id 1503946

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2603
  - Ceres seq\_id 1503947
  - Location of start within SEQ ID NO 2602: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15459
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2603: from 1 to 80 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15460
- gi No. 2833379
- % Identity 87.7
- Alignment Length 81

- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15461
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15462
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2603: from 1 to 80

- Alignment No. 15463
- gi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15464
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15465
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15466
- gi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2604
- Ceres seq\_id 1503948
- Location of start within SEQ ID NO 2602: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15467
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2604: from 1 to 54 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15468
- gi No. 2833379
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15469
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55



- Alignment No. 15470
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2604: from 1 to 54
  
- Alignment No. 15471
- gi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
  
- Alignment No. 15472
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
  
- Alignment No. 15473
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
  
- Alignment No. 15474
- gi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2605
- Ceres seq\_id 1503949
- Location of start within SEQ ID NO 2602: at 280 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15475
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2605: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15476
- gi No. 4902849
- % Identity 71.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2605: from 1 to 70

Maximum Length Sequence corresponding to clone ID 316227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2606
- Ceres seq\_id 1503969

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2607
- Ceres seq\_id 1503970
- Location of start within SEQ ID NO 2606: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15477
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
  
- Alignment No. 15478
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
  
- Alignment No. 15479
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2608
- Ceres seq\_id 1503971
- Location of start within SEQ ID NO 2606: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15480
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48
  
- Alignment No. 15481
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48
  
- Alignment No. 15482
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2609
- Ceres seq\_id 1503972
- Location of start within SEQ ID NO 2606: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316265

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2610
- Ceres seq\_id 1503989

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2611
- Ceres seq\_id 1503990
- Location of start within SEQ ID NO 2610: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15483
- EF hand
- Location within SEQ ID NO 2611: from 48 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15484
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15485
- gi No. 1076792
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15486
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15487
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15488
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15489
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
- Alignment No. 15490
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15491
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15492
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15493
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15494
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
  
- Alignment No. 15495
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15496
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15497
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
  
- Alignment No. 15498
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15499
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15500
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15501
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15502
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15503
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2611: from 75 to 104
  
- Alignment No. 15504
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15505
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15506
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15507
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15508
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15509
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15510
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15511
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
  
- Alignment No. 15512
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15513

- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15514
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15515
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
  
- Alignment No. 15516
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15517
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15518
- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15519
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15520
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 12 to 142
  
- Alignment No. 15521
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15522
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15523
- gi No. 1168749

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15524
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15525
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15526
- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15527
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2611: from 77 to 145
  
- Alignment No. 15528
- gi No. 1345451
- % Identity 94.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2611: from 2 to 59
  
- Alignment No. 15529
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15530
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15531
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15532
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15533
- gi No. 1421816
- % Identity 85.5

- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15534
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15535
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15536
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
  
- Alignment No. 15537
- gi No. 166655
- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2611: from 7 to 145
  
- Alignment No. 15538
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
  
- Alignment No. 15539
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15540
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 41 to 115
  
- Alignment No. 15541
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15542
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
  
- Alignment No. 15543
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121



- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15544
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15545
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15546
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 16 to 145
- Alignment No. 15547
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15548
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15549
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15550
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2611: from 77 to 127
- Alignment No. 15551
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15552
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15553
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145

- Alignment No. 15554
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15555
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 94 to 113
  
- Alignment No. 15556
- gi No. 2129557
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31
  
- Alignment No. 15557
- gi No. 2129558
- % Identity 93.5
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31
  
- Alignment No. 15558
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15559
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15560
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15561
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2611: from 8 to 143
  
- Alignment No. 15562
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15563
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15564
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15565
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
  
- Alignment No. 15566
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
  
- Alignment No. 15567
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
  
- Alignment No. 15568
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
  
- Alignment No. 15569
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15570
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 79 to 145
  
- Alignment No. 15571
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2611: from 81 to 145
  
- Alignment No. 15572
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2611: from 9 to 126
  
- Alignment No. 15573
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2611: from 1 to 104
  
- Alignment No. 15574

- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15575
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 61 to 145
  
- Alignment No. 15576
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2611: from 32 to 70
  
- Alignment No. 15577
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2611: from 77 to 133
  
- Alignment No. 15578
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 108 to 127
  
- Alignment No. 15579
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 2 to 76
  
- Alignment No. 15580
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15581
- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 38 to 123
  
- Alignment No. 15582
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2611: from 96 to 129
  
- Alignment No. 15583
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2611: from 20 to 129
  
- Alignment No. 15584
- gi No. 2809481

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15585
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2611: from 8 to 141
  
- Alignment No. 15586
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15587
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2611: from 8 to 129
  
- Alignment No. 15588
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 74 to 141
  
- Alignment No. 15589
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15590
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15591
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15592
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15593
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2611: from 77 to 111
  
- Alignment No. 15594
- gi No. 3336912
- % Identity 93.8

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15595
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2611: from 28 to 145
  
- Alignment No. 15596
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15597
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2611: from 32 to 60
  
- Alignment No. 15598
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 108 to 126
  
- Alignment No. 15599
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 128 to 145
  
- Alignment No. 15600
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15601
- gi No. 3561061
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15602
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15603
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15604
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15605
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15606
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15607
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15608
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15609
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15610
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15611
- gi No. 4098293
- % Identity 95.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2611: from 20 to 126
- Alignment No. 15612
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2611: from 20 to 126
- Alignment No. 15613
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2611: from 130 to 145
- Alignment No. 15614
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15615
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2611: from 82 to 145
  
- Alignment No. 15616
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2611: from 83 to 145
  
- Alignment No. 15617
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15618
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15619
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15620
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2611: from 21 to 67
  
- Alignment No. 15621
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15622
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15623
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15624
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145



- Alignment No. 15625
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
  
- Alignment No. 15626
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15627
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15628
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15629
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
  
- Alignment No. 15630
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 3 to 144
  
- Alignment No. 15631
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15632
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15633
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15634
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15635

- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15636
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15637
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15638
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15639
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15640
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15641
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15642
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15643
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15644
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15645
- gi No. 4959153

- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15646
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15647
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15648
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15649
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15650
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15651
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15652
- gi No. 4959161
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15653
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15654
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15655
- gi No. 4959164
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15656
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15657
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15658
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15659
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15660
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15661
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15662
- gi No. 4959171
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15663
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15664
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15665
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15666
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15667
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15668
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15669
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15670
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15671
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15672
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15673
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15674
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15675
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15676
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15677
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15678
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15679
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15680
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15681
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15682
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15683
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15684
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15685
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15686
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15687
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15688
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15689
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15690
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15691
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15692
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15693
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15694
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15695
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2611: from 49 to 70
  
- Alignment No. 15696

- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2611: from 49 to 70
  
- Alignment No. 15697
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2611: from 49 to 71
  
- Alignment No. 15698
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2611: from 49 to 71
  
- Alignment No. 15699
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 1 to 131
  
- Alignment No. 15700
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15701
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2611: from 75 to 100
  
- Alignment No. 15702
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2611: from 61 to 140
  
- Alignment No. 15703
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15704
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 6 to 145
  
- Alignment No. 15705
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2611: from 10 to 145
  
- Alignment No. 15706
- gi No. 625985



- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2611: from 1 to 46
  
- Alignment No. 15707
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15708
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
  
- Alignment No. 15709
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15710
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15711
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15712
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15713
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15714
- gi No. 729010
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15715
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15716
- gi No. 729012
- % Identity 87.3

- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
  
- Alignment No. 15717
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15718
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 2 to 142
  
- Alignment No. 15719
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15720
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2611: from 3 to 74

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2612
- Ceres seq\_id 1503991
- Location of start within SEQ ID NO 2610: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15721
- EF hand
- Location within SEQ ID NO 2612: from 12 to 40 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15722
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15723
- gi No. 1076792
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15724
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15725
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15726
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15727
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15728
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15729
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15730
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15731
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15732
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15733
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15734
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15735
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15736
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15737
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15738
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15739
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15740
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15741
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2612: from 39 to 68
  
- Alignment No. 15742
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15743
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15744
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15745
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15746
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15747
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15748
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15749
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15750
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15751
- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15752
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15753
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109
  
- Alignment No. 15754
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15755
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15756

- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15757
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15758
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 106
  
- Alignment No. 15759
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15760
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15761
- gi No. 1168749
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15762
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15763
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15764
- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15765
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2612: from 41 to 109
  
- Alignment No. 15766
- gi No. 1345451

- % Identity 94.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2612: from 1 to 23
  
- Alignment No. 15767
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15768
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15769
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15770
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15771
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15772
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15773
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15774
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15775
- gi No. 166655
- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15776
- gi No. 167676
- % Identity 87.4

- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15777
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15778
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 5 to 79
  
- Alignment No. 15779
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15780
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15781
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15782
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15783
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
  
- Alignment No. 15784
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15785
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
  
- Alignment No. 15786
- gi No. 20186
- % Identity 99.3
- Alignment Length 146



- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15787
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15788
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2612: from 41 to 91
- Alignment No. 15789
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15790
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15791
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15792
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15793
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 58 to 77
- Alignment No. 15794
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15795
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15796
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15797
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2612: from 1 to 107
  
- Alignment No. 15798
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15799
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15800
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15801
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15802
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15803
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15804
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15805
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15806
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 43 to 109

- Alignment No. 15807
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2612: from 45 to 109
  
- Alignment No. 15808
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2612: from 1 to 90
  
- Alignment No. 15809
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2612: from 1 to 68
  
- Alignment No. 15810
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15811
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 25 to 109
  
- Alignment No. 15812
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2612: from 1 to 34
  
- Alignment No. 15813
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2612: from 41 to 97
  
- Alignment No. 15814
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 72 to 91
  
- Alignment No. 15815
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 1 to 40
  
- Alignment No. 15816
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15817

- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 2 to 87
  
- Alignment No. 15818
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2612: from 60 to 93
  
- Alignment No. 15819
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2612: from 1 to 93
  
- Alignment No. 15820
- gi No. 2809481
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15821
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2612: from 1 to 105
  
- Alignment No. 15822
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15823
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2612: from 1 to 93
  
- Alignment No. 15824
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 38 to 105
  
- Alignment No. 15825
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15826
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15827
- gi No. 3121849

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15828
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15829
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2612: from 41 to 75
  
- Alignment No. 15830
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15831
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15832
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15833
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2612: from 1 to 24
  
- Alignment No. 15834
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 72 to 90
  
- Alignment No. 15835
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 92 to 109
  
- Alignment No. 15836
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15837
- gi No. 3561061
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15838
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15839
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15840
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15841
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15842
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15843
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15844
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15845
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15846
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15847
- gi No. 4098293
- % Identity 95.3
- Alignment Length 107

- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15848
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15849
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2612: from 94 to 109
- Alignment No. 15850
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15851
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2612: from 46 to 109
- Alignment No. 15852
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2612: from 47 to 109
- Alignment No. 15853
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15854
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15855
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15856
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2612: from 1 to 31
- Alignment No. 15857
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15858
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15859
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15860
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15861
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109
  
- Alignment No. 15862
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15863
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15864
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15865
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109
  
- Alignment No. 15866
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 108
  
- Alignment No. 15867
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109



- Alignment No. 15868
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15869
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15870
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15871
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15872
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15873
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15874
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15875
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15876
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15877
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15878

- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15879
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15880
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15881
- gi No. 4959153
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15882
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15883
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15884
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15885
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15886
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15887
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15888
- gi No. 4959161

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15889
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15890
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15891
- gi No. 4959164
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15892
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15893
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15894
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15895
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15896
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15897
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15898
- gi No. 4959171
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15899
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15900
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15901
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15902
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15903
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15904
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15905
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15906
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15907
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15908
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15909
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15910
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15911
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15912
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15913
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15914
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15915
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15916
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15917
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15918
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15919
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15920
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15921
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15922
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15923
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15924
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15925
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15926
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15927
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15928
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15929
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15930
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15931
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2612: from 13 to 34
  
- Alignment No. 15932
- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2612: from 13 to 34
  
- Alignment No. 15933
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2612: from 13 to 35
  
- Alignment No. 15934
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2612: from 13 to 35
  
- Alignment No. 15935
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 95
  
- Alignment No. 15936
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15937
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2612: from 39 to 64
  
- Alignment No. 15938
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2612: from 25 to 104
  
- Alignment No. 15939

- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15940
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15941
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15942
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15943
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15944
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15945
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15946
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15947
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15948
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15949
- gi No. 729010



- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15950
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15951
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15952
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15953
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 106
  
- Alignment No. 15954
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15955
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2612: from 1 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2613
- Ceres seq\_id 1503992
- Location of start within SEQ ID NO 2610: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15956
- EF hand
- Location within SEQ ID NO 2613: from 1 to 25 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15957
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15958
- gi No. 1076792
- % Identity 97.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15959
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15960
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15961
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15962
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15963
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15964
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15965
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15966
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15967
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15968
- gi No. 115503
- % Identity 89.7
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15969
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15970
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15971
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15972
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15973
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15974
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15975
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15976
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2613: from 24 to 53
- Alignment No. 15977
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15978
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15979
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15980
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15981
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15982
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15983
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15984
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15985
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15986
- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15987
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15988
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94

- Alignment No. 15989
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15990
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15991
- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15992
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15993
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 91
  
- Alignment No. 15994
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15995
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15996
- gi No. 1168749
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15997
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15998
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15999

- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16000
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2613: from 26 to 94
  
- Alignment No. 16001
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16002
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16003
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16004
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16005
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16006
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16007
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16008
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16009
- gi No. 166655

- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16010
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16011
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16012
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 64
  
- Alignment No. 16013
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16014
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16015
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16016
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16017
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68
  
- Alignment No. 16018
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16019
- gi No. 1785958
- % Identity 87.3

- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68
  
- Alignment No. 16020
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16021
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16022
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2613: from 26 to 76
  
- Alignment No. 16023
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16024
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16025
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16026
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16027
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2613: from 43 to 62
  
- Alignment No. 16028
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16029
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146



- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16030
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16031
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2613: from 1 to 92
- Alignment No. 16032
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16033
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16034
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16035
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16036
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16037
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16038
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16039
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16040
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2613: from 28 to 94
  
- Alignment No. 16041
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2613: from 30 to 94
  
- Alignment No. 16042
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2613: from 1 to 75
  
- Alignment No. 16043
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2613: from 1 to 53
  
- Alignment No. 16044
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16045
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2613: from 10 to 94
  
- Alignment No. 16046
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
  
- Alignment No. 16047
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2613: from 26 to 82
  
- Alignment No. 16048
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2613: from 57 to 76
  
- Alignment No. 16049
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 25

- Alignment No. 16050
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16051
- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2613: from 1 to 72
  
- Alignment No. 16052
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2613: from 45 to 78
  
- Alignment No. 16053
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2613: from 1 to 78
  
- Alignment No. 16054
- gi No. 2809481
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16055
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2613: from 1 to 90
  
- Alignment No. 16056
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16057
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2613: from 1 to 78
  
- Alignment No. 16058
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2613: from 23 to 90
  
- Alignment No. 16059
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16060

- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16061
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16062
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16063
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2613: from 26 to 60
  
- Alignment No. 16064
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16065
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16066
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16067
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 57 to 75
  
- Alignment No. 16068
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 77 to 94
  
- Alignment No. 16069
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16070
- gi No. 3561061

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16071
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16072
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16073
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16074
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16075
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16076
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16077
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16078
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16079
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16080
- gi No. 4098293
- % Identity 95.3

- Alignment Length 107
- Location of Alignment in SEQ ID NO 2613: from 1 to 75
  
- Alignment No. 16081
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2613: from 1 to 75
  
- Alignment No. 16082
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2613: from 79 to 94
  
- Alignment No. 16083
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16084
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2613: from 31 to 94
  
- Alignment No. 16085
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2613: from 32 to 94
  
- Alignment No. 16086
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16087
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16088
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16089
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2613: from 1 to 16
  
- Alignment No. 16090
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16091
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16092
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16093
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16094
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16095
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16096
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16097
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16098
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16099
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 93
- Alignment No. 16100
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16101
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16102
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16103
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16104
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16105
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16106
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16107
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16108
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16109
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16110
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94



- Alignment No. 16111
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16112
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16113
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16114
- gi No. 4959153
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16115
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16116
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16117
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16118
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16119
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16120
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16121

- gi No. 4959161
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16122
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16123
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16124
- gi No. 4959164
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16125
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16126
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16127
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16128
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16129
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16130
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16131
- gi No. 4959171

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16132
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16133
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16134
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16135
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16136
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16137
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16138
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16139
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16140
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16141
- gi No. 4959604
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16142
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16143
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16144
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16145
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16146
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16147
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16148
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16149
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16150
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16151
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16152
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16153
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16154
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16155
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16156
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16157
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16158
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16159
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16160
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16161
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16162
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16163
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16164
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
  
- Alignment No. 16165
- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
  
- Alignment No. 16166
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2613: from 1 to 20
  
- Alignment No. 16167
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2613: from 1 to 20
  
- Alignment No. 16168
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 80
  
- Alignment No. 16169
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16170
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2613: from 24 to 49
  
- Alignment No. 16171
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2613: from 10 to 89

- Alignment No. 16172
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16173
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16174
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16175
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16176
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16177
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16178
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16179
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16180
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16181
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16182

- gi No. 729010
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16183
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16184
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16185
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16186
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 91
  
- Alignment No. 16187
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16188
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2613: from 1 to 23

Maximum Length Sequence corresponding to clone ID 316301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2614
- Ceres seq\_id 1504001

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2615
- Ceres seq\_id 1504002
- Location of start within SEQ ID NO 2614: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2616
- Ceres seq\_id 1504003
- Location of start within SEQ ID NO 2614: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)



- Alignment No. 16189
- Ribosomal protein L5
- Location within SEQ ID NO 2616: from 34 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16190
- gi No. 1125808
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16191
- gi No. 1172816
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16192
- gi No. 1172817
- % Identity 90.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2616: from 27 to 79
- Alignment No. 16193
- gi No. 1172952
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2616: from 35 to 79
- Alignment No. 16194
- gi No. 1172954
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76
- Alignment No. 16195
- gi No. 1172969
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16196
- gi No. 1173055
- % Identity 94.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16197
- gi No. 132649
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16198
- gi No. 132951
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
- Alignment No. 16199
- gi No. 132992

- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2616: from 36 to 79
  
- Alignment No. 16200
- gi No. 1350658
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
  
- Alignment No. 16201
- gi No. 1350659
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76
  
- Alignment No. 16202
- gi No. 1710494
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2616: from 30 to 79
  
- Alignment No. 16203
- gi No. 2500240
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
  
- Alignment No. 16204
- gi No. 2500241
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
  
- Alignment No. 16205
- gi No. 2570507
- % Identity 85.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
  
- Alignment No. 16206
- gi No. 4322
- % Identity 77.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
  
- Alignment No. 16207
- gi No. 4432750
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2616: from 41 to 76
  
- Alignment No. 16208
- gi No. 4512679
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 36 to 79
  
- Alignment No. 16209
- gi No. 4586222
- % Identity 76.5

- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16210
- gi No. 71107
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2617
- Ceres seq\_id 1504004
- Location of start within SEQ ID NO 2614: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316327

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2618
- Ceres seq\_id 1504016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2619
- Ceres seq\_id 1504017
- Location of start within SEQ ID NO 2618: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2620
- Ceres seq\_id 1504018
- Location of start within SEQ ID NO 2618: at 310 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16211
- gi No. 2224915
- % Identity 81.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2620: from 1 to 55
- Alignment No. 16212
- gi No. 729944
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2620: from 1 to 55

Maximum Length Sequence corresponding to clone ID 316354

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2621
- Ceres seq\_id 1504025

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2622
- Ceres seq\_id 1504026
- Location of start within SEQ ID NO 2621: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 16213
- Sugar (and other) transporter
- Location within SEQ ID NO 2622: from 1 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16214
- gi No. 2760325
- % Identity 73.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2622: from 1 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2623
- Ceres seq\_id 1504027
- Location of start within SEQ ID NO 2621: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 16215
- Sugar (and other) transporter
- Location within SEQ ID NO 2623: from 1 to 87 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16216
- gi No. 2760325
- % Identity 73.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2623: from 1 to 87

Maximum Length Sequence corresponding to clone ID 316377

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2624
- Ceres seq\_id 1504036

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2625
- Ceres seq\_id 1504037
- Location of start within SEQ ID NO 2624: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16217
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2625: from 1 to 152

- Alignment No. 16218
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2625: from 1 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2626
- Ceres seq\_id 1504038
- Location of start within SEQ ID NO 2624: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16219
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2626: from 1 to 128
  
- Alignment No. 16220
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2626: from 1 to 114

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2627
- Ceres seq\_id 1504039
- Location of start within SEQ ID NO 2624: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16221
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2627: from 1 to 126
  
- Alignment No. 16222
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2627: from 1 to 112

Maximum Length Sequence corresponding to clone ID 316388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2628
- Ceres seq\_id 1504044

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2629
- Ceres seq\_id 1504045
- Location of start within SEQ ID NO 2628: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16223
- gi No. 3057044
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16224
- gi No. 3337356
- % Identity 93.9
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16225
- gi No. 3834321

- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16226
- gi No. 3881191
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2629: from 65 to 142
  
- Alignment No. 16227
- gi No. 4689112
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16228
- gi No. 585957
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16229
- gi No. 585959
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

Maximum Length Sequence corresponding to clone ID 316451

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2630
- Ceres seq\_id 1504050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2631
- Ceres seq\_id 1504051
- Location of start within SEQ ID NO 2630: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16230
- WD domain, G-beta repeat
- Location within SEQ ID NO 2631: from 85 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16231
- gi No. 3122386
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 2631: from 1 to 166
  
- Alignment No. 16232
- gi No. 3122387
- % Identity 86.8
- Alignment Length 167
- Location of Alignment in SEQ ID NO 2631: from 1 to 166

Maximum Length Sequence corresponding to clone ID 316638

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2632
- Ceres seq\_id 1504098

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2633
- Ceres seq\_id 1504099
- Location of start within SEQ ID NO 2632: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16233
- ADP-ribosylation factor family
- Location within SEQ ID NO 2633: from 2 to 75 aa.
- Alignment No. 16234
- Ras family
- Location within SEQ ID NO 2633: from 19 to 80 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16235
- gi No. 114122
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2633: from 1 to 75
- Alignment No. 16236
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2633: from 18 to 75
- Alignment No. 16237
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2633: from 19 to 75
- Alignment No. 16238
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2633: from 19 to 75
- Alignment No. 16239
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2633: from 1 to 75
- Alignment No. 16240
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2633: from 22 to 42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2634
- Ceres seq\_id 1504100
- Location of start within SEQ ID NO 2632: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16241
- ADP-ribosylation factor family
- Location within SEQ ID NO 2634: from 1 to 58 aa.

- Alignment No. 16242
- Ras family
- Location within SEQ ID NO 2634: from 2 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16243
- gi No. 114122
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2634: from 1 to 58
- Alignment No. 16244
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2634: from 1 to 58
- Alignment No. 16245
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2634: from 2 to 58
- Alignment No. 16246
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2634: from 2 to 58
- Alignment No. 16247
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2634: from 1 to 58
- Alignment No. 16248
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2634: from 5 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2635
- Ceres seq\_id 1504101
- Location of start within SEQ ID NO 2632: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16249
- ADP-ribosylation factor family
- Location within SEQ ID NO 2635: from 1 to 54 aa.
- Alignment No. 16250
- Ras family
- Location within SEQ ID NO 2635: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16251
- gi No. 114122
- % Identity 70.7



- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
  
- Alignment No. 16252
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
  
- Alignment No. 16253
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
  
- Alignment No. 16254
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
  
- Alignment No. 16255
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
  
- Alignment No. 16256
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2635: from 1 to 21

Maximum Length Sequence corresponding to clone ID 316643

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2636
- Ceres seq\_id 1504102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2637
- Ceres seq\_id 1504103
- Location of start within SEQ ID NO 2636: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16257
- gi No. 462338
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2637: from 95 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2638
- Ceres seq\_id 1504104
- Location of start within SEQ ID NO 2636: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2639
- Ceres seq\_id 1504105
- Location of start within SEQ ID NO 2636: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16258
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 2639: from 20 to 98 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316664

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2640
- Ceres seq\_id 1504107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2641
- Ceres seq\_id 1504108
- Location of start within SEQ ID NO 2640: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16259
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2641: from 65 to 155 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16260
- gi No. 1172977
- % Identity 78.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2641: from 55 to 155
  
- Alignment No. 16261
- gi No. 2529670
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2641: from 56 to 155
  
- Alignment No. 16262
- gi No. 3021348
- % Identity 75.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2641: from 58 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2642
- Ceres seq\_id 1504109
- Location of start within SEQ ID NO 2640: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2643
- Ceres seq\_id 1504110
- Location of start within SEQ ID NO 2640: at 164 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16263
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2643: from 11 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16264
- gi No. 1172977
- % Identity 78.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2643: from 1 to 101
- Alignment No. 16265
- gi No. 2529670
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2643: from 2 to 101
- Alignment No. 16266
- gi No. 3021348
- % Identity 75.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2643: from 4 to 101

Maximum Length Sequence corresponding to clone ID 316675

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2644
- Ceres seq\_id 1504111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2645
- Ceres seq\_id 1504112
- Location of start within SEQ ID NO 2644: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16267
- gi No. 121928
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2645: from 30 to 40
- Alignment No. 16268
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2645: from 17 to 42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2646
- Ceres seq\_id 1504113
- Location of start within SEQ ID NO 2644: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16269
- gi No. 121928
- % Identity 75
- Alignment Length 12

- Location of Alignment in SEQ ID NO 2646: from 14 to 24
- Alignment No. 16270
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2646: from 1 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2647
- Ceres seq\_id 1504114
- Location of start within SEQ ID NO 2644: at 212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16271
- linker histone H1 and H5 family
- Location within SEQ ID NO 2647: from 1 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16272
- gi No. 121906
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2647: from 1 to 22
- Alignment No. 16273
- gi No. 121950
- % Identity 87.6
- Alignment Length 97
- Location of Alignment in SEQ ID NO 2647: from 1 to 73
- Alignment No. 16274
- gi No. 121958
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16275
- gi No. 5230781
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16276
- gi No. 5230783
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16277
- gi No. 5230785
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16278
- gi No. 5230788
- % Identity 71.6
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

- Alignment No. 16279
- gi No. 5230790
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

Maximum Length Sequence corresponding to clone ID 316686

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2648
- Ceres seq\_id 1504119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2649
- Ceres seq\_id 1504120
- Location of start within SEQ ID NO 2648: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16280
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2649: from 74 to 84

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2650
- Ceres seq\_id 1504121
- Location of start within SEQ ID NO 2648: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16281
- gi No. 137715
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2650: from 24 to 37

- Alignment No. 16282
- gi No. 1389772
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

- Alignment No. 16283
- gi No. 1914851
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 57 to 70

- Alignment No. 16284
- gi No. 2388805
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

- Alignment No. 16285
- gi No. 3183204
- % Identity 76.9
- Alignment Length 13

- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16286
- gi No. 322755
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38
- Alignment No. 16287
- gi No. 333063
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2650: from 24 to 37
- Alignment No. 16288
- gi No. 465445
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16289
- gi No. 539029
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38
- Alignment No. 16290
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2650: from 58 to 69
- Alignment No. 16291
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16292
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2650: from 59 to 69
- Alignment No. 16293
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16294
- gi No. 93144
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2651
- Ceres seq\_id 1504122
- Location of start within SEQ ID NO 2648: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16295
- gi No. 1389772
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16296
- gi No. 1914851
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2651: from 28 to 41
  
- Alignment No. 16297
- gi No. 2388805
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16298
- gi No. 3183204
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16299
- gi No. 465445
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16300
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2651: from 29 to 40
  
- Alignment No. 16301
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16302
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2651: from 30 to 40
  
- Alignment No. 16303
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16304
- gi No. 93144
- % Identity 76.9
- Alignment Length 13

- Location of Alignment in SEQ ID NO 2651: from 28 to 40

Maximum Length Sequence corresponding to clone ID 316862

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2652
- Ceres seq\_id 1504161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2653
- Ceres seq\_id 1504162
- Location of start within SEQ ID NO 2652: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16305
- gi No. 1916974
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2653: from 7 to 21
- Alignment No. 16306
- gi No. 477833
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2653: from 7 to 21

Maximum Length Sequence corresponding to clone ID 316893

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2654
- Ceres seq\_id 1504170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2655
- Ceres seq\_id 1504171
- Location of start within SEQ ID NO 2654: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16307
- gi No. 404077
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2655: from 30 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2656
- Ceres seq\_id 1504172
- Location of start within SEQ ID NO 2654: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16308
- gi No. 4972116
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2656: from 26 to 36

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2657
- Ceres seq\_id 1504173



- Location of start within SEQ ID NO 2654: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16309
- gi No. 4996642
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2657: from 17 to 27

Maximum Length Sequence corresponding to clone ID 316929

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2658
- Ceres seq\_id 1504178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2659
- Ceres seq\_id 1504179
- Location of start within SEQ ID NO 2658: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16310
- GDP dissociation inhibitor
- Location within SEQ ID NO 2659: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16311
- gi No. 1550740
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16312
- gi No. 1655424
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16313
- gi No. 2384758
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16314
- gi No. 2384760
- % Identity 85.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16315
- gi No. 2446981
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16316
- gi No. 2501850
- % Identity 90.2
- Alignment Length 61

- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16317
- gi No. 3175990
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

Maximum Length Sequence corresponding to clone ID 316935

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2660
- Ceres seq\_id 1504180

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2661
- Ceres seq\_id 1504181
- Location of start within SEQ ID NO 2660: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2662
- Ceres seq\_id 1504182
- Location of start within SEQ ID NO 2660: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16318
- Globin
- Location within SEQ ID NO 2662: from 44 to 168 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2663
- Ceres seq\_id 1504183
- Location of start within SEQ ID NO 2660: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16319
- Globin
- Location within SEQ ID NO 2663: from 11 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316946

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2664
- Ceres seq\_id 1504184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2665
- Ceres seq\_id 1504185
- Location of start within SEQ ID NO 2664: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16320
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2665: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16321
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2665: from 3 to 139
  
- Alignment No. 16322
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2665: from 1 to 154
  
- Alignment No. 16323
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2665: from 1 to 145
  
- Alignment No. 16324
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2665: from 1 to 145
  
- Alignment No. 16325
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2665: from 3 to 139

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2666
- Ceres seq\_id 1504186
- Location of start within SEQ ID NO 2664: at 6 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16326
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2666: from 1 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16327
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138
  
- Alignment No. 16328
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2666: from 1 to 153
  
- Alignment No. 16329
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144

- Alignment No. 16330
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144
  
- Alignment No. 16331
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2667
- Ceres seq\_id 1504187
- Location of start within SEQ ID NO 2664: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16332
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2667: from 1 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16333
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2667: from 1 to 89
  
- Alignment No. 16334
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2667: from 1 to 104
  
- Alignment No. 16335
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2667: from 1 to 95
  
- Alignment No. 16336
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2667: from 1 to 95
  
- Alignment No. 16337
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2667: from 1 to 89

Maximum Length Sequence corresponding to clone ID 316976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2668
- Ceres seq\_id 1504192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2669

- Ceres seq\_id 1504193
- Location of start within SEQ ID NO 2668: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16338
- gi No. 5042432
- % Identity 70.6
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2669: from 93 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2670
- Ceres seq\_id 1504194
- Location of start within SEQ ID NO 2668: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16339
- gi No. 5042432
- % Identity 70.6
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2670: from 65 to 131

Maximum Length Sequence corresponding to clone ID 317012

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2671
- Ceres seq\_id 1504201

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2672
- Ceres seq\_id 1504202
- Location of start within SEQ ID NO 2671: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2673
- Ceres seq\_id 1504203
- Location of start within SEQ ID NO 2671: at 369 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16340
- gi No. 2642447
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46

- Alignment No. 16341

- gi No. 4335730

- % Identity 76.9

- Alignment Length 26

- Location of Alignment in SEQ ID NO 2673: from 22 to 46

- Alignment No. 16342

- gi No. 4544385

- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2674
- Ceres seq\_id 1504204
- Location of start within SEQ ID NO 2671: at 378 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16343
- gi No. 2642447
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2674: from 20 to 43
  
- Alignment No. 16344
- gi No. 4335730
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2674: from 19 to 43
  
- Alignment No. 16345
- gi No. 4544385
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2674: from 20 to 43

Maximum Length Sequence corresponding to clone ID 317151

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2675
- Ceres seq\_id 1504231

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2676
- Ceres seq\_id 1504232
- Location of start within SEQ ID NO 2675: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16346
- gi No. 1076389
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16347
- gi No. 1076390
- % Identity 95.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16348
- gi No. 1076396
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16349

- gi No. 1262171
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16350
- gi No. 1568511
- % Identity 94.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16351
- gi No. 2129734
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16352
- gi No. 2146743
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16353
- gi No. 261767
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2676: from 125 to 144
  
- Alignment No. 16354
- gi No. 3928142
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16355
- gi No. 476923
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2676: from 125 to 144
  
- Alignment No. 16356
- gi No. 543715
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16357
- gi No. 5679684
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16358
- gi No. 683506
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2677

- Ceres seq\_id 1504233
- Location of start within SEQ ID NO 2675: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16359
- gi No. 1076389
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16360
- gi No. 1076390
- % Identity 95.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16361
- gi No. 1076396
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16362
- gi No. 1262171
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16363
- gi No. 1568511
- % Identity 94.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16364
- gi No. 2129734
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16365
- gi No. 2146743
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16366
- gi No. 261767
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2677: from 111 to 130
  
- Alignment No. 16367
- gi No. 3928142
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16368



- gi No. 476923
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2677: from 111 to 130
  
- Alignment No. 16369
- gi No. 543715
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16370
- gi No. 5679684
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16371
- gi No. 683506
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130

Maximum Length Sequence corresponding to clone ID 317164

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2678
- Ceres seq\_id 1504239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2679
- Ceres seq\_id 1504240
- Location of start within SEQ ID NO 2678: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16372
- PCI domain
- Location within SEQ ID NO 2679: from 7 to 86 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317195

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2680
- Ceres seq\_id 1504254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2681
- Ceres seq\_id 1504255
- Location of start within SEQ ID NO 2680: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16373
- gi No. 1076294
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2681: from 92 to 107
  
- Alignment No. 16374
- gi No. 1279640
- % Identity 71.1

- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
  
- Alignment No. 16375
- gi No. 1321924
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
  
- Alignment No. 16376
- gi No. 1944132
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
  
- Alignment No. 16377
- gi No. 4972066
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2681: from 89 to 107
  
- Alignment No. 16378
- gi No. 5679845
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2681: from 89 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2682
- Ceres seq\_id 1504256
- Location of start within SEQ ID NO 2680: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16379
- gi No. 1279640
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
  
- Alignment No. 16380
- gi No. 1321924
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
  
- Alignment No. 16381
- gi No. 1944132
- % Identity 90.9
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
  
- Alignment No. 16382
- gi No. 2894607
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
  
- Alignment No. 16383
- gi No. 4585977

- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2682: from 9 to 32
  
- Alignment No. 16384
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
  
- Alignment No. 16385
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
  
- Alignment No. 16386
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
  
- Alignment No. 16387
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2683
- Ceres seq\_id 1504257
- Location of start within SEQ ID NO 2680: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16388
- gi No. 1279640
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
  
- Alignment No. 16389
- gi No. 1321924
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
  
- Alignment No. 16390
- gi No. 1944132
- % Identity 90.9
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
  
- Alignment No. 16391
- gi No. 2894607
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
  
- Alignment No. 16392

- gi No. 4585977
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2683: from 1 to 24
  
- Alignment No. 16393
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
  
- Alignment No. 16394
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
  
- Alignment No. 16395
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
  
- Alignment No. 16396
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

Maximum Length Sequence corresponding to clone ID 317200

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2684
- Ceres seq\_id 1504258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2685
- Ceres seq\_id 1504259
- Location of start within SEQ ID NO 2684: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2686
- Ceres seq\_id 1504260
- Location of start within SEQ ID NO 2684: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2687
- Ceres seq\_id 1504261
- Location of start within SEQ ID NO 2684: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16397
- gi No. 2642154

- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2687: from 1 to 35

Maximum Length Sequence corresponding to clone ID 317211

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2688
- Ceres seq\_id 1504270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2689
- Ceres seq\_id 1504271
- Location of start within SEQ ID NO 2688: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2690
- Ceres seq\_id 1504272
- Location of start within SEQ ID NO 2688: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16398
- gi No. 1546779
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32
- Alignment No. 16399
- gi No. 2136108
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32
- Alignment No. 16400
- gi No. 3858885
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2691
- Ceres seq\_id 1504273
- Location of start within SEQ ID NO 2688: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317217

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2692
- Ceres seq\_id 1504274

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2693
- Ceres seq\_id 1504275
- Location of start within SEQ ID NO 2692: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16401
- Metallothionein
- Location within SEQ ID NO 2693: from 37 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16402
- gi No. 1944205
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2693: from 37 to 73
- Alignment No. 16403
- gi No. 225131
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2693: from 40 to 59
- Alignment No. 16404
- gi No. 225144
- % Identity 71.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2693: from 39 to 59
- Alignment No. 16405
- gi No. 225146
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2693: from 40 to 59
- Alignment No. 16406
- gi No. 2407285
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2693: from 37 to 73
- Alignment No. 16407
- gi No. 2497897
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84
- Alignment No. 16408
- gi No. 2497903
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2693: from 37 to 88
- Alignment No. 16409
- gi No. 2662415
- % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2693: from 38 to 88
- Alignment No. 16410
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2693: from 37 to 83

- Alignment No. 16411
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2694
- Ceres seq\_id 1504276
- Location of start within SEQ ID NO 2692: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16412
- Metallothionein
- Location within SEQ ID NO 2694: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16413
- gi No. 1944205
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2694: from 1 to 37
  
- Alignment No. 16414
- gi No. 225131
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2694: from 4 to 23
  
- Alignment No. 16415
- gi No. 225144
- % Identity 71.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2694: from 3 to 23
  
- Alignment No. 16416
- gi No. 225146
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2694: from 4 to 23
  
- Alignment No. 16417
- gi No. 2407285
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2694: from 1 to 37
  
- Alignment No. 16418
- gi No. 2497897
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48
  
- Alignment No. 16419
- gi No. 2497903
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 1 to 52
  
- Alignment No. 16420

- gi No. 2662415
- % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 2 to 52
  
- Alignment No. 16421
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2694: from 1 to 47
  
- Alignment No. 16422
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48

Maximum Length Sequence corresponding to clone ID 317283

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2695
- Ceres seq\_id 1504277

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2696
- Ceres seq\_id 1504278
- Location of start within SEQ ID NO 2695: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16423
- gi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2696: from 70 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2697
- Ceres seq\_id 1504279
- Location of start within SEQ ID NO 2695: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16424
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2697: from 7 to 57 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16425
- gi No. 1042189
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16426
- gi No. 1042189
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16427
- gi No. 131036



- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16428
- gi No. 131036
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16429
- gi No. 1703594
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 3 to 13
  
- Alignment No. 16430
- gi No. 2134213
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 27 to 37
  
- Alignment No. 16431
- gi No. 2134213
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16432
- gi No. 2134213
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2697: from 25 to 38
  
- Alignment No. 16433
- gi No. 2498095
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16434
- gi No. 462338
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16435
- gi No. 462338
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2698
- Ceres seq\_id 1504280
- Location of start within SEQ ID NO 2695: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16436

- gi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2698: from 31 to 41

Maximum Length Sequence corresponding to clone ID 317408

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2699
- Ceres seq\_id 1504299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2700
- Ceres seq\_id 1504300
- Location of start within SEQ ID NO 2699: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16437
- Chitin recognition protein
- Location within SEQ ID NO 2700: from 42 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16438
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2700: from 26 to 76

- Alignment No. 16439
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2700: from 26 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2701
- Ceres seq\_id 1504301
- Location of start within SEQ ID NO 2699: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16440
- Chitin recognition protein
- Location within SEQ ID NO 2701: from 31 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16441
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2701: from 15 to 65

- Alignment No. 16442
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2701: from 15 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2702
- Ceres seq\_id 1504302
- Location of start within SEQ ID NO 2699: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16443
- Chitin recognition protein
- Location within SEQ ID NO 2702: from 29 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16444
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2702: from 13 to 63
- Alignment No. 16445
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2702: from 13 to 63

Maximum Length Sequence corresponding to clone ID 317416

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2703
- Ceres seq\_id 1504303

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2704
- Ceres seq\_id 1504304
- Location of start within SEQ ID NO 2703: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16446
- PCI domain
- Location within SEQ ID NO 2704: from 99 to 149 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2705
- Ceres seq\_id 1504305
- Location of start within SEQ ID NO 2703: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16447
- PCI domain
- Location within SEQ ID NO 2705: from 64 to 114 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2706
- Ceres seq\_id 1504306
- Location of start within SEQ ID NO 2703: at 196 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16448
- PCI domain
- Location within SEQ ID NO 2706: from 34 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317417

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2707
- Ceres seq\_id 1504307

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2708
- Ceres seq\_id 1504308
- Location of start within SEQ ID NO 2707: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2709
- Ceres seq\_id 1504309
- Location of start within SEQ ID NO 2707: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16449
- gi No. 133902
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16450
- gi No. 1350971
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16451
- gi No. 1350972
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16452
- gi No. 2078466
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16453
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16454
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16455
- gi No. 3098456

- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2709: from 11 to 54
  
- Alignment No. 16456
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
  
- Alignment No. 16457
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
  
- Alignment No. 16458
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2709: from 7 to 54
  
- Alignment No. 16459
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
  
- Alignment No. 16460
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2710
- Ceres seq\_id 1504310
- Location of start within SEQ ID NO 2707: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16461
- gi No. 133902
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16462
- gi No. 1350971
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16463
- gi No. 1350972
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16464

- gi No. 2078466
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16465
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16466
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16467
- gi No. 3098456
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16468
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16469
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16470
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16471
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16472
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

Maximum Length Sequence corresponding to clone ID 317418

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2711
- Ceres seq\_id 1504311

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2712
- Ceres seq\_id 1504312
- Location of start within SEQ ID NO 2711: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2713
- Ceres seq\_id 1504313
- Location of start within SEQ ID NO 2711: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16473
- gi No. 100789
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16474
- gi No. 100883
- % Identity 93.2
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16475
- gi No. 1122313
- % Identity 79.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16476
- gi No. 1122315
- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16477
- gi No. 123541
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22
- Alignment No. 16478
- gi No. 123545
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16479
- gi No. 123546
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22
- Alignment No. 16480
- gi No. 1536911
- % Identity 75
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43

- Alignment No. 16481
- gi No. 232272
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21
  
- Alignment No. 16482
- gi No. 445136
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
  
- Alignment No. 16483
- gi No. 507209
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21
  
- Alignment No. 16484
- gi No. 81638
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22

Maximum Length Sequence corresponding to clone ID 317460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2714
- Ceres seq\_id 1504333

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2715
- Ceres seq\_id 1504334
- Location of start within SEQ ID NO 2714: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16485
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2715: from 1 to 99
  
- Alignment No. 16486
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2715: from 1 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2716
- Ceres seq\_id 1504335
- Location of start within SEQ ID NO 2714: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16487
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2716: from 1 to 93



- Alignment No. 16488
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2716: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2717
- Ceres seq\_id 1504336
- Location of start within SEQ ID NO 2714: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16489
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2717: from 1 to 64
- Alignment No. 16490
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2717: from 1 to 48

Maximum Length Sequence corresponding to clone ID 317528

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2718
- Ceres seq\_id 1504370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2719
- Ceres seq\_id 1504371
- Location of start within SEQ ID NO 2718: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2720
- Ceres seq\_id 1504372
- Location of start within SEQ ID NO 2718: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16491
- gi No. 2997589
- % Identity 87.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2720: from 1 to 116
- Alignment No. 16492
- gi No. 2997591
- % Identity 84.6
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- Alignment No. 16493

- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
  
- Alignment No. 16494
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2720: from 93 to 116
  
- Alignment No. 16495
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2721
- Ceres seq\_id 1504373
- Location of start within SEQ ID NO 2718: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16496
- gi No. 2997589
- % Identity 87.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2721: from 1 to 109
  
- Alignment No. 16497
- gi No. 2997591
- % Identity 84.6
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110
  
- Alignment No. 16498
- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110
  
- Alignment No. 16499
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2721: from 86 to 109
  
- Alignment No. 16500
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110

Maximum Length Sequence corresponding to clone ID 317547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2722
- Ceres seq\_id 1504374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2723

- Ceres seq\_id 1504375
- Location of start within SEQ ID NO 2722: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16501
- E1-E2 ATPases
- Location within SEQ ID NO 2723: from 2 to 149 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16502
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

- Alignment No. 16503
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

- Alignment No. 16504
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2724
- Ceres seq\_id 1504376
- Location of start within SEQ ID NO 2722: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16505
- E1-E2 ATPases
- Location within SEQ ID NO 2724: from 1 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16506
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

- Alignment No. 16507
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

- Alignment No. 16508
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2725
- Ceres seq\_id 1504377

- Location of start within SEQ ID NO 2722: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16509
- E1-E2 ATPases
- Location within SEQ ID NO 2725: from 1 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16510
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136
- Alignment No. 16511
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136
- Alignment No. 16512
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136

Maximum Length Sequence corresponding to clone ID 317650

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2726
- Ceres seq\_id 1504382

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2727
- Ceres seq\_id 1504383
- Location of start within SEQ ID NO 2726: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16513
- gi No. 100490
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2727: from 36 to 47
- Alignment No. 16514
- gi No. 100490
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16515
- gi No. 100490
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16516
- gi No. 100490
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16517
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16518
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16519
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16520
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16521
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16522
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16523
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16524
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16525
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16526
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16527
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16528
- gi No. 100598
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16529
- gi No. 100599
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16530
- gi No. 100812
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16531
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16532
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16533
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16534
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16535
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16536
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16537
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16538
- gi No. 102062
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16539
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16540
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16541
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16542
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16543
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16544
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16545
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16546
- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16547

- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16548
- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16549
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16550
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16551
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16552
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16553
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16554
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16555
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16556
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16557
- gi No. 102281



- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16558
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16559
- gi No. 102389
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16560
- gi No. 103436
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16561
- gi No. 1044940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16562
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16563
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16564
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16565
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16566
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16567
- gi No. 10673
- % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16568
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16569
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16570
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16571
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16572
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16573
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16574
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16575
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16576
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16577
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16578
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16579
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16580
- gi No. 1076678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16581
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16582
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16583
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16584
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16585
- gi No. 1078777
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2727: from 27 to 51
- Alignment No. 16586
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16587
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16588
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
  
- Alignment No. 16589
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16590
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16591
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16592
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16593
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16594
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16595
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16596
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16597
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16598
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16599
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16600
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16601
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16602
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16603
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16604
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16605
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16606
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16607
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16608

- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16609
- gi No. 1101013
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16610
- gi No. 1101015
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16611
- gi No. 1101021
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16612
- gi No. 1101021
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16613
- gi No. 1107481
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 16614
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16615
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16616
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16617
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16618
- gi No. 1143188

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16619
- gi No. 1167510
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 16620
- gi No. 1167510
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16621
- gi No. 1174859
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16622
- gi No. 1174860
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16623
- gi No. 1174861
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16624
- gi No. 1184755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16625
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16626
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16627
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16628
- gi No. 1197093
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16629
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16630
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16631
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16632
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16633
- gi No. 1304128
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16634
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16635
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16636
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16637
- gi No. 1304357
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16638
- gi No. 1321735
- % Identity 85.7
- Alignment Length 21



- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16639
- gi No. 1321735
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16640
- gi No. 1326022
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16641
- gi No. 1326022
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16642
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16643
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16644
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16645
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16646
- gi No. 1332579
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16647
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16648
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16649
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16650
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16651
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16652
- gi No. 1351348
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16653
- gi No. 1351349
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16654
- gi No. 1353755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16655
- gi No. 1353757
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 28 to 47
  
- Alignment No. 16656
- gi No. 1353757
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16657
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16658
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16659
- gi No. 1362008
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16660
- gi No. 1362008
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16661
- gi No. 1362009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16662
- gi No. 1362010
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16663
- gi No. 1362010
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16664
- gi No. 1362010
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16665
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16666
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16667
- gi No. 136665
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16668
- gi No. 136666
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16669

- gi No. 136667
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16670
- gi No. 136668
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16671
- gi No. 136669
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
  
- Alignment No. 16672
- gi No. 136670
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16673
- gi No. 136671
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16674
- gi No. 136672
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16675
- gi No. 136673
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16676
- gi No. 136674
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16677
- gi No. 136675
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16678
- gi No. 136676
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16679
- gi No. 136677

- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16680
- gi No. 136678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16681
- gi No. 1421797
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16682
- gi No. 156480
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16683
- gi No. 158759
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16684
- gi No. 158763
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16685
- gi No. 158765
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16686
- gi No. 158767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16687
- gi No. 158769
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16688
- gi No. 158771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16689
- gi No. 161281
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16690
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16691
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16692
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16693
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16694
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16695
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16696
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16697
- gi No. 166336
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16698
- gi No. 1666175
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16699
- gi No. 1675359
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16700
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16701
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16702
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16703
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16704
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16705
- gi No. 167941
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 28 to 48
- Alignment No. 16706
- gi No. 167945
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16707
- gi No. 167945
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16708
- gi No. 167945
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16709
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16710
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16711
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16712
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16713
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16714
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16715
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16716
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16717
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16718
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16719
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48



- Alignment No. 16720
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16721
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16722
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16723
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16724
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16725
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16726
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16727
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16728
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16729
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16730

- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16731
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16732
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16733
- gi No. 170354
- % Identity 88.2
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2727: from 31 to 47
  
- Alignment No. 16734
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16735
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16736
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16737
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16738
- gi No. 1762374
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16739
- gi No. 1762935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16740
- gi No. 1763015

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16741
- gi No. 1771780
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16742
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16743
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16744
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16745
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16746
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16747
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16748
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16749
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16750
- gi No. 1800281
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16751
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16752
- gi No. 1805696
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16753
- gi No. 1805696
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16754
- gi No. 1839584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16755
- gi No. 1841849
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42
  
- Alignment No. 16756
- gi No. 208558
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16757
- gi No. 208560
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16758
- gi No. 208562
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16759
- gi No. 208564
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16760
- gi No. 208566
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16761
- gi No. 208568
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16762
- gi No. 208891
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16763
- gi No. 208891
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16764
- gi No. 209603
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16765
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16766
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16767
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16768
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16769
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16770
- gi No. 2118959
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16771
- gi No. 2118959
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16772
- gi No. 2118959
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16773
- gi No. 2118960
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16774
- gi No. 2118960
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16775
- gi No. 2118961
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16776
- gi No. 2118961
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16777
- gi No. 2118962
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16778
- gi No. 2118962
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16779
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16780
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16781
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16782
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16783
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16784
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16785
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16786
- gi No. 2129452
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16787
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16788
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16789
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16790
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16791

- gi No. 2133278
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
  
- Alignment No. 16792
- gi No. 2133549
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16793
- gi No. 2144011
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16794
- gi No. 2144275
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16795
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16796
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16797
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16798
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16799
- gi No. 2149467
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16800
- gi No. 2209091
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16801
- gi No. 2209091



- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16802
- gi No. 223061
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16803
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16804
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16805
- gi No. 225317
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16806
- gi No. 225319
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16807
- gi No. 225320
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16808
- gi No. 2281952
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16809
- gi No. 2281954
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16810
- gi No. 2281955
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16811
- gi No. 2281959
- % Identity 73.3

- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16812
- gi No. 2330875
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16813
- gi No. 2408009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16814
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16815
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16816
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16817
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16818
- gi No. 247308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16819
- gi No. 248865
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 16820
- gi No. 2558539
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16821
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16822
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16823
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16824
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16825
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16826
- gi No. 2627129
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16827
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16828
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16829
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16830
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16831
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16832
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16833
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16834
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16835
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16836
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16837
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16838
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16839
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16840
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16841
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16842
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16843
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16844
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16845
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16846
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16847
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16848
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16849
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16850
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16851
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16852

- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16853
- gi No. 2641213
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16854
- gi No. 2641213
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16855
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16856
- gi No. 2654141
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16857
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16858
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16859
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16860
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16861
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16862
- gi No. 2707837

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16863
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16864
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16865
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16866
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16867
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16868
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16869
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16870
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16871
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16872
- gi No. 2760347
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16873
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16874
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16875
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16876
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16877
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16878
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16879
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16880
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16881
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16882
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21



- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16883
- gi No. 279635
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16884
- gi No. 279636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16885
- gi No. 280386
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16886
- gi No. 281276
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16887
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16888
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16889
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16890
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16891
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16892
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16893
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16894
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16895
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16896
- gi No. 2894306
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16897
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16898
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16899
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16900
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16901
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16902
- gi No. 2995949
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16903
- gi No. 3047314
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16904
- gi No. 3047316
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16905
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16906
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16907
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16908
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16909
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16910
- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16911
- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16912
- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16913

- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16914
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16915
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16916
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16917
- gi No. 3126967
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16918
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16919
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16920
- gi No. 3152950
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16921
- gi No. 3158372
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16922
- gi No. 3158372
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16923
- gi No. 320608

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16924
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16925
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16926
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16927
- gi No. 322750
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16928
- gi No. 323071
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16929
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16930
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16931
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16932
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16933
- gi No. 323157
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16934
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16935
- gi No. 323208
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16936
- gi No. 323230
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16937
- gi No. 3265058
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16938
- gi No. 3319208
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16939
- gi No. 3335355
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 16940
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16941
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16942
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16943
- gi No. 340062
- % Identity 88.2
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2727: from 31 to 47
- Alignment No. 16944
- gi No. 3452083
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16945
- gi No. 348148
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16946
- gi No. 3603456
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16947
- gi No. 3603456
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16948
- gi No. 3603456
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16949
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16950
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16951
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16952
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16953
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16954
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16955
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16956
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16957
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16958
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16959
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16960
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16961
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16962
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16963
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47



- Alignment No. 16964
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16965
- gi No. 3789940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16966
- gi No. 3789940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16967
- gi No. 3789940
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16968
- gi No. 3789940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16969
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16970
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16971
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16972
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16973
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16974

- gi No. 385076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16975
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16976
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16977
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16978
- gi No. 3885463
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 30 to 47
  
- Alignment No. 16979
- gi No. 3892189
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2727: from 27 to 51
  
- Alignment No. 16980
- gi No. 402242
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16981
- gi No. 4105408
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2727: from 36 to 47
  
- Alignment No. 16982
- gi No. 4105408
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16983
- gi No. 4105408
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16984
- gi No. 4105408

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16985
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16986
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16987
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16988
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16989
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16990
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16991
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16992
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16993
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16994
- gi No. 4150898
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16995
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16996
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16997
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16998
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16999
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17000
- gi No. 4150914
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 17001
- gi No. 4150914
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17002
- gi No. 4151082
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17003
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17004
- gi No. 418854
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17005
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17006
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17007
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17008
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17009
- gi No. 421735
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17010
- gi No. 421867
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17011
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17012
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17013
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17014
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17015
- gi No. 421929
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17016
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17017
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17018
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17019
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17020
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17021
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17022
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17023
- gi No. 422269
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17024
- gi No. 422270
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17025
- gi No. 422271
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17026
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17027
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17028
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17029
- gi No. 433970
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17030
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17031
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17032
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17033
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17034
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17035

- gi No. 4506713
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17036
- gi No. 4507761
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17037
- gi No. 456779
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17038
- gi No. 4586594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17039
- gi No. 4586594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17040
- gi No. 4587232
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17041
- gi No. 4587234
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17042
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17043
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17044
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17045
- gi No. 4587236



- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17046
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17047
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17048
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17049
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17050
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17051
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17052
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17053
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17054
- gi No. 4589760
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
  
- Alignment No. 17055
- gi No. 4589760
- % Identity 75

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
  
- Alignment No. 17056
- gi No. 463363
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 17057
- gi No. 463369
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17058
- gi No. 463373
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17059
- gi No. 463375
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17060
- gi No. 464989
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17061
- gi No. 464990
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17062
- gi No. 468272
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17063
- gi No. 4737
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17064
- gi No. 477630
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17065
- gi No. 477815
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17066
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17067
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17068
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17069
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17070
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17071
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17072
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17073
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17074
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17075
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17076
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17077
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17078
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17079
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17080
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17081
- gi No. 485427
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17082
- gi No. 485518
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17083
- gi No. 49586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17084
- gi No. 49586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17085
- gi No. 49586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17086
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17087
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17088
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17089
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17090
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17091
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17092
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17093
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17094
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17095
- gi No. 510476
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17096

- gi No. 5107695
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17097
- gi No. 539404
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17098
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17099
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17100
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17101
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17102
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17103
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17104
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17105
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17106
- gi No. 541546

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17107
- gi No. 541953
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17108
- gi No. 541954
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17109
- gi No. 5441519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17110
- gi No. 552237
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17111
- gi No. 5523967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17112
- gi No. 5523969
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17113
- gi No. 5523969
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17114
- gi No. 5523971
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17115
- gi No. 5523973
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17116
- gi No. 5523975
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17117
- gi No. 5523977
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17118
- gi No. 5523979
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17119
- gi No. 5523979
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2727: from 19 to 47
  
- Alignment No. 17120
- gi No. 5523981
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17121
- gi No. 5523985
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17122
- gi No. 5523987
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17123
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17124
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17125
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17126
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21



- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17127
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17128
- gi No. 5531278
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17129
- gi No. 5531281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17130
- gi No. 554564
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17131
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17132
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17133
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17134
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17135
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17136
- gi No. 571519
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17137
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17138
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17139
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17140
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17141
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17142
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17143
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17144
- gi No. 576775
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17145
- gi No. 578545
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17146
- gi No. 578545
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17147
- gi No. 578546
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17148
- gi No. 578546
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17149
- gi No. 578546
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17150
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17151
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17152
- gi No. 578551
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2727: from 29 to 47
  
- Alignment No. 17153
- gi No. 578551
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17154
- gi No. 600539
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17155
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17156
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17157

- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17158
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17159
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17160
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17161
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17162
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 17163
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17164
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17165
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17166
- gi No. 630455
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17167
- gi No. 630479

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17168
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17169
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17170
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17171
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17172
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17173
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17174
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17175
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17176
- gi No. 70637
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17177
- gi No. 70639
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17178
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17179
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17180
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17181
- gi No. 70640
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17182
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17183
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17184
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17185
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17186
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17187
- gi No. 70643
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17188
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17189
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17190
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17191
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17192
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17193
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17194
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17195
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17196
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17197
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17198
- gi No. 70646
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17199
- gi No. 70647
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17200
- gi No. 70647
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17201
- gi No. 70647
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17202
- gi No. 70648
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17203
- gi No. 70650
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
  
- Alignment No. 17204
- gi No. 70653
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17205
- gi No. 70654
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17206
- gi No. 70657
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17207
- gi No. 70658
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47



- Alignment No. 17208
- gi No. 70659
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 32 to 47
  
- Alignment No. 17209
- gi No. 70660
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17210
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17211
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17212
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17213
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17214
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17215
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17216
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17217
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17218

- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17219
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17220
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17221
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17222
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17223
- gi No. 82040
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17224
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17225
- gi No. 82284
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17226
- gi No. 82287
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17227
- gi No. 82426
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17228
- gi No. 82426

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17229
- gi No. 82512
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17230
- gi No. 82512
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17231
- gi No. 82733
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17232
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17233
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17234
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17235
- gi No. 83594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17236
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17237
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17238
- gi No. 83596
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17239
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17240
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17241
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17242
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17243
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17244
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17245
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17246
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17247
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17248
- gi No. 84152
- % Identity 86.4
- Alignment Length 22

- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17249
  - gi No. 84337
  - % Identity 83.3
  - Alignment Length 18
  - Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17250
  - gi No. 84337
  - % Identity 81
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17251
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17252
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17253
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17254
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17255
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17256
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17257
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17258
  - gi No. 84478
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17259
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17260
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17261
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17262
- gi No. 84834
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42
  
- Alignment No. 17263
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17264
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17265
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17266
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17267
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17268
- gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17269
- gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17270
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17271
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17272
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17273
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17274
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17275
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17276
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17277
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17278
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17279

- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17280
- gi No. 902525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17281
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17282
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17283
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17284
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17285
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17286
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17287
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17288
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17289
- gi No. 902586



- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17290
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17291
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17292
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17293
- gi No. 91870
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 17294
- gi No. 91870
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17295
- gi No. 91871
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17296
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17297
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17298
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17299
- gi No. 940395
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17300
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17301
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17302
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17303
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17304
- gi No. 967985
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
  
- Alignment No. 17305
- gi No. 99771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17306
- gi No. 99772
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17307
- gi No. 99975
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2728
- Ceres seq\_id 1504384
- Location of start within SEQ ID NO 2726: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 17308
- Ubiquitin family
- Location within SEQ ID NO 2728: from 1 to 49 aa.

(D) Related Amino Acid Sequences

- Alignment No. 17309
- gi No. 100490
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17310
- gi No. 100490
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17311
- gi No. 100490
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17312
- gi No. 100490
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17313
- gi No. 100524
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17314
- gi No. 100524
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17315
- gi No. 100524
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17316
- gi No. 100524
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17317
- gi No. 100524
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17318
- gi No. 100524
- % Identity 79.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17319
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17320
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17321
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17322
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17323
- gi No. 100598
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17324
- gi No. 100599
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17325
- gi No. 100812
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17326
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17327
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17328
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17329
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17330
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17331
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17332
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17333
- gi No. 100981
- % Identity 76.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2728: from 9 to 51
  
- Alignment No. 17334
- gi No. 102062
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17335
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17336
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17337
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17338
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17339

- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17340
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17341
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17342
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17343
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17344
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17345
- gi No. 102280
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17346
- gi No. 102280
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17347
- gi No. 102280
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17348
- gi No. 102280
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17349
- gi No. 102280

- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17350
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17351
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17352
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17353
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17354
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17355
- gi No. 102389
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17356
- gi No. 103436
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17357
- gi No. 1044940
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17358
- gi No. 104829
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17359
- gi No. 104829
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17360
- gi No. 104829
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17361
- gi No. 1050930
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17362
- gi No. 10673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17363
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17364
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17365
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17366
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17367
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17368
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17369
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53



- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17370
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17371
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17372
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17373
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17374
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17375
- gi No. 1076678
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17376
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17377
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17378
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17379
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17380
- gi No. 1078777
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17381
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17382
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17383
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17384
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17385
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17386
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17387
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17388
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17389
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17390
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17391
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17392
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17393
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17394
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17395
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17396
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17397
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17398
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17399
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17400

- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17401
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17402
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17403
- gi No. 1101013
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2728: from 1 to 18
  
- Alignment No. 17404
- gi No. 1101021
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17405
- gi No. 1101023
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 10 to 49
  
- Alignment No. 17406
- gi No. 1107481
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17407
- gi No. 1107481
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17408
- gi No. 1143188
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17409
- gi No. 1143188
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17410
- gi No. 1143188

- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17411
- gi No. 1167510
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17412
- gi No. 1174859
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17413
- gi No. 1174860
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17414
- gi No. 1174861
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17415
- gi No. 1184755
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17416
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17417
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17418
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17419
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17420
- gi No. 1304128
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17421
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17422
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17423
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17424
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17425
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17426
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17427
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17428
- gi No. 1321735
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36
  
- Alignment No. 17429
- gi No. 1321735
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17430
- gi No. 1326021
- % Identity 79.4
- Alignment Length 34

- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17431
- gi No. 1326022
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49
- Alignment No. 17432
- gi No. 1326022
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17433
- gi No. 1326022
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17434
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17435
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17436
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17437
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17438
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17439
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17440
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17441
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17442
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17443
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17444
- gi No. 1351348
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17445
- gi No. 1351349
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17446
- gi No. 1353755
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2728: from 14 to 49
  
- Alignment No. 17447
- gi No. 1353755
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17448
- gi No. 1353757
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2728: from 1 to 18
  
- Alignment No. 17449
- gi No. 1353757
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17450
- gi No. 1362008
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49



- Alignment No. 17451
- gi No. 1362008
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17452
- gi No. 1362008
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17453
- gi No. 1362008
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17454
- gi No. 1362009
- % Identity 79.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17455
- gi No. 1362010
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17456
- gi No. 1362010
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17457
- gi No. 1362010
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17458
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17459
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17460
- gi No. 136665
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17461

- gi No. 136666
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17462
- gi No. 136667
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17463
- gi No. 136668
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17464
- gi No. 136669
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17465
- gi No. 136670
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17466
- gi No. 136671
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17467
- gi No. 136672
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17468
- gi No. 136673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17469
- gi No. 136674
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17470
- gi No. 136675
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17471
- gi No. 136676

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17472
- gi No. 136677
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17473
- gi No. 136678
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17474
- gi No. 1421797
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17475
- gi No. 1480012
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17476
- gi No. 158759
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17477
- gi No. 158763
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17478
- gi No. 158765
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17479
- gi No. 158767
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17480
- gi No. 158769
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17481
- gi No. 158771
- % Identity 77.4

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17482
- gi No. 161281
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17483
- gi No. 163575
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17484
- gi No. 163575
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17485
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17486
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17487
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17488
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17489
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17490
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17491
- gi No. 1666175
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17492
- gi No. 1675359
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2728: from 1 to 13
- Alignment No. 17493
- gi No. 167935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17494
- gi No. 167935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17495
- gi No. 167935
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17496
- gi No. 167935
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17497
- gi No. 167935
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17498
- gi No. 167941
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53
- Alignment No. 17499
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17500
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17501
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17502
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17503
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17504
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17505
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17506
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17507
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17508
- gi No. 167947
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17509
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17510
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17511
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17512
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17513
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17514
- gi No. 1684855
- % Identity 81.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 17 to 49
  
- Alignment No. 17515
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17516
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17517
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17518
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17519
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17520
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17521
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17522

- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17523
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17524
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17525
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17526
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17527
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17528
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17529
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17530
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17531
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17532
- gi No. 170354



- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17533
- gi No. 1762374
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44
  
- Alignment No. 17534
- gi No. 1762935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17535
- gi No. 1763015
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17536
- gi No. 1771780
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17537
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17538
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17539
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17540
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17541
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17542
- gi No. 1800281
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17543
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17544
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17545
- gi No. 1800281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17546
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17547
- gi No. 1805696
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 1 to 38
  
- Alignment No. 17548
- gi No. 1805696
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17549
- gi No. 1841849
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49
  
- Alignment No. 17550
- gi No. 208558
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17551
- gi No. 208560
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17552
- gi No. 208562
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17553
- gi No. 208564
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17554
- gi No. 208566
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17555
- gi No. 208568
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17556
- gi No. 208891
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17557
- gi No. 209603
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17558
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17559
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17560
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17561
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17562
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17563
- gi No. 2118959
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17564
- gi No. 2118960
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17565
- gi No. 2118960
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17566
- gi No. 2118961
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17567
- gi No. 2118961
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17568
- gi No. 2118962
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17569
- gi No. 2118962
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17570
- gi No. 2118963
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49
  
- Alignment No. 17571
- gi No. 2118963
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
  
- Alignment No. 17572
- gi No. 2118964
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2728: from 9 to 49

- Alignment No. 17573
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17574
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17575
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17576
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17577
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17578
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17579
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17580
- gi No. 2129452
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17581
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17582
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17583

- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17584
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17585
- gi No. 2133278
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17586
- gi No. 2133549
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
  
- Alignment No. 17587
- gi No. 2133549
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 16 to 49
  
- Alignment No. 17588
- gi No. 2133549
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17589
- gi No. 2144011
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17590
- gi No. 2144275
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17591
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17592
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17593
- gi No. 2144734

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17594
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17595
- gi No. 2149467
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17596
- gi No. 2209091
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17597
- gi No. 2209091
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17598
- gi No. 223061
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
  
- Alignment No. 17599
- gi No. 224321
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49
  
- Alignment No. 17600
- gi No. 224321
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17601
- gi No. 224321
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17602
- gi No. 225317
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
  
- Alignment No. 17603
- gi No. 225319
- % Identity 78.3

- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
  
- Alignment No. 17604
- gi No. 225320
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
  
- Alignment No. 17605
- gi No. 2281952
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
  
- Alignment No. 17606
- gi No. 2281954
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
  
- Alignment No. 17607
- gi No. 2281955
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2728: from 1 to 24
  
- Alignment No. 17608
- gi No. 2281959
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44
  
- Alignment No. 17609
- gi No. 2330875
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17610
- gi No. 2408009
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17611
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17612
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17613
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53



- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17614
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17615
- gi No. 2558539
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17616
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17617
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17618
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17619
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17620
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17621
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17622
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17623
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17624
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17625
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17626
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17627
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17628
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17629
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17630
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17631
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17632
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17633
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17634
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17635
- gi No. 2627133
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17636
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17637
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17638
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17639
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17640
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17641
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17642
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17643
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17644

- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17645
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17646
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17647
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17648
- gi No. 2641213
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36
  
- Alignment No. 17649
- gi No. 2641213
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17650
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17651
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17652
- gi No. 2654141
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17653
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17654
- gi No. 2654141

- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17655
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17656
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17657
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17658
- gi No. 2707837
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17659
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17660
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17661
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17662
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17663
- gi No. 2760345
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17664
- gi No. 2760345
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17665
- gi No. 2760345
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17666
- gi No. 2760345
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17667
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17668
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17669
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17670
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17671
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17672
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17673
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17674
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17675
- gi No. 2760349
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17676
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17677
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17678
- gi No. 279635
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17679
- gi No. 279636
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17680
- gi No. 280386
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17681
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17682
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17683
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17684
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17685
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17686
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17687
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17688
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17689
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17690
- gi No. 2894306
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17691
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17692
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17693
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17694
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49



- Alignment No. 17695
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17696
- gi No. 2995277
- % Identity 83.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2728: from 20 to 49
  
- Alignment No. 17697
- gi No. 2995949
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2728: from 15 to 49
  
- Alignment No. 17698
- gi No. 2995949
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17699
- gi No. 3047314
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17700
- gi No. 3047316
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17701
- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17702
- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17703
- gi No. 3047318
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17704
- gi No. 3047318
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17705

- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17706
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17707
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17708
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17709
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17710
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17711
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17712
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17713
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17714
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17715
- gi No. 3126967

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17716
- gi No. 3152950
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17717
- gi No. 3158372
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2728: from 24 to 49
  
- Alignment No. 17718
- gi No. 3158372
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17719
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17720
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17721
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17722
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17723
- gi No. 322750
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17724
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17725
- gi No. 323157
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17726
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17727
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17728
- gi No. 323157
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17729
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17730
- gi No. 323208
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2728: from 3 to 49
  
- Alignment No. 17731
- gi No. 323208
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17732
- gi No. 323230
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
  
- Alignment No. 17733
- gi No. 3265058
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17734
- gi No. 3319208
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17735
- gi No. 3335355
- % Identity 86.4
- Alignment Length 22

- Location of Alignment in SEQ ID NO 2728: from 29 to 50
- Alignment No. 17736
- gi No. 3335355
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2728: from 1 to 23
- Alignment No. 17737
- gi No. 3335355
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17738
- gi No. 3335355
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17739
- gi No. 3335355
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17740
- gi No. 340062
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17741
- gi No. 3452083
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17742
- gi No. 348148
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 17743
- gi No. 348148
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17744
- gi No. 348149
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17745
- gi No. 3603456
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2728: from 13 to 49

- Alignment No. 17746
- gi No. 3603456
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17747
- gi No. 3603456
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17748
- gi No. 3603456
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17749
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17750
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17751
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17752
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17753
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17754
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17755
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17756
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17757
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17758
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17759
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17760
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17761
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17762
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17763
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17764
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17765
- gi No. 3789940
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17766

- gi No. 3789940
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17767
- gi No. 3789940
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17768
- gi No. 3789940
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17769
- gi No. 3789942
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17770
- gi No. 3789942
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17771
- gi No. 3789942
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17772
- gi No. 3789942
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17773
- gi No. 3789942
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17774
- gi No. 385076
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17775
- gi No. 3882081
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17776
- gi No. 3882081



- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17777
- gi No. 3882081
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17778
- gi No. 3885463
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17779
- gi No. 3892189
- % Identity 78.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17780
- gi No. 402242
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17781
- gi No. 4049712
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17782
- gi No. 4102845
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17783
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17784
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17785
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17786
- gi No. 4105408
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17787
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17788
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17789
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17790
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17791
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17792
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17793
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17794
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17795
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17796
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17797
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17798
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17799
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17800
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17801
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17802
- gi No. 4150914
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17803
- gi No. 4150914
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17804
- gi No. 4151082
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17805
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17806
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17807
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17808
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17809
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17810
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17811
- gi No. 421867
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17812
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17813
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17814
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17815
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17816
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17817
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17818
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17819
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17820
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17821
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17822
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17823
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17824
- gi No. 422269
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17825
- gi No. 422270
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17826
- gi No. 422271
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17827

- gi No. 433970
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49
  
- Alignment No. 17828
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17829
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17830
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17831
- gi No. 433970
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17832
- gi No. 433970
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17833
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17834
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17835
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17836
- gi No. 444791
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17837
- gi No. 4506713

- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17838
- gi No. 4507761
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17839
- gi No. 4510359
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49
  
- Alignment No. 17840
- gi No. 4586594
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17841
- gi No. 4587232
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17842
- gi No. 4587234
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17843
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17844
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17845
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17846
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17847
- gi No. 4587236
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17848
- gi No. 4587236
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17849
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17850
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17851
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17852
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17853
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17854
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17855
- gi No. 4589760
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17856
- gi No. 4589760
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17857
- gi No. 463363
- % Identity 73.6
- Alignment Length 53



- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17858
- gi No. 463365
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17859
- gi No. 463367
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17860
- gi No. 463369
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17861
- gi No. 463371
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17862
- gi No. 463373
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17863
- gi No. 463375
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17864
- gi No. 464990
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17865
- gi No. 468272
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17866
- gi No. 4737
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2728: from 1 to 19
- Alignment No. 17867
- gi No. 477630
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17868
- gi No. 477630
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17869
- gi No. 477815
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17870
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17871
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17872
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17873
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17874
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17875
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17876
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17877
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17878
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17879
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17880
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17881
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17882
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17883
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17884
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17885
- gi No. 485427
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
  
- Alignment No. 17886
- gi No. 485518
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17887
- gi No. 49586
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44
  
- Alignment No. 17888

- gi No. 49586
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17889
- gi No. 49586
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17890
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17891
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17892
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17893
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17894
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17895
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17896
- gi No. 510473
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17897
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17898
- gi No. 510473

- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17899
- gi No. 510476
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17900
- gi No. 5107695
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17901
- gi No. 539404
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17902
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17903
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17904
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17905
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17906
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17907
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17908
- gi No. 541546
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17909
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17910
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17911
- gi No. 541953
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17912
- gi No. 541954
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17913
- gi No. 542395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17914
- gi No. 5441519
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17915
- gi No. 552237
- % Identity 78.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49
  
- Alignment No. 17916
- gi No. 5523967
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17917
- gi No. 5523969
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17918
- gi No. 5523969
- % Identity 77.4
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17919
- gi No. 5523971
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2728: from 31 to 49
- Alignment No. 17920
- gi No. 5523971
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17921
- gi No. 5523973
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17922
- gi No. 5523975
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17923
- gi No. 5523977
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17924
- gi No. 5523979
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17925
- gi No. 5523979
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17926
- gi No. 5523981
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17927
- gi No. 5523983
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17928
- gi No. 5523985
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 2 to 49

- Alignment No. 17929
- gi No. 5523985
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17930
- gi No. 5523987
- % Identity 79.2
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 2 to 49
  
- Alignment No. 17931
- gi No. 5523987
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17932
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17933
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17934
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17935
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17936
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17937
- gi No. 5531278
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17938
- gi No. 5531281
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51



- Alignment No. 17939
- gi No. 554564
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17940
- gi No. 567767
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17941
- gi No. 567767
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17942
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17943
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17944
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17945
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17946
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17947
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17948
- gi No. 576773
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17949

- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17950
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17951
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17952
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17953
- gi No. 576775
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17954
- gi No. 578545
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
  
- Alignment No. 17955
- gi No. 578545
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17956
- gi No. 578545
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17957
- gi No. 578545
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17958
- gi No. 578545
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17959
- gi No. 578546

- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
  
- Alignment No. 17960
- gi No. 578546
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17961
- gi No. 578546
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17962
- gi No. 578549
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17963
- gi No. 578549
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17964
- gi No. 578551
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17965
- gi No. 578551
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
  
- Alignment No. 17966
- gi No. 578551
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17967
- gi No. 578551
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17968
- gi No. 578551
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17969
- gi No. 600539
- % Identity 76.4

- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17970
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17971
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17972
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17973
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17974
- gi No. 625174
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17975
- gi No. 625174
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17976
- gi No. 625174
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 17977
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2728: from 30 to 49
  
- Alignment No. 17978
- gi No. 625509
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2728: from 1 to 23
  
- Alignment No. 17979
- gi No. 625509
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17980
- gi No. 625509
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17981
- gi No. 625509
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17982
- gi No. 630455
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17983
- gi No. 630479
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17984
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17985
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17986
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17987
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17988
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17989
- gi No. 70636
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17990
- gi No. 70636
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17991
- gi No. 70636
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17992
- gi No. 70637
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2728: from 1 to 47
  
- Alignment No. 17993
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17994
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17995
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17996
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17997
- gi No. 70640
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17998
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17999
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18000
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18001
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18002
- gi No. 70642
- % Identity 81.5
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 18003
- gi No. 70643
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18004
- gi No. 70644
- % Identity 83.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2728: from 20 to 49
  
- Alignment No. 18005
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18006
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18007
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18008
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18009
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18010

- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18011
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18012
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18013
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18014
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18015
- gi No. 70646
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18016
- gi No. 70647
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18017
- gi No. 70647
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18018
- gi No. 70647
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 18019
- gi No. 70648
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18020
- gi No. 70653



- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18021
- gi No. 70654
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18022
- gi No. 70657
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18023
- gi No. 70658
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18024
- gi No. 70659
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18025
- gi No. 70660
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53
  
- Alignment No. 18026
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18027
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18028
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18029
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18030
- gi No. 726391
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18031
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18032
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18033
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18034
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18035
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18036
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18037
- gi No. 82040
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49
  
- Alignment No. 18038
- gi No. 82040
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18039
- gi No. 82040
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18040
- gi No. 82040
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18041
- gi No. 82284
- % Identity 78.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 1 to 29
- Alignment No. 18042
- gi No. 82286
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2728: from 30 to 49
- Alignment No. 18043
- gi No. 82287
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 18044
- gi No. 82288
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2728: from 9 to 49
- Alignment No. 18045
- gi No. 82426
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2728: from 32 to 49
- Alignment No. 18046
- gi No. 82426
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18047
- gi No. 82426
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18048
- gi No. 82512
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2728: from 13 to 49
- Alignment No. 18049
- gi No. 82512
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18050
- gi No. 82512
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18051
- gi No. 825728
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2728: from 12 to 49
  
- Alignment No. 18052
- gi No. 82733
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18053
- gi No. 82734
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2728: from 7 to 49
  
- Alignment No. 18054
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18055
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18056
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18057
- gi No. 829173
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18058
- gi No. 83594
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18059
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18060
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18061
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18062
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18063
- gi No. 83596
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 18064
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18065
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18066
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18067
- gi No. 84152
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18068
- gi No. 84152
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18069
- gi No. 84152
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18070
- gi No. 84152
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18071

- gi No. 84152
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 18072
- gi No. 84336
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18073
- gi No. 84337
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18074
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18075
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18076
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18077
- gi No. 84478
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18078
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18079
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18080
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18081
- gi No. 84478

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18082
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18083
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18084
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18085
- gi No. 84834
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18086
- gi No. 84834
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 18087
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18088
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18089
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18090
- gi No. 86473
- % Identity 76.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 17 to 50
  
- Alignment No. 18091
- gi No. 86474
- % Identity 87.5

- Alignment Length 16
- Location of Alignment in SEQ ID NO 2728: from 34 to 49
  
- Alignment No. 18092
- gi No. 870794
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18093
- gi No. 870794
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18094
- gi No. 89311
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2728: from 24 to 49
  
- Alignment No. 18095
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18096
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18097
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18098
- gi No. 899115
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18099
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18100
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18101
- gi No. 899608
- % Identity 81.1
- Alignment Length 53



- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18102
- gi No. 899608
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18103
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18104
- gi No. 902525
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18105
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18106
- gi No. 902584
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18107
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18108
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18109
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18110
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18111
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18112
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18113
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18114
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18115
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18116
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18117
- gi No. 91870
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18118
- gi No. 91871
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18119
- gi No. 9295
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18120
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18121
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18122
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18123
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18124
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18125
- gi No. 940395
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18126
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18127
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 18128
- gi No. 967985
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18129
- gi No. 99469
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 10 to 49
  
- Alignment No. 18130
- gi No. 99771
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18131
- gi No. 99772
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
  
- Alignment No. 18132

- gi No. 99975
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

Maximum Length Sequence corresponding to clone ID 317675

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2729
- Ceres seq\_id 1504393

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2730
- Ceres seq\_id 1504394
- Location of start within SEQ ID NO 2729: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2731
- Ceres seq\_id 1504395
- Location of start within SEQ ID NO 2729: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 18133
- gi No. 132962
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46
  
- Alignment No. 18134
- gi No. 132963
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46
  
- Alignment No. 18135
- gi No. 2500379
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46
  
- Alignment No. 18136
- gi No. 3142154
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2731: from 22 to 38
  
- Alignment No. 18137
- gi No. 3142154
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2731: from 22 to 40
  
- Alignment No. 18138
- gi No. 3492819
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18139
- gi No. 3914754
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2731: from 27 to 46
  
- Alignment No. 18140
- gi No. 4581465
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46
  
- Alignment No. 18141
- gi No. 464638
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

Maximum Length Sequence corresponding to clone ID 317687

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2732
- Ceres seq\_id 1504400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2733
- Ceres seq\_id 1504401
- Location of start within SEQ ID NO 2732: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18142
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2733: from 1 to 64 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18143
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2733: from 1 to 69
  
- Alignment No. 18144
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2733: from 1 to 66
  
- Alignment No. 18145
- gi No. 3451392
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2733: from 1 to 66
  
- Alignment No. 18146
- gi No. 4063007
- % Identity 72.7
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2733: from 1 to 66

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2734

- Ceres seq\_id 1504402
- Location of start within SEQ ID NO 2732: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18147
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2734: from 1 to 56 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18148
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2734: from 1 to 61
- Alignment No. 18149
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2734: from 1 to 58
- Alignment No. 18150
- gi No. 3451392
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2734: from 1 to 58
- Alignment No. 18151
- gi No. 4063007
- % Identity 72.7
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2734: from 1 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2735
- Ceres seq\_id 1504403
- Location of start within SEQ ID NO 2732: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18152
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2735: from 1 to 55 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18153
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2735: from 1 to 60
- Alignment No. 18154
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2735: from 1 to 57
- Alignment No. 18155
- gi No. 3451392
- % Identity 83.3



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..789
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atcatcaaca	aaaacaattc	tcaatacaca	aaacacaaaa	cacaaagaag	tttaattctc	60
tgaagaaaga	tgagttctac	aagcaaagca	tggacagtgg	cagtgagcat	cggagccgta	120
gaggcattaa	aagaccaact	aggtctttgt	cggtggaact	acatactccg	gtcggttaat	180
caacatctcc	ggaacaacgt	tagatctggt	tctcaaggga	aaaggttctc	ttcgtcttct	240
gtctccgcag	ccgttacctc	ctctggtgag	agcgagaaga	cgaagagaac	cttttccctt	300
gagaaacaat	tgatcagagc	tttaaagaaa	aagatggaat	tcaccgcaga	gcagctaagc	360
caatacaacg	gcaccgacga	atcaaagccg	atctacgtcg	caatcaaagg	ccgtgtgttc	420
gaygtcacca	ccggaaaatc	cttctacggc	tccggaggcg	attactcgat	gttcgccgga	480
aaagacgcga	gcagagcttt	gggtaagatg	agtaagaacg	aagaagatgt	gtctccttct	540
cttgaaggtc	tactgagaa	agagatcaat	actcttaatg	attgggagac	caaatttgaa	600
gctaagtatc	ctgtcgttgg	ccgtgttgtc	tcttaggtct	ctcttctgag	attgcactat	660
gttatgtaac	tattgtgtgt	gaggatcttt	gtgttggtgt	ttttctgatt	tcgtgtttgg	720
atctgatcgt	tttgatacaa	ttaccataag	taccaaatta	tctatgaaat	aaatcgggga	780
tttcgtggt						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Thr	Ser	Lys	Ala	Trp	Thr	Val	Ala	Val	Ser	Ile	Gly	Ala
1				5					10					15	
Val	Glu	Ala	Leu	Lys	Asp	Gln	Leu	Gly	Leu	Cys	Arg	Trp	Asn	Tyr	Ile
			20					25					30		
Leu	Arg	Ser	Val	Asn	Gln	His	Leu	Arg	Asn	Asn	Val	Arg	Ser	Val	Ser
			35				40					45			
Gln	Gly	Lys	Arg	Phe	Ser	Ser	Ser	Val	Ser	Ala	Ala	Val	Thr	Ser	
			50			55				60					
Ser	Gly	Glu	Ser	Glu	Lys	Thr	Lys	Arg	Thr	Phe	Ser	Leu	Glu	Lys	Gln
65					70				75					80	
Leu	Ile	Arg	Ala	Leu	Lys	Lys	Lys	Met	Glu	Phe	Thr	Ala	Glu	Gln	Leu
				85				90					95		
Ser	Gln	Tyr	Asn	Gly	Thr	Asp	Glu	Ser	Lys	Pro	Ile	Tyr	Val	Ala	Ile
			100				105						110		
Lys	Gly	Arg	Val	Phe	Xaa	Val	Thr	Gly	Lys	Ser	Phe	Tyr	Gly	Ser	
			115				120					125			
Gly	Gly	Asp	Tyr	Ser	Met	Phe	Ala	Gly	Lys	Asp	Ala	Ser	Arg	Ala	Leu
			130			135				140					
Gly	Lys	Met	Ser	Lys	Asn	Glu	Glu	Asp	Val	Ser	Pro	Ser	Leu	Glu	Gly
145					150				155					160	
Leu	Thr	Glu	Lys	Glu	Ile	Asn	Thr	Leu	Asn	Asp	Trp	Glu	Thr	Lys	Phe
				165				170						175	
Glu	Ala	Lys	Tyr	Pro	Val	Val	Gly	Arg	Val	Val	Ser				



180 185  
(2) INFORMATION FOR SEQ ID NO:3:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 100 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..100  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1497853  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
Met Glu Phe Thr Ala Glu Gln Leu Ser Gln Tyr Asn Gly Thr Asp Glu  
1                    5                    10                    15  
Ser Lys Pro Ile Tyr Val Ala Ile Lys Gly Arg Val Phe Xaa Val Thr  
                    20                    25                    30  
Thr Gly Lys Ser Phe Tyr Gly Ser Gly Gly Asp Tyr Ser Met Phe Ala  
                    35                    40                    45  
Gly Lys Asp Ala Ser Arg Ala Leu Gly Lys Met Ser Lys Asn Glu Glu  
50                    55                    60  
Asp Val Ser Pro Ser Leu Glu Gly Leu Thr Glu Lys Glu Ile Asn Thr  
65                    70                    75                    80  
Leu Asn Asp Trp Glu Thr Lys Phe Glu Ala Lys Tyr Pro Val Val Gly  
                    85                    90                    95  
Arg Val Val Ser  
100

(2) INFORMATION FOR SEQ ID NO:4:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 1005 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..1005  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1497854  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
aaaaacaaac aaaaaaatca gtgttcggct ctaacacgct cgacgaccat ggcgggtctcg 60  
tttaatacaa cgcttcacca gccttctctg agtcccagct gtagcatcaa gctttattct 120  
gggttaaagc ctcaatctgc aagctttttg gcaagtgggt atcagaattt gaataaggag 180  
ttctatggaa gagttcataa gagtctgcaa tctgggactg gcaaagcgag caggtcacgg 240  
gtaaagatga tgccaatagg aacaccgaga gtgccctaca gaaaccgtga agaaggcact 300  
tggcaakggg ttgatatatg gaatgccctt tatcgagagc gtgtaatctt cattggacaa 360  
aacattgatg aagagtttag caaccagata ttagcaacca tgttgtaacct tgatactctt 420  
gatgactcga ggaggattta tatgtacctt aatggtccgg gtggtgatct tactccaagt 480  
ctagccatct atgatacaat gaagagcttg aaaagtccgg ttgggacaca ttgcgttggg 540  
cttgcttaca accttgcagg ttttcttctt gcggttgagg aaaaggggtca ccgatttgcg 600  
atgccattgt caagaatcgc cctccaatca ccagctgggt cagcccgtgg ccaggctgat 660  
gatatccaaa atgaagcaaa agagctttca aggataagag actacctctt caatgaacta 720  
gccaaagaata caggccagcc tgcggaaaag gtcttcaaaag acttgagccg ggtgaaaagg 780  
ttcaatgcag aggaagcaat cgagtattga ctatttgata agattgttag accaccgcgc 840  
atcaaagaag acgctcctcg ccaagacgaa agcgcagggc taggctagtc tttttgttt 900  
gtttgttatg tcaaaagttt taatctttat gttattgtga ttgtgattgt tacctaaaaa 960  
aatcactgat tattgttttt tcattccacc gattttctga tttct

(2) INFORMATION FOR SEQ ID NO:5:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 295 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..295  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys	Asn	Lys	Gln	Lys	Asn	Gln	Cys	Ser	Ala	Leu	Thr	Arg	Ser	Thr	Thr
1			5						10					15	
Met	Ala	Val	Ser	Phe	Asn	Thr	Thr	Leu	His	Gln	Pro	Ser	Leu	Ser	Pro
			20					25				30			
Ser	Cys	Ser	Ile	Lys	Leu	Tyr	Ser	Gly	Leu	Lys	Pro	Gln	Ser	Ala	Ser
		35					40					45			
Phe	Leu	Ala	Ser	Gly	Tyr	Gln	Asn	Leu	Asn	Lys	Glu	Phe	Tyr	Gly	Arg
	50					55					60				
Val	His	Lys	Ser	Leu	Gln	Ser	Gly	Thr	Gly	Lys	Ala	Ser	Arg	Ser	Arg
65					70					75					80
Val	Lys	Met	Met	Pro	Ile	Gly	Thr	Pro	Arg	Val	Pro	Tyr	Arg	Asn	Arg
				85					90					95	
Glu	Glu	Gly	Thr	Trp	Gln	Xaa	Val	Asp	Ile	Trp	Asn	Ala	Leu	Tyr	Arg
			100					105					110		
Glu	Arg	Val	Ile	Phe	Ile	Gly	Gln	Asn	Ile	Asp	Glu	Glu	Phe	Ser	Asn
		115				120						125			
Gln	Ile	Leu	Ala	Thr	Met	Leu	Tyr	Leu	Asp	Thr	Leu	Asp	Asp	Ser	Arg
		130				135					140				
Arg	Ile	Tyr	Met	Tyr	Leu	Asn	Gly	Pro	Gly	Gly	Asp	Leu	Thr	Pro	Ser
145					150					155					160
Leu	Ala	Ile	Tyr	Asp	Thr	Met	Lys	Ser	Leu	Lys	Ser	Pro	Val	Gly	Thr
			165						170					175	
His	Cys	Val	Gly	Leu	Ala	Tyr	Asn	Leu	Ala	Gly	Phe	Leu	Leu	Ala	Ala
			180					185					190		
Gly	Glu	Lys	Gly	His	Arg	Phe	Ala	Met	Pro	Leu	Ser	Arg	Ile	Ala	Leu
		195					200					205			
Gln	Ser	Pro	Ala	Gly	Ala	Ala	Arg	Gly	Gln	Ala	Asp	Asp	Ile	Gln	Asn
	210					215					220				
Glu	Ala	Lys	Glu	Leu	Ser	Arg	Ile	Arg	Asp	Tyr	Leu	Phe	Asn	Glu	Leu
225					230					235					240
Ala	Lys	Asn	Thr	Gly	Gln	Pro	Ala	Glu	Arg	Val	Phe	Lys	Asp	Leu	Ser
			245						250					255	
Arg	Val	Lys	Arg	Phe	Asn	Ala	Glu	Glu	Ala	Ile	Glu	Tyr	Gly	Leu	Ile
			260					265					270		
Asp	Lys	Ile	Val	Arg	Pro	Pro	Arg	Ile	Lys	Glu	Asp	Ala	Pro	Arg	Gln
	275						280					285			
Asp	Glu	Ser	Ala	Gly	Leu	Gly									
	290					295									

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 279 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..279  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Val	Ser	Phe	Asn	Thr	Thr	Leu	His	Gln	Pro	Ser	Leu	Ser	Pro
1			5						10					15	
Ser	Cys	Ser	Ile	Lys	Leu	Tyr	Ser	Gly	Leu	Lys	Pro	Gln	Ser	Ala	Ser
			20					25					30		

```

Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
  35          40          45
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
  50          55          60
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
  65          70          75          80
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
          85          90          95
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
          100          105          110
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg
          115          120          125
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser
          130          135          140
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr
          145          150          155          160
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala
          165          170          175
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu
          180          185          190
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn
          195          200          205
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu
          210          215          220
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser
          225          230          235          240
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile
          245          250          255
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln
          260          265          270
Asp Glu Ser Ala Gly Leu Gly
          275

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1497857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg Glu Glu
  1          5          10          15
Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg Glu Arg
          20          25          30
Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn Gln Ile
          35          40          45
Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg Arg Ile
          50          55          60
Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser Leu Ala
          65          70          75          80
Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr His Cys
          85          90          95
Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala Gly Glu
          100          105          110
Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu Gln Ser
          115          120          125
Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn Glu Ala

```

```

      130              135              140
Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu Ala Lys
145              150              155              160
Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser Arg Val
      165              170              175
Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile Asp Lys
      180              185              190
Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln Asp Glu
      195              200              205
Ser Ala Gly Leu Gly
210
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

aatcgcatc tccgatcgaa tagccgacgg agaaatgacc aagttcagga agctcggccg      60
cccagcaggt caccgtatgt ccatgctcag gactatgggt tctcaattgg tgcaacacga      120
gcgaattgag accactgtta caaaggctat agaagttcgt cgtcttgctg ataatatgat      180
tcaactcgga aaagagggtt cactagctgc agcaagaaga gctgctgggt ttgttagagg      240
agatgatgta cttcacaaga tttttacaga attggckcat cgatacaaag atagagctgg      300
tggtatcaca agaatgcttc gtactcgcat tctgtttggt gatgctgccc caatggccta      360
tatcgagttt atcgatagag agaacgagct aaggcaatca aaaccagcta ctctcaacc      420
tccacctcga gtgccacttg atccatgggc tagatcccgt ctcaccaggc agtatgctcc      480
accaaaggag gcaaaaaact tctgattctg acctataaat agaagaagat ctctctcgct      540
ctctcacacc agaagatcat gtttttttcc cccttgccca tgttgtttct ccttcaaccc      600
atagctttgt atgtctggca cttattcat cactgtcatt cacaatgtgt ttaaaacagt      660
ttaaatgtag tttccttg
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Ile Ala Phe Ser Asp Arg Ile Ala Asp Gly Glu Met Thr Lys Phe Arg
1              5              10              15
Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser Met Leu Arg Thr Met
      20              25              30
Val Ser Gln Leu Val Gln His Glu Arg Ile Glu Thr Thr Val Thr Lys
      35              40              45
Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met Ile Gln Leu Gly Lys
      50              55              60
Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala Gly Phe Val Arg Gly
      65              70              75              80
Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu Xaa His Arg Tyr Lys
      85              90              95
Asp Arg Ala Gly Tyr Thr Arg Met Leu Arg Thr Arg Ile Arg Val
      100              105              110
```

Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe Ile Asp Arg Glu Asn  
 115 120 125  
 Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln Pro Pro Pro Arg Val  
 130 135 140  
 Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr Arg Gln Tyr Ala Pro  
 145 150 155 160  
 Pro Lys Glu Ala Lys Asn Phe  
 165

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1497862

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser  
 1 5 10 15  
 Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg Ile Glu  
 20 25 30  
 Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met  
 35 40 45  
 Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala  
 50 55 60  
 Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu  
 65 70 75 80  
 Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg  
 85 90 95  
 Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe  
 100 105 110  
 Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln  
 115 120 125  
 Pro Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr  
 130 135 140  
 Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1497863

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg  
 1 5 10 15  
 Ile Glu Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp  
 20 25 30  
 Asn Met Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Ala Arg Arg  
 35 40 45  
 Ala Ala Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr  
 50 55 60  
 Glu Leu Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met

65					70					75					80
Leu	Arg	Thr	Arg	Ile	Arg	Val	Gly	Asp	Ala	Ala	Pro	Met	Ala	Tyr	Ile
				85					90					95	
Glu	Phe	Ile	Asp	Arg	Glu	Asn	Glu	Leu	Arg	Gln	Ser	Lys	Pro	Ala	Thr
			100					105					110		
Pro	Gln	Pro	Pro	Pro	Arg	Val	Pro	Leu	Asp	Pro	Trp	Ala	Arg	Ser	Arg
		115					120					125			
Leu	Thr	Arg	Gln	Tyr	Ala	Pro	Pro	Lys	Glu	Ala	Lys	Asn	Phe		
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

atcaatcgga ttatctgcac ttgtttcaat ggtgcatcta atatctctca agctggtgct	60
cttgcttgcc ttacacccga aggacttgag gcaatgcata aggtgattgg attctataaa	120
gaaaacacaa acataatcat tgacacattc acatctctcg ggtatgatgt atatggagga	180
aatgcgcctt acgtatgggt tcaattcccc aaccaaagct catgggatgt gtttgctgag	240
attctggaga agactcatgt ggttacaact ccaggaagtg ggtttgacc agggggtgaa	300
gggttcgttc gtgtcagtgc ctttggtcac agagagaaca tcttagaggc atgtcgaaga	360
ttcaagcagc ttacaaatg aagaaccttg tttgtaatcg ttcctcatca tcatcacct	420
ctttaatgac atgatttgag ttaaaataat gtcgtttcca ttgtkktstg gaattttag	480
aagacacttt tgacaccagt gtttc	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Asn Arg Ile Ile Cys Thr Cys Phe Asn Gly Ala Ser Asn Ile Ser			
1	5	10	15
Gln Ala Gly Ala Leu Ala Cys Leu Thr Pro Glu Gly Leu Glu Ala Met			
	20	25	30
His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Ile Asp			
	35	40	45
Thr Phe Thr Ser Leu Gly Tyr Asp Val Tyr Gly Gly Asn Ala Pro Tyr			
	50	55	60
Val Trp Val His Phe Pro Asn Gln Ser Ser Trp Asp Val Phe Ala Glu			
65	70	75	80
Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly			
	85	90	95
Pro Gly Gly Glu Gly Phe Val Arg Val Ser Ala Phe Gly His Arg Glu			
	100	105	110
Asn Ile Leu Glu Ala Cys Arg Arg Phe Lys Gln Leu Tyr Lys			
	115	120	125

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..95
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497866
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	His	Lys	Val	Ile	Gly	Phe	Tyr	Lys	Glu	Asn	Thr	Asn	Ile	Ile	Ile
1			5						10				15		
Asp	Thr	Phe	Thr	Ser	Leu	Gly	Tyr	Asp	Val	Tyr	Gly	Gly	Asn	Ala	Pro
			20					25					30		
Tyr	Val	Trp	Val	His	Phe	Pro	Asn	Gln	Ser	Ser	Trp	Asp	Val	Phe	Ala
			35				40					45			
Glu	Ile	Leu	Glu	Lys	Thr	His	Val	Val	Thr	Thr	Pro	Gly	Ser	Gly	Phe
	50					55					60				
Gly	Pro	Gly	Gly	Glu	Gly	Phe	Val	Arg	Val	Ser	Ala	Phe	Gly	His	Arg
65				70					75					80	
Glu	Asn	Ile	Leu	Glu	Ala	Cys	Arg	Arg	Phe	Lys	Gln	Leu	Tyr	Lys	
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..431
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497867
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

atttcctaaa	agaacgaacg	acgccatata	caccgagaag	ctcaacgttc	gtcatcactc	60
ttctcgcttc	tcggcgcttc	catcgccgtc	tctatcta	ttcgctcctgc	gtcgacctgg	120
tgagctactt	cagattccgg	ccatcacgca	gctccagttg	tatgctttgt	ggctaataca	180
aagatgacaa	caatcaaaac	cggtcagaaa	actcaaaagt	cttctccttc	cggttctgct	240
actaccgcta	ctggtactct	taagcagtc	tcagcatcgt	ttaawagggtg	gggaaggaga	300
cacccgtttg	taagatatgg	acttccgatg	atatctctca	ctgtatttgg	agccctcgga	360
ctcggccaac	tccttcaagg	cagtaaggat	attgcaaagg	taaaagatga	ccaagaatgg	420
gagattatag a						

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497868
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Phe	Pro	Lys	Arg	Thr	Asn	Asp	Ala	Ile	Tyr	Thr	Glu	Lys	Leu	Asn	Val
1				5					10					15	
Arg	His	His	Ser	Ser	Arg	Phe	Ser	Ala	Ser	Pro	Ser	Pro	Ser	Leu	Ser
			20					25					30		
Asn	Phe	Val	Leu	Arg	Arg	Pro	Gly	Glu	Leu	Leu	Gln	Ile	Pro	Ala	Ile
			35				40					45			
Thr	Gln	Leu	Gln	Leu	Tyr	Ala	Leu	Trp	Leu	Ile	Gln	Arg			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe	Leu	Lys	Glu	Arg	Thr	Thr	Pro	Tyr	Thr	Pro	Arg	Ser	Ser	Thr	Phe
1				5					10					15	
Val	Ile	Thr	Leu	Leu	Ala	Ser	Arg	Arg	Leu	His	Arg	Arg	Leu	Tyr	Leu
			20					25					30		
Ile	Ser	Ser	Cys	Val	Asp	Leu	Val	Ser	Tyr	Phe	Arg	Phe	Arg	Pro	Ser
			35				40					45			
Arg	Ser	Ser	Ser	Cys	Met	Leu	Cys	Gly							
50						55									

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Thr	Thr	Ile	Lys	Thr	Gly	Gln	Lys	Thr	Gln	Lys	Ser	Ser	Pro	Ser
1				5					10					15	
Gly	Ser	Ala	Thr	Thr	Ala	Thr	Gly	Thr	Leu	Lys	Gln	Ser	Ser	Ala	Ser
			20					25					30		
Phe	Xaa	Arg	Trp	Gly	Arg	Arg	His	Pro	Phe	Val	Arg	Tyr	Gly	Leu	Pro
			35				40					45			
Met	Ile	Ser	Leu	Thr	Val	Phe	Gly	Ala	Leu	Gly	Leu	Gly	Gln	Leu	Leu
			50				55				60				
Gln	Gly	Ser	Lys	Asp	Ile	Ala	Lys	Val	Lys	Asp	Asp	Gln	Glu	Trp	Glu
65					70					75				80	
Ile	Ile														

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2584
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

aaacacacca	aatcaaaag	ctgagagctc	tcttacattg	aagctacttt	cgaagatagc	60
attcactgat	tggtaaagag	ttctagaagc	gacgagcatc	ttcttttagtt	cccagagttt	120
ctgcgtttga	gaagtctgtt	ctagaaagta	atgggtgaca	gcgaggccat	ggtttccgag	180
ggttatactt	ctgctccata	tggagactat	aatgcttctg	ctgctactgt	ggaatcgacc	240
gggcaagaga	ctgcaccaat	tgttgatgca	tcacactcgg	tcaacaatga	ttctttggtc	300



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aatggtactg cgccagttga gaacggaagt gcaacagata atgtggctgt gactgctcca 360
gcagcggagc atggagacaa tactggctct acactctcaa cggaagagga gcgcttgtgg 420
aatattgtaa gggcaaattc tttagagttt aatgcttgga ctgccttgat tgatgagacg 480
gagaggatag cgcaggacaa tatagcaaaa atccggaagg tctatgatgc tttcttagct 540
gaatttcctc tgtgttatgg ctattggaaa aagtttgccg atcatgaggc tcgggtgggg 600
gcaatggaca aagtcgtgga ggtttatgaa agagcagtgc tgggagtgc atattcagt 660
gatatctggt tgcattattg cacttttgcc atcaatacat atggagatcc agaaacgatc 720
agaaggcttt ttgaacgagc ttgtggttac gttggaactg attttctttc ctctccgttg 780
tgggacaaat acattgagta tgagtacatg cagcaggact ggagccgagt tgccttgatt 840
tacaccagaa tattggagaa tccaattcaa aatctggata gatatttcag cagttttaag 900
gagctagctg aaacacggcc tctgtcggaa ctaaggagtg ctgaggaatc cgcagctgct 960
gctgttgctg ttgctggtga tgcttctgaa agtgcagcat ctgagtccgg tgaaaaggca 1020
gatgaaggac gatctcaagt tgatggttcc accgaacaat cccctaaatt ggaaagtgct 1080
agttcaactg aacctgagga gttgaagaag tatgtaggca tcagggaagc catgtacata 1140
aaatcgaaag agtttgaatc taaaatcatt ggttatgaaa tggctataag gaggccctat 1200
ttccatgtgc gtccctctgaa tgtcgcagaa ctggagaatt ggcacaacta tctggatttc 1260
attgagaggg atggagactt caataagggt gtcaagctgt atgaaagatg tgtggttacc 1320
tgtgcaaatt acccagaata ctggattcgt tatgtgacaa acatggaagc aagtggaggt 1380
gcggaccttg cagaaaatgc ccttgctcga gcaactcaag tctttgtcaa gaaacaacca 1440
gagattcacc tatttgctgc tcgattaaaa gagcagaatg gagatatagc tgggtgctaga 1500
gctgcatacc aattagtgc cttctgaaatt tctcctggac ttcttgaagc agtaatcaag 1560
catgcaaata tggaaataccg actaggtaat ctggatgatg ctttctcttt gtatgagcaa 1620
gtgattgctg ttgaaaaggg gaaagaacat tccacaatac tgccactgct gtatgcgcag 1680
tattcaagggt tttcatactt ggtctccagg gatgctgaga aagctaggag gattattgtc 1740
gaagcacttg accatgtaca accgtcaaaa cctctcatgg aagcactgat tcattttgag 1800
gcgattcagc caccaccaag agagattgat taccttgagc cacttgtaga gaaagttata 1860
aagccagatg cagatgcccc aaacattgca agttccactg agagggaaga gctatcctta 1920
atatatatag agttcctggg tatttttgga gatgtgaagt ccattaaaaa agcggaagat 1980
caacatgtta aactgtttta tctcatcgg agcacgtcg agctgaaaaa gcgtagcgca 2040
gatgattttc tgcatacaga taggacgaaa atggcaaaaa cttacaacgg cactccacct 2100
gctcagccag tatccaatgc atatccaaat gctcaggctc aatgggtctg tggttatgct 2160
gcgcagcctc agacttgccc accagcacia gctgctcctg ctcaaccaca gcaatggaac 2220
cctgcctacg gtcaacaggc tgcttatggt gcatatgggg gatatcctgc tggctatacc 2280
gctccacaag caccaacacc tgtgccacag gccgcagctt atggagcgta tctgctcag 2340
acatacccaa cgcagagtta tgcacctcca gttgcagcag cagcaccagc ggctgcaccg 2400
gtgcagcaac cggctgctgc tgttgctcct caagcgact acaacacgta ctactgacc 2460
tattactgct gctggctggt tttgtagtgt aattgataac catttgcttc tatctactca 2520
aatttagtgt ctggatgttt acatgtctct cttttctcga tcagtgacaa tagatattta 2580
cttt

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..768
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Gly Asp Ser Glu Ala Met Val Ser Glu Gly Tyr Thr Ser Ala Pro
1           5           10           15
Tyr Gly Asp Tyr Asn Ala Ser Ala Ala Thr Val Glu Ser Thr Gly Gln
20           25           30
Glu Thr Ala Pro Ile Val Asp Ala Ser His Ser Val Asn Asn Asp Ser
35           40           45
Leu Val Asn Gly Thr Ala Pro Val Glu Asn Gly Ser Ala Thr Asp Asn
50           55           60
Val Ala Val Thr Ala Pro Ala Ala Glu His Gly Asp Asn Thr Gly Ser
65           70           75           80

```

Thr	Leu	Ser	Thr	Glu	Glu	Glu	Arg	Leu	Trp	Asn	Ile	Val	Arg	Ala	Asn	
				85					90						95	
Ser	Leu	Glu	Phe	Asn	Ala	Trp	Thr	Ala	Leu	Ile	Asp	Glu	Thr	Glu	Arg	
			100					105						110		
Ile	Ala	Gln	Asp	Asn	Ile	Ala	Lys	Ile	Arg	Lys	Val	Tyr	Asp	Ala	Phe	
			115				120						125			
Leu	Ala	Glu	Phe	Pro	Leu	Cys	Tyr	Gly	Tyr	Trp	Lys	Lys	Phe	Ala	Asp	
	130					135					140					
His	Glu	Ala	Arg	Val	Gly	Ala	Met	Asp	Lys	Val	Val	Glu	Val	Tyr	Glu	
145					150					155					160	
Arg	Ala	Val	Leu	Gly	Val	Thr	Tyr	Ser	Val	Asp	Ile	Trp	Leu	His	Tyr	
				165					170						175	
Cys	Thr	Phe	Ala	Ile	Asn	Thr	Tyr	Gly	Asp	Pro	Glu	Thr	Ile	Arg	Arg	
			180					185						190		
Leu	Phe	Glu	Arg	Ala	Leu	Val	Tyr	Val	Gly	Thr	Asp	Phe	Leu	Ser	Ser	
	195						200					205				
Pro	Leu	Trp	Asp	Lys	Tyr	Ile	Glu	Tyr	Glu	Tyr	Met	Gln	Gln	Asp	Trp	
	210					215					220					
Ser	Arg	Val	Ala	Leu	Ile	Tyr	Thr	Arg	Ile	Leu	Glu	Asn	Pro	Ile	Gln	
225					230					235					240	
Asn	Leu	Asp	Arg	Tyr	Phe	Ser	Ser	Phe	Lys	Glu	Leu	Ala	Glu	Thr	Arg	
				245					250						255	
Pro	Leu	Ser	Glu	Leu	Arg	Ser	Ala	Glu	Glu	Ser	Ala	Ala	Ala	Ala	Val	
			260					265						270		
Ala	Val	Ala	Gly	Asp	Ala	Ser	Glu	Ser	Ala	Ala	Ser	Glu	Ser	Gly	Glu	
	275						280					285				
Lys	Ala	Asp	Glu	Gly	Arg	Ser	Gln	Val	Asp	Gly	Ser	Thr	Glu	Gln	Ser	
	290					295					300					
Pro	Lys	Leu	Glu	Ser	Ala	Ser	Ser	Thr	Glu	Pro	Glu	Glu	Leu	Lys	Lys	
305					310					315					320	
Tyr	Val	Gly	Ile	Arg	Glu	Ala	Met	Tyr	Ile	Lys	Ser	Lys	Glu	Phe	Glu	
				325					330						335	
Ser	Lys	Ile	Ile	Gly	Tyr	Glu	Met	Ala	Ile	Arg	Arg	Pro	Tyr	Phe	His	
			340					345					350			
Val	Arg	Pro	Leu	Asn	Val	Ala	Glu	Leu	Glu	Asn	Trp	His	Asn	Tyr	Leu	
		355					360					365				
Asp	Phe	Ile	Glu	Arg	Asp	Gly	Asp	Phe	Asn	Lys	Val	Val	Lys	Leu	Tyr	
	370					375					380					
Glu	Arg	Cys	Val	Val	Thr	Cys	Ala	Asn	Tyr	Pro	Glu	Tyr	Trp	Ile	Arg	
385					390					395					400	
Tyr	Val	Thr	Asn	Met	Glu	Ala	Ser	Gly	Ser	Ala	Asp	Leu	Ala	Glu	Asn	
				405					410						415	
Ala	Leu	Ala	Arg	Ala	Thr	Gln	Val	Phe	Val	Lys	Lys	Gln	Pro	Glu	Ile	
			420					425					430			
His	Leu	Phe	Ala	Ala	Arg	Leu	Lys	Glu	Gln	Asn	Gly	Asp	Ile	Ala	Gly	
		435					440					445				
Ala	Arg	Ala	Ala	Tyr	Gln	Leu	Val	His	Ser	Glu	Ile	Ser	Pro	Gly	Leu	
	450					455					460					
Leu	Glu	Ala	Val	Ile	Lys	His	Ala	Asn	Met	Glu	Tyr	Arg	Leu	Gly	Asn	
465					470					475					480	
Leu	Asp	Asp	Ala	Phe	Ser	Leu	Tyr	Glu	Gln	Val	Ile	Ala	Val	Glu	Lys	
				485					490					495		
Gly	Lys	Glu	His	Ser	Thr	Ile	Leu	Pro	Leu	Leu	Tyr	Ala	Gln	Tyr	Ser	
			500					505					510			
Arg	Phe	Ser	Tyr	Leu	Val	Ser	Arg	Asp	Ala	Glu	Lys	Ala	Arg	Arg	Ile	
		515					520					525				
Ile	Val	Glu	Ala	Leu	Asp	His	Val	Gln	Pro	Ser	Lys	Pro	Leu	Met	Glu	
	530					535					540					
Ala	Leu	Ile	His	Phe	Glu	Ala	Ile	Gln	Pro	Pro	Pro	Arg	Glu	Ile	Asp	
545					550					555					560	
Tyr	Leu	Glu	Pro	Leu	Val	Glu	Lys	Val	Ile	Lys	Pro	Asp	Ala	Asp	Ala	

(2) INFORMATION FOR SEQ ID NO:21:

(A) LENGTH: 762 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..762

(D) OTHER INFORMATION: / Ceres Seq. ID 1497877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Val	Ser	Glu	Gly	Tyr	Thr	Ser	Ala	Pro	Tyr	Gly	Asp	Tyr	Asn	Ala
1				5					10					15	
Ser	Ala	Ala	Thr	Val	Glu	Ser	Thr	Gly	Gln	Glu	Thr	Ala	Pro	Ile	Val
			20					25					30		
Asp	Ala	Ser	His	Ser	Val	Asn	Asn	Asp	Ser	Leu	Val	Asn	Gly	Thr	Ala
		35					40					45			
Pro	Val	Glu	Asn	Gly	Ser	Ala	Thr	Asp	Asn	Val	Ala	Val	Thr	Ala	Pro
	50					55					60				
Ala	Ala	Glu	His	Gly	Asp	Asn	Thr	Gly	Ser	Thr	Leu	Ser	Thr	Glu	Glu
65				70						75				80	
Glu	Arg	Leu	Trp	Asn	Ile	Val	Arg	Ala	Asn	Ser	Leu	Glu	Phe	Asn	Ala
				85					90					95	
Trp	Thr	Ala	Leu	Ile	Asp	Glu	Thr	Glu	Arg	Ile	Ala	Gln	Asp	Asn	Ile
			100					105					110		
Ala	Lys	Ile	Arg	Lys	Val	Tyr	Asp	Ala	Phe	Leu	Ala	Glu	Phe	Pro	Leu
		115					120					125			
Cys	Tyr	Gly	Tyr	Trp	Lys	Lys	Phe	Ala	Asp	His	Glu	Ala	Arg	Val	Gly
	130					135					140				
Ala	Met	Asp	Lys	Val	Val	Glu	Val	Tyr	Glu	Arg	Ala	Val	Leu	Gly	Val
145				150						155				160	
Thr	Tyr	Ser	Val	Asp	Ile	Trp	Leu	His	Tyr	Cys	Thr	Phe	Ala	Ile	Asn
				165					170					175	

Thr	Tyr	Gly	Asp	Pro	Glu	Thr	Ile	Arg	Arg	Leu	Phe	Glu	Arg	Ala	Leu
			180					185					190		
Val	Tyr	Val	Gly	Thr	Asp	Phe	Leu	Ser	Ser	Pro	Leu	Trp	Asp	Lys	Tyr
		195					200					205			
Ile	Glu	Tyr	Glu	Tyr	Met	Gln	Gln	Asp	Trp	Ser	Arg	Val	Ala	Leu	Ile
	210					215					220				
Tyr	Thr	Arg	Ile	Leu	Glu	Asn	Pro	Ile	Gln	Asn	Leu	Asp	Arg	Tyr	Phe
225					230					235					240
Ser	Ser	Phe	Lys	Glu	Leu	Ala	Glu	Thr	Arg	Pro	Leu	Ser	Glu	Leu	Arg
				245					250					255	
Ser	Ala	Glu	Glu	Ser	Ala	Ala	Ala	Ala	Val	Ala	Val	Ala	Gly	Asp	Ala
			260					265					270		
Ser	Glu	Ser	Ala	Ala	Ser	Glu	Ser	Gly	Glu	Lys	Ala	Asp	Glu	Gly	Arg
		275					280					285			
Ser	Gln	Val	Asp	Gly	Ser	Thr	Glu	Gln	Ser	Pro	Lys	Leu	Glu	Ser	Ala
	290					295					300				
Ser	Ser	Thr	Glu	Pro	Glu	Glu	Leu	Lys	Lys	Tyr	Val	Gly	Ile	Arg	Glu
305					310					315					320
Ala	Met	Tyr	Ile	Lys	Ser	Lys	Glu	Phe	Glu	Ser	Lys	Ile	Ile	Gly	Tyr
				325					330					335	
Glu	Met	Ala	Ile	Arg	Arg	Pro	Tyr	Phe	His	Val	Arg	Pro	Leu	Asn	Val
			340					345					350		
Ala	Glu	Leu	Glu	Asn	Trp	His	Asn	Tyr	Leu	Asp	Phe	Ile	Glu	Arg	Asp
		355					360					365			
Gly	Asp	Phe	Asn	Lys	Val	Val	Lys	Leu	Tyr	Glu	Arg	Cys	Val	Val	Thr
	370					375					380				
Cys	Ala	Asn	Tyr	Pro	Glu	Tyr	Trp	Ile	Arg	Tyr	Val	Thr	Asn	Met	Glu
385					390					395					400
Ala	Ser	Gly	Ser	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Leu	Ala	Arg	Ala	Thr
				405					410					415	
Gln	Val	Phe	Val	Lys	Lys	Gln	Pro	Glu	Ile	His	Leu	Phe	Ala	Ala	Arg
			420					425					430		
Leu	Lys	Glu	Gln	Asn	Gly	Asp	Ile	Ala	Gly	Ala	Arg	Ala	Ala	Tyr	Gln
		435					440					445			
Leu	Val	His	Ser	Glu	Ile	Ser	Pro	Gly	Leu	Leu	Glu	Ala	Val	Ile	Lys
	450					455					460				
His	Ala	Asn	Met	Glu	Tyr	Arg	Leu	Gly	Asn	Leu	Asp	Asp	Ala	Phe	Ser
465					470					475					480
Leu	Tyr	Glu	Gln	Val	Ile	Ala	Val	Glu	Lys	Gly	Lys	Glu	His	Ser	Thr
				485					490					495	
Ile	Leu	Pro	Leu	Leu	Tyr	Ala	Gln	Tyr	Ser	Arg	Phe	Ser	Tyr	Leu	Val
			500					505					510		
Ser	Arg	Asp	Ala	Glu	Lys	Ala	Arg	Arg	Ile	Ile	Val	Glu	Ala	Leu	Asp
		515					520					525			
His	Val														

Ala	Gln	Ala	Ala	Pro	Ala	Gln	Pro	Gln	Gln	Trp	Asn	Pro	Ala	Tyr	Gly
		675					680					685			
Gln	Gln	Ala	Ala	Tyr	Gly	Ala	Tyr	Gly	Gly	Tyr	Pro	Ala	Gly	Tyr	Thr
		690					695				700				
Ala	Pro	Gln	Ala	Pro	Thr	Pro	Val	Pro	Gln	Ala	Ala	Ala	Tyr	Gly	Ala
705					710					715					720
Tyr	Pro	Ala	Gln	Thr	Tyr	Pro	Thr	Gln	Ser	Tyr	Ala	Pro	Pro	Val	Ala
				725					730					735	
Ala	Ala	Ala	Pro	Ala	Ala	Ala	Pro	Val	Gln	Gln	Pro	Ala	Ala	Ala	Val
			740					745				750			
Ala	Pro	Gln	Ala	Tyr	Tyr	Asn	Thr	Tyr	Tyr						
		755				760									

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..617
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Asp	Lys	Val	Val	Glu	Val	Tyr	Glu	Arg	Ala	Val	Leu	Gly	Val	Thr
1			5						10					15	
Tyr	Ser	Val	Asp	Ile	Trp	Leu	His	Tyr	Cys	Thr	Phe	Ala	Ile	Asn	Thr
			20					25					30		
Tyr	Gly	Asp	Pro	Glu	Thr	Ile	Arg	Arg	Leu	Phe	Glu	Arg	Ala	Leu	Val
		35					40				45				
Tyr	Val	Gly	Thr	Asp	Phe	Leu	Ser	Ser	Pro	Leu	Trp	Asp	Lys	Tyr	Ile
	50					55				60					
Glu	Tyr	Glu	Tyr	Met	Gln	Gln	Asp	Trp	Ser	Arg	Val	Ala	Leu	Ile	Tyr
65					70					75				80	
Thr	Arg	Ile	Leu	Glu	Asn	Pro	Ile	Gln	Asn	Leu	Asp	Arg	Tyr	Phe	Ser
			85					90					95		
Ser	Phe	Lys	Glu	Leu	Ala	Glu	Thr	Arg	Pro	Leu	Ser	Glu	Leu	Arg	Ser
		100						105				110			
Ala	Glu	Glu	Ser	Ala	Ala	Ala	Ala	Val	Ala	Val	Ala	Gly	Asp	Ala	Ser
		115					120					125			
Glu	Ser	Ala	Ala	Ser	Glu	Ser	Gly	Glu	Lys	Ala	Asp	Glu	Gly	Arg	Ser
		130				135					140				
Gln	Val	Asp	Gly	Ser	Thr	Glu	Gln	Ser	Pro	Lys	Leu	Glu	Ser	Ala	Ser
145					150					155					160
Ser	Thr	Glu	Pro	Glu	Glu	Leu	Lys	Lys	Tyr	Val	Gly	Ile	Arg	Glu	Ala
			165						170					175	
Met	Tyr	Ile	Lys	Ser	Lys	Glu	Phe	Glu	Ser	Lys	Ile	Ile	Gly	Tyr	Glu
		180						185					190		
Met	Ala	Ile	Arg	Arg	Pro	Tyr	Phe	His	Val	Arg	Pro	Leu	Asn	Val	Ala
		195					200					205			
Glu	Leu	Glu	Asn	Trp	His	Asn	Tyr	Leu	Asp	Phe	Ile	Glu	Arg	Asp	Gly
	210					215					220				
Asp	Phe	Asn	Lys	Val	Val	Lys	Leu	Tyr	Glu	Arg	Cys	Val	Val	Thr	Cys
225					230					235					240
Ala	Asn	Tyr	Pro	Glu	Tyr	Trp	Ile	Arg	Tyr	Val	Thr	Asn	Met	Glu	Ala
			245						250					255	
Ser	Gly	Ser	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Leu	Ala	Arg	Ala	Thr	Gln
		260					265					270			
Val	Phe	Val	Lys	Lys	Gln	Pro	Glu	Ile	His	Leu	Phe	Ala	Ala	Arg	Leu
		275					280					285			

```

Lys Glu Gln Asn Gly Asp Ile Ala Gly Ala Arg Ala Ala Tyr Gln Leu
290                               295                               300
Val His Ser Glu Ile Ser Pro Gly Leu Leu Glu Ala Val Ile Lys His
305                               310                               315                               320
Ala Asn Met Glu Tyr Arg Leu Gly Asn Leu Asp Asp Ala Phe Ser Leu
                               325                               330                               335
Tyr Glu Gln Val Ile Ala Val Glu Lys Gly Lys Glu His Ser Thr Ile
340                               345                               350
Leu Pro Leu Leu Tyr Ala Gln Tyr Ser Arg Phe Ser Tyr Leu Val Ser
355                               360                               365
Arg Asp Ala Glu Lys Ala Arg Arg Ile Ile Val Glu Ala Leu Asp His
370                               375                               380
Val Gln Pro Ser Lys Pro Leu Met Glu Ala Leu Ile His Phe Glu Ala
385                               390                               395                               400
Ile Gln Pro Pro Pro Arg Glu Ile Asp Tyr Leu Glu Pro Leu Val Glu
405                               410                               415
Lys Val Ile Lys Pro Asp Ala Asp Ala Gln Asn Ile Ala Ser Ser Thr
420                               425                               430
Glu Arg Glu Glu Leu Ser Leu Ile Tyr Ile Glu Phe Leu Gly Ile Phe
435                               440                               445
Gly Asp Val Lys Ser Ile Lys Lys Ala Glu Asp Gln His Val Lys Leu
450                               455                               460
Phe Tyr Pro His Arg Ser Thr Ser Glu Leu Lys Lys Arg Ser Ala Asp
465                               470                               475                               480
Asp Phe Leu Ala Ser Asp Arg Thr Lys Met Ala Lys Thr Tyr Asn Gly
485                               490                               495
Thr Pro Pro Ala Gln Pro Val Ser Asn Ala Tyr Pro Asn Ala Gln Ala
500                               505                               510
Gln Trp Ser Gly Gly Tyr Ala Ala Gln Pro Gln Thr Trp Pro Pro Ala
515                               520                               525
Gln Ala Ala Pro Ala Gln Pro Gln Gln Trp Asn Pro Ala Tyr Gly Gln
530                               535                               540
Gln Ala Ala Tyr Gly Ala Tyr Gly Gly Tyr Pro Ala Gly Tyr Thr Ala
545                               550                               555                               560
Pro Gln Ala Pro Thr Pro Val Pro Gln Ala Ala Tyr Gly Ala Tyr
565                               570                               575
Pro Ala Gln Thr Tyr Pro Thr Gln Ser Tyr Ala Pro Pro Val Ala Ala
580                               585                               590
Ala Ala Pro Ala Ala Ala Pro Val Gln Gln Pro Ala Ala Ala Val Ala
595                               600                               605
Pro Gln Ala Tyr Tyr Asn Thr Tyr Tyr
610                               615

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

caaaccaagt tttcttctaa gctgtatttg aaatgggata tatttcacac accaaacaga      60
tcagaagcta aaaggtaata atataatggc ggatttgagg gacgaaaaag gtaacccaat      120
ccatctaacc gacacacagg gaaacccaat tgctgacctg actgatgagc acggtaaccc      180
catgtacctt accggtgttg ttagctccac tctcagcat aaggagagta ctaccagcga      240
cattgcagag caccctacta gcaccgttgg agaaacacat ccggcagctg ctccaactgg      300
tgctgggtgct gccaccgctg ccactgcgac aggagtctct gctgggtactg gagcaaccac      360
cacagggcag caacaccatg ggctcgcttga agagcatctt cgtcgggtctg gaagttcatc      420

```

```
tagctctagc tcggaggatg acgggcaagg agggaggagg aagaagagca taaaggagaa      480
aattaaagag aagttcagta gcggcaaaca caaggacgaa caaacaccaa ccaccgccac      540
aacaacagga cctgccacta ccgaccaacc tcacgagaag aagggcattc tcgagaagat      600
caaggacaag cttcccggcc accataacca caaccaccca tgaacaccaa tcatatgacg      660
tctttgttac atgaataaat cgtttgcacg aatttcatta gggcttatga agaatacaata      720
tatatgtcta gtgaagttta ctaaatttta gttgtgtttg cttgcagttt gtgaatgtga      780
ccatcgtgtt atcatgttct tgttatttta taaagaagga actgtatttt gct
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1497884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Met Ala Asp Leu Arg Asp Glu Lys Gly Asn Pro Ile His Leu Thr Asp
1           5           10           15
Thr Gln Gly Asn Pro Ile Val Asp Leu Thr Asp Glu His Gly Asn Pro
20          25          30
Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser
35          40          45
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr
50          55          60
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Thr Ala Ala Thr
65          70          75          80
Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln
85          90          95
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser
100         105         110
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser
115         120         125
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp
130         135         140
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp
145         150         155         160
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu
165         170         175
Pro Gly His His Asn His Asn His Pro
180         185
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1497885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser
1           5           10           15
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr
20          25          30
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Ala Thr Ala Ala Thr
35          40          45
```

Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln  
50 55 60  
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser  
65 70 75 80  
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser  
85 90 95  
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp  
100 105 110  
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp  
115 120 125  
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu  
130 135 140  
Pro Gly His His Asn His Asn His Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

agtctagtca	tttctcagac	tctgacctca	ctgactctcca	atggcgaaaa	ccctagctcg	60
ctccacagcg	tcacgcatca	ccaagcgctt	attctccacc	tccggagcca	ccactccttc	120
cccttcttat	atcctctccc	gtcgatcaac	cccggtgttc	tcccatgccg	tcggattcat	180
ctcttctctg	aatcggttca	caacgattcg	aactcgaatg	gataggtccg	gtggatcgta	240
ctctcctcta	aaatccgggt	cgaatttcag	cgaccgagca	cccactgaga	tggcgccgtt	300
gtttcctggc	tgcgattatg	agcattgggt	gattgtaatg	gacaaacctg	gaggcgaaaa	360
cgctactaag	cagcaaataa	ttgattgtta	tgttcaaacc	ctagctaaaa	ttatcggcag	420
tgaggaagaa	gctaagaaga	agatttataa	tgtatcgtgt	gaaaggtatt	ttggatttgg	480
ttgtgagatt	gatgaagaga	catcaaacaa	acttgaagga	cttcctgggt	ttctcttcat	540
caatctcaca	accaaataca	aaaaactttt	ctcctccatc	aaaatcctcc	gacgatgaca	600
accatagctg	cagctggcct	caacgtcgcg	actccacgag	tggtcgttcg	acctgtggct	660
cgtgtattag	gtccgggtccg	gttgaattac	ccgtggaaat	tcggttcgat	gaagcggatg	720
gttgtgggta	aggctacatc	ggaaggagag	atatcgagaa	aggtggagaa	gagtatacaa	780
gaagctaagg	agacatgcgc	tgatgatccg	gtgagcgggg	agtgtgtagc	ggcttggggc	840
gaggtggagg	agctgagtg	ggcggcgagt	catgctaggg	acaagaagaa	agctggtggc	900
tccgatcctt	tggagagata	ttgcaatgat	aaycctgaga	ctgatgagtg	tcgtacttat	960
gataattaaa	aaatatgttt	ttgatgttcg	aattatgaaa	ctttaggtat	ggatcaatgt	1020
ttgttcttct	tgtcccttgt	tgttatgttt	gtgttttttg	tttggttgat	gattgtaatg	1080
tgataaatga	atatgaatag	tacaatacac	aacatatgtt	tc		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Ala Lys Thr Leu Ala Arg Ser Thr Ala Ser Arg Ile Thr Lys Arg  
1 5 10 15  
Leu Phe Ser Thr Ser Gly Ala Thr Thr Pro Ser Pro Ser Tyr Ile Leu  
20 25 30



Ser Arg Arg Ser Thr Pro Val Phe Ser His Ala Val Gly Phe Ile Ser  
35 40 45  
Ser Leu Asn Arg Phe Thr Thr Ile Arg Thr Arg Met Asp Arg Ser Gly  
50 55 60  
Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn Phe Ser Asp Arg Ala  
65 70 75 80  
Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys Asp Tyr Glu His Trp  
85 90 95  
Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn Ala Thr Lys Gln Gln  
100 105 110  
Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys Ile Ile Gly Ser Glu  
115 120 125  
Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser Cys Glu Arg Tyr Phe  
130 135 140  
Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser Asn Lys Leu Glu Gly  
145 150 155 160  
Leu Pro Gly Val Leu Phe Ile Asn Leu Thr Lys Ser Lys Lys Leu  
165 170 175  
Phe Ser Ser Ile Lys Ile Leu Arg Arg  
180 185

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Arg Ser Gly Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn  
1 5 10 15  
Phe Ser Asp Arg Ala Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys  
20 25 30  
Asp Tyr Glu His Trp Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn  
35 40 45  
Ala Thr Lys Gln Gln Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys  
50 55 60  
Ile Ile Gly Ser Glu Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser  
65 70 75 80  
Cys Glu Arg Tyr Phe Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser  
85 90 95  
Asn Lys Leu Glu Gly Leu Pro Gly Val Leu Phe Ile Asn Leu Thr Thr  
100 105 110  
Lys Ser Lys Lys Leu Phe Ser Ser Ile Lys Ile Leu Arg Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Thr Thr Ile Ala Ala Ala Gly Leu Asn Val Ala Thr Pro Arg Val

(2) INFORMATION FOR SEQ ID NO:30:

(A) LENGTH: 1025 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1025

(D) OTHER INFORMATION: / Ceres Seq. ID 1497890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

acccacc	aacttacttt	ctattcagac	aagacatttc	gatatgttat	ttctatggtc	60
tgatcacacg	atagtgtatt	ctgatatcat	cactctacca	aagagataacc	aaattatgga	120
aggagaatct	atcactttcc	ggtgaagata	aaccggagat	ccaatctcca	attccaccaa	180
atcagatctt	catactctct	ggacaaaagca	atatggccgg	acgcggcggc	gtcgtcaaag	240
atcaccacca	caatogctgg	gtctgggata	aaatcctccc	accggaatgc	gcaccaaact	300
catcgatcct	ccgcctgtcc	gcagatctcc	ggtgggaaga	agcacacgag	ccactacacg	360
ttgacattga	cacaggtaaa	gtgtgtggag	taggtccagg	aatggcggtc	gctaaccggg	420
tgaagaatcg	cgtgggaaca	gattccggctg	tgatcgggtt	ggtgccgtgc	gcttcgggtg	480
gaacggcgat	aaaagagtg	gagcgtggaa	gccacttgta	cgagaggatg	gtcaagagaa	540
cggaggagag	taggaaatgc	ggcggagaga	tcaaggcgg	gttgtggtat	caaggagaga	600
gtgacgtgtt	ggacatccat	gacgccgaga	gctacgggaa	caatatggat	cgtttgatta	660
agaacctccg	tcatgatctc	aaccttcctt	ctcttcccat	tattcagggtg	gcaatagcat	720
cgggaggagg	atacatagat	aagggtgagag	aagcacagtt	gggactgaaa	ctgtcgaatg	780
tggctctgtg	agatgctaag	ggattgccgc	taaagtccga	caatcttcac	ttaaccaccg	840
aggctcaagt	ccagcttggt	ctctccttag	cacaagctta	cctttccaac	tttgcttaga	900
caatcaagta	agttcgtgat	aaggttcatg	aatctttctg	aatgatgtg	gtggactagt	960
tatatggata	tcacaaaaact	ttgtaataat	ggattggtaa	aacattgatg	ttcatagtga	1020
aqaac						

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1497891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Ala	Gly	Arg	Gly	Gly	Val	Val	Lys	Asp	His	His	His	Asn	Arg	Trp
1				5					10					15	
Val	Trp	Asp	Lys	Ile	Leu	Pro	Pro	Glu	Cys	Ala	Pro	Asn	Ser	Ser	Ile
			20					25					30		

Leu Arg Leu Ser Ala Asp Leu Arg Trp Glu Glu Ala His Glu Pro Leu  
35 40 45  
His Val Asp Ile Asp Thr Gly Lys Val Cys Gly Val Gly Pro Gly Met  
50 55 60  
Ala Phe Ala Asn Ala Val Lys Asn Arg Val Glu Thr Asp Ser Ala Val  
65 70 75 80  
Ile Gly Leu Val Pro Cys Ala Ser Gly Gly Thr Ala Ile Lys Glu Trp  
85 90 95  
Glu Arg Gly Ser His Leu Tyr Glu Arg Met Val Lys Arg Thr Glu Glu  
100 105 110  
Ser Arg Lys Cys Gly Gly Glu Ile Lys Ala Val Leu Trp Tyr Gln Gly  
115 120 125  
Glu Ser Asp Val Leu Asp Ile His Asp Ala Glu Ser Tyr Gly Asn Asn  
130 135 140  
Met Asp Arg Leu Ile Lys Asn Leu Arg His Asp Leu Asn Leu Pro Ser  
145 150 155 160  
Leu Pro Ile Ile Gln Val Ala Ile Ala Ser Gly Gly Gly Tyr Ile Asp  
165 170 175  
Lys Val Arg Glu Ala Gln Leu Gly Leu Lys Leu Ser Asn Val Val Cys  
180 185 190  
Val Asp Ala Lys Gly Leu Pro Leu Lys Ser Asp Asn Leu His Leu Thr  
195 200 205  
Thr Glu Ala Gln Val Gln Leu Gly Leu Ser Leu Ala Gln Ala Tyr Leu  
210 215 220  
Ser Asn Phe Cys  
225

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Phe Ala Asn Ala Val Lys Asn Arg Val Glu Thr Asp Ser Ala  
1 5 10 15  
Val Ile Gly Leu Val Pro Cys Ala Ser Gly Gly Thr Ala Ile Lys Glu  
20 25 30  
Trp Glu Arg Gly Ser His Leu Tyr Glu Arg Met Val Lys Arg Thr Glu  
35 40 45  
Glu Ser Arg Lys Cys Gly Gly Glu Ile Lys Ala Val Leu Trp Tyr Gln  
50 55 60  
Gly Glu Ser Asp Val Leu Asp Ile His Asp Ala Glu Ser Tyr Gly Asn  
65 70 75 80  
Asn Met Asp Arg Leu Ile Lys Asn Leu Arg His Asp Leu Asn Leu Pro  
85 90 95  
Ser Leu Pro Ile Ile Gln Val Ala Ile Ala Ser Gly Gly Gly Tyr Ile  
100 105 110  
Asp Lys Val Arg Glu Ala Gln Leu Gly Leu Lys Leu Ser Asn Val Val  
115 120 125  
Cys Val Asp Ala Lys Gly Leu Pro Leu Lys Ser Asp Asn Leu His Leu  
130 135 140  
Thr Thr Glu Ala Gln Val Gln Leu Gly Leu Ser Leu Ala Gln Ala Tyr  
145 150 155 160  
Leu Ser Asn Phe Cys  
165

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 123 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..123  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497893  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  
Met Val Lys Arg Thr Glu Glu Ser Arg Lys Cys Gly Gly Glu Ile Lys  
1                    5                    10                    15  
Ala Val Leu Trp Tyr Gln Gly Glu Ser Asp Val Leu Asp Ile His Asp  
                    20                    25                    30  
Ala Glu Ser Tyr Gly Asn Asn Met Asp Arg Leu Ile Lys Asn Leu Arg  
                    35                    40                    45  
His Asp Leu Asn Leu Pro Ser Leu Pro Ile Ile Gln Val Ala Ile Ala  
                    50                    55                    60  
Ser Gly Gly Gly Tyr Ile Asp Lys Val Arg Glu Ala Gln Leu Gly Leu  
65                    70                    75                    80  
Lys Leu Ser Asn Val Val Cys Val Asp Ala Lys Gly Leu Pro Leu Lys  
                    85                    90                    95  
Ser Asp Asn Leu His Leu Thr Thr Glu Ala Gln Val Gln Leu Gly Leu  
                    100                    105                    110  
Ser Leu Ala Gln Ala Tyr Leu Ser Asn Phe Cys  
                    115                    120

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1166 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1166  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

atatatacaa cgaggaaaaa tagtactatt ttctacgaac ttcagaatct ttcgtctctc 60  
ttaattatatt ttctcaaatt tctcgaaaca tctagttttc ttttcaacca gccaatcatg 120  
ggtagtgatc atcatcatcg aaagctccac gttatgttct tccctttcat ggcttatggg 180  
cacatgatac caactctaga catggctaag cttttctcta gcagaggagc caaatccaca 240  
atcctcacca catctctcaa ctccaagatc ctccaaaaac ccatcgacac attcaagaat 300  
ctgaatccgg gtctcgaaat cgacatccag atcttcgatt tcccttgcggt ggagctgggg 360  
ttaccagaag gatgtgaaaa cgttgatttc ttcacttcaa acaacaatga tgataaaaaac 420  
gagatgatcg tgaaattctt tttctcgaca aggtttttca aagaccagct tgagaaactc 480  
ctcgggacaa cgagaccaga ctgtcttata gccgacatgt tcttcccctg ggctactgaa 540  
gctgctggga agttcaatgt gccaagactt gtgttccacg gcaactggcta cttctcttta 600  
tgcgctgggt attgcatcgg agtgcataaa ccacagaaga gagtggcttc aagctctgag 660  
ccatttgtga ttcccagact ccctgggaac attgtgataa ctgaagaaca gatcatagat 720  
ggcgatggag aatccgacat gggaaagttt atgactgaag ttagggaatc ggaagtgaag 780  
agctcaggag ttgttttgaa tagtttctac gagctagaac atgattacgc cgatttttac 840  
aaaagttgtg taaaaaagag agcgtggcat atcggtcgcg tatcggttta caacagggga 900  
tttgaggaga aggtgagag aggaaagaaa gcgaacattg atgasgctga atgcctcaaa 960  
tggttgact ccaagaaacc aaattcagtc atttatgttt cctttgggag cgtggctttc 1020  
ttcaagaatg aacagttatt cgagatcgct gcagggttag aagcttccgg tacaagtttc 1080  
atttgggttg ttaggaaaac caaaggtatt gaaattgacg tttgaagcct atattatata 1140  
actgtaattt gggtagcttt gatattt

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..374  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497895  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ile	Tyr	Thr	Thr	Arg	Lys	Asn	Ser	Thr	Ile	Phe	Tyr	Glu	Leu	Gln	Asn
1				5					10					15	
Leu	Ser	Ser	Leu	Leu	Ile	Ile	Phe	Leu	Lys	Phe	Leu	Glu	Thr	Ser	Ser
			20					25					30		
Phe	Leu	Phe	Asn	Gln	Pro	Ile	Met	Gly	Ser	Asp	His	His	His	Arg	Lys
		35					40					45			
Leu	His	Val	Met	Phe	Phe	Pro	Phe	Met	Ala	Tyr	Gly	His	Met	Ile	Pro
	50					55					60				
Thr	Leu	Asp	Met	Ala	Lys	Leu	Phe	Ser	Ser	Arg	Gly	Ala	Lys	Ser	Thr
65					70					75					80
Ile	Leu	Thr	Thr	Ser	Leu	Asn	Ser	Lys	Ile	Leu	Gln	Lys	Pro	Ile	Asp
				85					90					95	
Thr	Phe	Lys	Asn	Leu	Asn	Pro	Gly	Leu	Glu	Ile	Asp	Ile	Gln	Ile	Phe
			100					105					110		
Asp	Phe	Pro	Cys	Val	Glu	Leu	Gly	Leu	Pro	Glu	Gly	Cys	Glu	Asn	Val
	115						120					125			
Asp	Phe	Phe	Thr	Ser	Asn	Asn	Asp	Asp	Lys	Asn	Glu	Met	Ile	Val	
	130					135				140					
Lys	Phe	Phe	Phe	Ser	Thr	Arg	Phe	Phe	Lys	Asp	Gln	Leu	Glu	Lys	Leu
145					150					155					160
Leu	Gly	Thr	Thr	Arg	Pro	Asp	Cys	Leu	Ile	Ala	Asp	Met	Phe	Phe	Pro
				165					170					175	
Trp	Ala	Thr	Glu	Ala	Ala	Gly	Lys	Phe	Asn	Val	Pro	Arg	Leu	Val	Phe
			180					185					190		
His	Gly	Thr	Gly	Tyr	Phe	Ser	Leu	Cys	Ala	Gly	Tyr	Cys	Ile	Gly	Val
	195						200					205			
His	Lys	Pro	Gln	Lys	Arg	Val	Ala	Ser	Ser	Ser	Glu	Pro	Phe	Val	Ile
	210					215					220				
Pro	Glu	Leu	Pro	Gly	Asn	Ile	Val	Ile	Thr	Glu	Glu	Gln	Ile	Ile	Asp
225					230					235					240
Gly	Asp	Gly	Glu	Ser	Asp	Met	Gly	Lys	Phe	Met	Thr	Glu	Val	Arg	Glu
				245					250					255	
Ser	Glu	Val	Lys	Ser	Ser	Gly	Val	Val	Leu	Asn	Ser	Phe	Tyr	Glu	Leu
		260						265					270		
Glu	His	Asp	Tyr	Ala	Asp	Phe	Tyr	Lys	Ser	Cys	Val	Gln	Lys	Arg	Ala
	275						280					285			
Trp	His	Ile	Gly	Pro	Leu	Ser	Val	Tyr	Asn	Arg	Gly	Phe	Glu	Glu	Lys
	290					295					300				
Ala	Glu	Arg	Gly	Lys	Lys	Ala	Asn	Ile	Asp	Xaa	Ala	Glu	Cys	Leu	Lys
305					310					315					320
Trp	Leu	Asp	Ser	Lys	Lys	Pro	Asn	Ser	Val	Ile	Tyr	Val	Ser	Phe	Gly
				325					330					335	
Ser	Val	Ala	Phe	Phe	Lys	Asn	Glu	Gln	Leu	Phe	Glu	Ile	Ala	Ala	Gly
			340					345					350		
Leu	Glu	Ala	Ser	Gly	Thr	Ser	Phe	Ile	Trp	Val	Val	Arg	Lys	Thr	Lys
		355					360					365			
Gly	Ile	Glu	Ile	Asp	Val										
	370														

(2) INFORMATION FOR SEQ ID NO:36:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..335  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Gly	Ser	Asp	His	His	His	Arg	Lys	Leu	His	Val	Met	Phe	Phe	Pro
1				5					10					15	
Phe	Met	Ala	Tyr	Gly	His	Met	Ile	Pro	Thr	Leu	Asp	Met	Ala	Lys	Leu
			20					25					30		
Phe	Ser	Ser	Arg	Gly	Ala	Lys	Ser	Thr	Ile	Leu	Thr	Thr	Ser	Leu	Asn
		35					40					45			
Ser	Lys	Ile	Leu	Gln	Lys	Pro	Ile	Asp	Thr	Phe	Lys	Asn	Leu	Asn	Pro
	50					55					60				
Gly	Leu	Glu	Ile	Asp	Ile	Gln	Ile	Phe	Asp	Phe	Pro	Cys	Val	Glu	Leu
65					70					75					80
Gly	Leu	Pro	Glu	Gly	Cys	Glu	Asn	Val	Asp	Phe	Phe	Thr	Ser	Asn	Asn
			85						90					95	
Asn	Asp	Asp	Lys	Asn	Glu	Met	Ile	Val	Lys	Phe	Phe	Phe	Ser	Thr	Arg
			100					105						110	
Phe	Phe	Lys	Asp	Gln	Leu	Glu	Lys	Leu	Leu	Gly	Thr	Thr	Arg	Pro	Asp
		115					120					125			
Cys	Leu	Ile	Ala	Asp	Met	Phe	Phe	Pro	Trp	Ala	Thr	Glu	Ala	Ala	Gly
	130					135					140				
Lys	Phe	Asn	Val	Pro	Arg	Leu	Val	Phe	His	Gly	Thr	Gly	Tyr	Phe	Ser
145					150					155					160
Leu	Cys	Ala	Gly	Tyr	Cys	Ile	Gly	Val	His	Lys	Pro	Gln	Lys	Arg	Val
			165						170					175	
Ala	Ser	Ser	Ser	Glu	Pro	Phe	Val	Ile	Pro	Glu	Leu	Pro	Gly	Asn	Ile
			180					185					190		
Val	Ile	Thr	Glu	Glu	Gln	Ile	Ile	Asp	Gly	Asp	Gly	Glu	Ser	Asp	Met
	195						200					205			
Gly	Lys	Phe	Met	Thr	Glu	Val	Arg	Glu	Ser	Glu	Val	Lys	Ser	Ser	Gly
	210					215					220				
Val	Val	Leu	Asn	Ser	Phe	Tyr	Glu	Leu	Glu	His	Asp	Tyr	Ala	Asp	Phe
225					230					235					240
Tyr	Lys	Ser	Cys	Val	Gln	Lys	Arg	Ala	Trp	His	Ile	Gly	Pro	Leu	Ser
			245					250						255	
Val	Tyr	Asn	Arg	Gly	Phe	Glu	Glu	Lys	Ala	Glu	Arg	Gly	Lys	Lys	Ala
		260						265					270		
Asn	Ile	Asp	Xaa	Ala	Glu	Cys	Leu	Lys	Trp	Leu	Asp	Ser	Lys	Lys	Pro
	275						280					285			
Asn	Ser	Val	Ile	Tyr	Val	Ser	Phe	Gly	Ser	Val	Ala	Phe	Phe	Lys	Asn
	290					295					300				
Glu	Gln	Leu	Phe	Glu	Ile	Ala	Ala	Gly	Leu	Glu	Ala	Ser	Gly	Thr	Ser
305					310					315					320
Phe	Ile	Trp	Val	Val	Arg	Lys	Thr	Lys	Gly	Ile	Glu	Ile	Asp	Val	
			325						330					335	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1497897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Phe Phe Pro Phe Met Ala Tyr Gly His Met Ile Pro Thr Leu Asp  
1 5 10 15  
Met Ala Lys Leu Phe Ser Ser Arg Gly Ala Lys Ser Thr Ile Leu Thr  
20 25 30  
Thr Ser Leu Asn Ser Lys Ile Leu Gln Lys Pro Ile Asp Thr Phe Lys  
35 40 45  
Asn Leu Asn Pro Gly Leu Glu Ile Asp Ile Gln Ile Phe Asp Phe Pro  
50 55 60  
Cys Val Glu Leu Gly Leu Pro Glu Gly Cys Glu Asn Val Asp Phe Phe  
65 70 75 80  
Thr Ser Asn Asn Asn Asp Asp Lys Asn Glu Met Ile Val Lys Phe Phe  
85 90 95  
Phe Ser Thr Arg Phe Phe Lys Asp Gln Leu Glu Lys Leu Leu Gly Thr  
100 105 110  
Thr Arg Pro Asp Cys Leu Ile Ala Asp Met Phe Phe Pro Trp Ala Thr  
115 120 125  
Glu Ala Ala Gly Lys Phe Asn Val Pro Arg Leu Val Phe His Gly Thr  
130 135 140  
Gly Tyr Phe Ser Leu Cys Ala Gly Tyr Cys Ile Gly Val His Lys Pro  
145 150 155 160  
Gln Lys Arg Val Ala Ser Ser Ser Glu Pro Phe Val Ile Pro Glu Leu  
165 170 175  
Pro Gly Asn Ile Val Ile Thr Glu Glu Gln Ile Ile Asp Gly Asp Gly  
180 185 190  
Glu Ser Asp Met Gly Lys Phe Met Thr Glu Val Arg Glu Ser Glu Val  
195 200 205  
Lys Ser Ser Gly Val Val Leu Asn Ser Phe Tyr Glu Leu Glu His Asp  
210 215 220  
Tyr Ala Asp Phe Tyr Lys Ser Cys Val Gln Lys Arg Ala Trp His Ile  
225 230 235 240  
Gly Pro Leu Ser Val Tyr Asn Arg Gly Phe Glu Glu Lys Ala Glu Arg  
245 250 255  
Gly Lys Lys Ala Asn Ile Asp Xaa Ala Glu Cys Leu Lys Trp Leu Asp  
260 265 270  
Ser Lys Lys Pro Asn Ser Val Ile Tyr Val Ser Phe Gly Ser Val Ala  
275 280 285  
Phe Phe Lys Asn Glu Gln Leu Phe Glu Ile Ala Ala Gly Leu Glu Ala  
290 295 300  
Ser Gly Thr Ser Phe Ile Trp Val Val Arg Lys Thr Lys Gly Ile Glu  
305 310 315 320  
Ile Asp Val

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..584

(D) OTHER INFORMATION: / Ceres Seq. ID 1497898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

aagtgattaa gcttatgcag agtttcaa	ccaaggagta tgtagggag acaattgcct	60
ggatgcatta ctattgggtt ttgaccaatg	aagggatoga gttcttgaga acttatctta	120
atcttccatc tgatgttggt cctgctactt	tgaagaagtc agctaagcct ggtggtcgtc	180
catttggttg cccacctggt gatcgctcaa	gaggacctcg ccatgaagga ggagaccgtc	240
ccaggttttg tgacctgat ggtaccgtg	caggtcctcg agctggtggt gagtttgga	300

```
gtgaaaaggg tggagctcct gcagattacc agccatcttt ccaaggaagt gggcgtggtt      360
ttggccgtgg tgctggtggc tacagcgagc ctgcaccatc tggttcaggt ttgccttgaa      420
aaagaaatgt ctttaggtga cagtaagacc atggaggagt tttcagcttt aaattttgct      480
tttgaatttc agattccgga atccttcata atctctatct gagtttagtt ttgttgttga      540
atcaaacatc cgatttaaag ttatgttcat tccatcttct cttc
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1497899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
Val Ile Lys Leu Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu
1          5          10          15
Thr Ile Ala Trp Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile
20        25        30
Glu Phe Leu Arg Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala
35        40        45
Thr Leu Lys Lys Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro
50        55        60
Pro Gly Asp Arg Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro
65        70        75        80
Arg Phe Gly Asp Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Gly
85        90        95
Glu Phe Gly Gly Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser
100       105       110
Phe Gln Gly Ser Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser
115       120       125
Ala Ala Ala Pro Ser Gly Ser Gly Leu Pro
130       135
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1497900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Ile Ala Trp
1          5          10          15
Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg
20        25        30
Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys
35        40        45
Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg
50        55        60
Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp
65        70        75        80
Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Gly Glu Phe Gly Gly
85        90        95
Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser
100       105       110
```



Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro  
115 120 125  
Ser Gly Ser Gly Leu Pro  
130

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1497901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg  
1 5 10 15  
Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys  
20 25 30  
Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg  
35 40 45  
Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp  
50 55 60  
Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Gly Glu Phe Gly Gly  
65 70 75 80  
Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser  
85 90 95  
Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro  
100 105 110  
Ser Gly Ser Gly Leu Pro  
115

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1128

(D) OTHER INFORMATION: / Ceres Seq. ID 1497902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

acatccttag	tttttctaaa	ccacaaaata	aaaactttcg	ttcatgaaat	cttatggtaa	60
gttttgagag	aaatatccga	gtattgcttc	agtcgtagc	atacgaatca	agcgagacga	120
tggtgcagcc	tggaaccgag	ataaaagcaa	gcgacctaac	cctactagta	atcacgatta	180
tactcttcgc	aatcttcata	gttggttg	smttcggtt	gcttcgctg	gacctctcgc	240
caattttact	cacaagaatc	catcaaccct	ttcactgact	ccgacgttga	atcccgtacg	300
agtattacgg	cggtgcgtgg	gctcgacgag	gctatcatca	actcatttcc	gacgtttctc	360
tactcggagg	tgaaggagcg	gagaatcggg	ataggtggcg	tcgagtgtgc	agtgtgtatc	420
tgtgagttcg	aagaccatga	aacgctccgt	ttgatgcctg	aatgctgcc	cgtgtttcat	480
gctgattgtg	taagtgtctg	gctctctgat	cactccacgt	gtccactctg	tcgtgtggat	540
ctttgcttac	aaccgggtga	gagaagctac	ttgaatccgg	aaccggatct	tgtagaatct	600
acaaactcgc	atttgtttga	tggtgtgacg	tggaccaata	ggaacagacc	gtctcgggtca	660
tggtcaacga	gattgtctca	atgtcgagtc	tcccagatat	taatctcgag	atcgcatctg	720
accggacatt	ctgtggttca	accgctagat	aatttagacc	ggtttacgct	tcggttacca	780
gaagaagtcc	ggaggcaact	gacgaagaaa	acggtggaca	acgtggcatt	ttctcaggct	840
aggagctcac	ggcgtggtta	cagaagcaga	agtcccgaa	gcgagaggag	tgtcttctcg	900
taccaacggc	ggatgcattc	cttctctgat	tgtgcatggt	ccacctcctg	tggcggagaa	960
gcggtggctc	cgtcaaagga	ttttcgccga	atatcagttg	aacaatcyca	gntagatgat	1020

cgagtgtagt agataggcaa ttttcttggt gtgtgttttn tgctaacaac atttgtgttt 1080  
gtctgtttgc tatcatttgc ttttogaaca tgaccaatat tcaagtcc

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Pro	Glu	Cys	Cys	His	Val	Phe	His	Ala	Asp	Cys	Val	Ser	Val	Trp
1				5					10					15	
Leu	Ser	Asp	His	Ser	Thr	Cys	Pro	Leu	Cys	Arg	Val	Asp	Leu	Cys	Leu
			20					25					30		
Gln	Pro	Gly	Glu	Arg	Ser	Tyr	Leu	Asn	Pro	Glu	Pro	Asp	Leu	Val	Glu
		35					40					45			
Ser	Thr	Asn	Ser	His	Leu	Phe	Asp	Gly	Val	Thr	Trp	Thr	Asn	Arg	Asn
	50					55					60				
Arg	Pro	Ser	Arg	Ser	Trp	Ser	Thr	Arg	Leu	Ser	Gln	Cys	Arg	Val	Ser
65					70				75					80	
Gln	Ile	Leu	Ile	Ser	Arg	Ser	His	Ser	Thr	Gly	His	Ser	Val	Val	Gln
				85					90					95	
Pro	Leu	Asp	Asn	Leu	Asp	Arg	Phe	Thr	Leu	Arg	Leu	Pro	Glu	Glu	Val
			100						105				110		
Arg	Arg	Gln	Leu	Thr	Lys	Lys	Thr	Val	Asp	Asn	Val	Ala	Phe	Ser	Gln
		115					120					125			
Ala	Arg	Ser	Ser	Arg	Arg	Gly	Tyr	Arg	Ser	Arg	Ser	Ala	Gly	Ser	Glu
	130					135					140				
Arg	Ser	Val	Phe	Ser	Tyr	Gln	Arg	Arg	Met	His	Ser	Phe	Ser	Asp	Cys
145					150				155					160	
Ala	Trp	Ser	Thr	Ser	Cys	Gly	Gly	Glu	Ala	Val	Ala	Pro	Ser	Lys	Asp
				165					170					175	
Phe	Arg	Arg	Ile	Ser	Val	Glu	Gln	Xaa	Gln	Xaa	Asp	Asp	Arg	Val	
			180				185						190		

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ataacgaagc	ggttggaaga	agatgaaact	gttcgacgog	cactgtcacc	ttcaagaccc	60
gaggattatc	accaaagctc	ctcagataat	cacctccgcc	gttgcttccg	gcgtctctgc	120
tttcgccgtc	aatggagtct	ccgagaaaga	ttggagtttg	gtcaaagaga	tgggagctaa	180
atacccttct	gttgctcctt	gctttgggat	ccatccatgg	tatgtagcag	agaggagtcc	240
tcaatgggtt	gagacataag	agtttctttg	agaccactcc	tactgctgct	gttgagaaaa	300
ttggtttgga	caaagggctc	aaggggaagg	agattgattt	ctcagaacag	gttaccgtct	360
ttcgtcaaca	gcttgaactt	gcaaaggaat	tgaagaaacc	tgcgtcagtt	cattgtgttc	420
gtgcatttgg	ggatctactc	gagatattaa	aatctgtagg	gccttttctt	tctgggggtca	480
tgcttcactc	gtatttgggt	tytgctgaga	tggttcctga	atttgctaag	ctcgggtgcat	540
atttctcctt	ctccggtttc	cttatgtcca	tgagtgaagaa	aaaagccaag	aagatgttga	600
aagcagttcc	atctgatagg	atcttatttg	agacggattc	accagatgca	ctaccaaagg	660

cagagtcagg	ttgtctctac	tttgtagacg	gagatccttc	tctacccgaa	gaaggaaatt	720
cagctcagga	tottgattct	gcttcatatg	ataagcctaa	tgtgtctagt	gactcgatga	780
agttaacaaa	ggaaacactt	aatcacccgg	ctaataattca	tatcgtactc	ggatatgtag	840
cgcagttggt	ggatatgaag	aatgaagaac	tcgcggaact	aagttatcaa	aatgctgttc	900
ggttattctc	ttacgaaggt	tcaaagatac	ttcttgacag	aggtactggg	gatgtctctg	960
gtcacactca	aaaccagtca	acaacacatg	tatcatgagt	tcttacttct	taagaaatcg	1020
tagtgtttct	catcactcta	ttacgagtc	ttgaatttgg	actctctctt	tttttttctt	1080
ttttttttga	atgtttgaat	ttggaattat	tgtactagt	ttatagacaa	tcacactttt	1140
ctttgtacaa	actacaaagg	ttctgatttt	gtgtgaaaat	taattcagtt	aatgatgtga	1200
ttagagcc						

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Leu	His	Ser	Tyr	Leu	Gly	Xaa	Ala	Glu	Met	Val	Pro	Glu	Phe	Ala	
1				5					10					15		
Lys	Leu	Gly	Ala	Tyr	Phe	Ser	Phe	Ser	Gly	Phe	Leu	Met	Ser	Met	Ser	
			20					25					30			
Glu	Lys	Lys	Ala	Lys	Lys	Met	Leu	Lys	Ala	Val	Pro	Ser	Asp	Arg	Ile	
		35					40					45				
Leu	Leu	Glu	Thr	Asp	Ser	Pro	Asp	Ala	Leu	Pro	Lys	Ala	Glu	Ser	Gly	
		50					55				60					
Cys	Leu	Tyr	Phe	Val	Asp	Gly	Asp	Pro	Ser	Leu	Pro	Glu	Glu	Gly	Asn	
65					70					75				80		
Ser	Ala	Gln	Asp	Leu	Asp	Ser	Ala	Ser	Tyr	Asp	Lys	Pro	Asn	Val	Ser	
			85						90					95		
Ser	Asp	Ser	Met	Lys	Leu	Thr	Lys	Glu	Thr	Leu	Asn	His	Pro	Ala	Asn	
			100					105					110			
Ile	His	Ile	Val	Leu	Gly	Tyr	Val	Ala	Gln	Leu	Leu	Asp	Met	Lys	Asn	
		115					120					125				
Glu	Glu	Leu	Ala	Glu	Leu	Ser	Tyr	Gln	Asn	Ala	Val	Arg	Leu	Phe	Ser	
		130				135					140					
Tyr	Glu	Gly	Ser	Lys	Ile	Leu	Leu	Asp	Arg	Gly	Thr	Gly	Asp	Val	Ser	
145					150					155				160		
Gly	His	Thr	Gln	Asn	Gln	Ser	Thr	Thr	His	Val	Ser					
			165					170								

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Val	Pro	Glu	Phe	Ala	Lys	Leu	Gly	Ala	Tyr	Phe	Ser	Phe	Ser	Gly	
1				5					10					15		
Phe	Leu	Met	Ser	Met	Ser	Glu	Lys	Lys	Ala	Lys	Lys	Met	Leu	Lys	Ala	
			20					25					30			
Val	Pro	Ser	Asp	Arg	Ile	Leu	Leu	Glu	Thr	Asp	Ser	Pro	Asp	Ala	Leu	

35	40	45
Pro Lys Ala Glu Ser Gly Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser		
50	55	60
Leu Pro Glu Glu Gly Asn Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr		
65	70	75
Asp Lys Pro Asn Val Ser Ser Asp Ser Met Lys Leu Thr Lys Glu Thr		
85	90	95
Leu Asn His Pro Ala Asn Ile His Ile Val Leu Gly Tyr Val Ala Gln		
100	105	110
Leu Leu Asp Met Lys Asn Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn		
115	120	125
Ala Val Arg Leu Phe Ser Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg		
130	135	140
Gly Thr Gly Asp Val Ser Gly His Thr Gln Asn Gln Ser Thr Thr His		
145	150	155
Val Ser		160

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1497907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ser Met Ser Glu Lys Lys Ala Lys Lys Met Leu Lys Ala Val Pro		
1	5	10
Ser Asp Arg Ile Leu Leu Glu Thr Asp Ser Pro Asp Ala Leu Pro Lys		
20	25	30
Ala Glu Ser Gly Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser Leu Pro		
35	40	45
Glu Glu Gly Asn Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr Asp Lys		
50	55	60
Pro Asn Val Ser Ser Asp Ser Met Lys Leu Thr Lys Glu Thr Leu Asn		
65	70	75
His Pro Ala Asn Ile His Ile Val Leu Gly Tyr Val Ala Gln Leu Leu		
85	90	95
Asp Met Lys Asn Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn Ala Val		
100	105	110
Arg Leu Phe Ser Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg Gly Thr		
115	120	125
Gly Asp Val Ser Gly His Thr Gln Asn Gln Ser Thr Thr His Val Ser		
130	135	140

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..765

(D) OTHER INFORMATION: / Ceres Seq. ID 1497908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

gttcgattga	tgaacagact	cttactgctt	ctaaaccggg	aaccgggtgtg	gttattgctg	60
tcaaaaaaact	taaccaagat	ggttggcaag	gtcaccagga	atggctggcg	gaagtgaatt	120
acttggggca	gttttcgcat	cctaactctt	tgaaaactgat	tggttattgc	ttagaggatg	180
agcatcgctc	tcttgtttat	gagttcatgc	ctcgtggaag	cttagagaat	catttgttca	240
gaagagggttc	ttattttcaa	cctttatctt	ggactctccg	gttgaaagtt	gctcctgggtg	300
cagcgaaagg	tcttgcggtt	cttcataacg	ccgagactag	tgatcatata	cgcgatttca	360
aaacgtcgaa	tatactgctt	gattcggagt	acaatgctaa	gctttctgat	ttcgggctag	420
ctaaagacgg	tccaacgggt	gataaaagcc	atgtctctac	gcggatcatg	ggtacttacg	480
gatacgcagc	tcctgaatat	cttgcaactg	gtcatttaac	aacccaaaagt	gatgtctata	540
gctacgggtg	tgtgcttttg	gaggtgttgt	ctggacggag	agctgtagac	aagaaccgtc	600
caccaggaga	gcaaaagcta	gtggaatggg	caagaccgtt	acttgctaac	aaaaggraag	660
ttattccgag	ttatcgataa	ccgtctacaa	gatcaatact	caatggaaga	agcttgtaag	720
tagctactct	tgcgctgaga	tgcttcacat	tcgagataag	ctgag		

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1497909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser	Ile	Asp	Glu	Gln	Thr	Leu	Thr	Ala	Ser	Lys	Pro	Gly	Thr	Gly	Val
1			5						10					15	
Val	Ile	Ala	Val	Lys	Lys	Leu	Asn	Gln	Asp	Gly	Trp	Gln	Gly	His	Gln
			20					25					30		
Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr	Leu	Gly	Gln	Phe	Ser	His	Pro	Asn
			35				40					45			
Leu	Val	Lys	Leu	Ile	Gly	Tyr	Cys	Leu	Glu	Asp	Glu	His	Arg	Leu	Leu
			50			55				60					
Val	Tyr	Glu	Phe	Met	Pro	Arg	Gly	Ser	Leu	Glu	Asn	His	Leu	Phe	Arg
65					70				75					80	
Arg	Gly	Ser	Tyr	Phe	Gln	Pro	Leu	Ser	Trp	Thr	Leu	Arg	Leu	Lys	Val
			85					90					95		
Ala	Leu	Gly	Ala	Ala	Lys	Gly	Leu	Ala	Phe	Leu	His	Asn	Ala	Glu	Thr
			100					105					110		
Ser	Val	Ile	Tyr	Arg	Asp	Phe	Lys	Thr	Ser	Asn	Ile	Leu	Leu	Asp	Ser
			115				120					125			
Glu	Tyr	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Gly	Pro
			130			135				140					
Thr	Gly	Asp	Lys	Ser	His	Val	Ser	Thr	Arg	Ile	Met	Gly	Thr	Tyr	Gly
145					150				155					160	
Tyr	Ala	Ala	Pro	Glu	Tyr	Leu	Ala	Thr	Gly	His	Leu	Thr	Thr	Lys	Ser
			165					170					175		
Asp	Val	Tyr	Ser	Tyr	Gly	Val	Val	Leu	Leu	Glu	Val	Leu	Ser	Gly	Arg
			180					185					190		
Arg	Ala	Val	Asp	Lys	Asn	Arg	Pro	Pro	Gly	Glu	Gln	Lys	Leu	Val	Glu
		195					200					205			
Trp	Ala	Arg	Pro	Leu	Leu	Ala	Asn	Lys	Arg	Xaa	Val	Ile	Pro	Ser	Tyr
		210				215					220				
Arg															
225															

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1497910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Pro	Arg	Gly	Ser	Leu	Glu	Asn	His	Leu	Phe	Arg	Arg	Gly	Ser	Tyr
1				5					10					15	
Phe	Gln	Pro	Leu	Ser	Trp	Thr	Leu	Arg	Leu	Lys	Val	Ala	Leu	Gly	Ala
			20					25					30		
Ala	Lys	Gly	Leu	Ala	Phe	Leu	His	Asn	Ala	Glu	Thr	Ser	Val	Ile	Tyr
		35					40					45			
Arg	Asp	Phe	Lys	Thr	Ser	Asn	Ile	Leu	Leu	Asp	Ser	Glu	Tyr	Asn	Ala
	50					55					60				
Lys	Leu	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Gly	Pro	Thr	Gly	Asp	Lys
65					70					75				80	
Ser	His	Val	Ser	Thr	Arg	Ile	Met	Gly	Thr	Tyr	Gly	Tyr	Ala	Ala	Pro
			85						90					95	
Glu	Tyr	Leu	Ala	Thr	Gly	His	Leu	Thr	Lys	Ser	Asp	Val	Tyr	Ser	
		100						105				110			
Tyr	Gly	Val	Val	Leu	Leu	Glu	Val	Leu	Ser	Gly	Arg	Arg	Ala	Val	Asp
		115					120					125			
Lys	Asn	Arg	Pro	Pro	Gly	Glu	Gln	Lys	Leu	Val	Glu	Trp	Ala	Arg	Pro
	130					135					140				
Leu	Leu	Ala	Asn	Lys	Arg	Xaa	Val	Ile	Pro	Ser	Tyr	Arg			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..888

(D) OTHER INFORMATION: / Ceres Seq. ID 1497911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

atccttataa	cctttcttct	cctcttctcc	ttcttctctt	tatgcaaaca	tatatttaca	60
taaacacaca	catatatata	gtaagagaga	gagagagaga	tctagcaaga	tagtgaaagc	120
ttcataatca	atggaagggg	ttgacaacac	aaatcctatg	ttaaccctag	aagaaggcga	180
aaacaacaat	cctttttctt	ccttagatga	caaaacatta	atgatgatgg	ctccttcggt	240
aatcttttcg	ggcgatgtag	gtccatcttc	ttcttcttgt	actccagcag	gttatcatct	300
atctgctcag	ctggagaact	ttcgaggagg	tggaggagag	atggcaggat	tagtgagtaa	360
taatagcaat	aatagtgatc	ataataagaa	ttgcaacaaa	ggaaaaggga	agagaacttc	420
ggcaatgcag	aggatagcct	tccatacaag	gagtgatgat	gatgttcttg	atgatggtta	480
tcgttggcga	aagtaagggt	agaaatctgt	caagaacaat	gctcatccca	ggagctatta	540
tagatgtaca	taccacacat	gcaacgtgaa	gaaacaagtg	caaagactgg	caaaagatcc	600
aaacgttgtc	gtaacaacct	acgaagggtg	tcataatcat	ccttgtgaga	agctcatgga	660
gactcttagc	cctctcctta	agcaacttca	gttctctctc	agagtttctg	atctgtaatt	720
attgaatggt	aattagtggg	gtaatacatt	aattatgctt	taatctctcc	attgaccctc	780
aatctccaaa	gagacaaatg	tatagaataa	atctcataac	atacatgctt	taggtttatt	840
gagacattga	tctatgtttt	gctttaattt	gattcgtcta	attgtccc		

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..195  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu Gly  
1 5 10 15  
Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met Met  
20 25 30  
Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser Ser  
35 40 45  
Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn Phe  
50 55 60  
Arg Gly Gly Gly Gly Glu Met Ala Gly Leu Val Ser Asn Asn Ser Asn  
65 70 75 80  
Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg Thr  
85 90 95  
Ser Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Val  
100 105 110  
Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys  
115 120 125  
Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys  
130 135 140  
Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val  
145 150 155 160  
Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met  
165 170 175  
Glu Thr Leu Ser Pro Leu Leu Lys Gln Leu Gln Phe Leu Ser Arg Val  
180 185 190  
Ser Asp Leu  
195

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..186  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Leu Thr Leu Glu Glu Gly Glu Asn Asn Pro Phe Ser Ser Leu  
1 5 10 15  
Asp Asp Lys Thr Leu Met Met Met Ala Pro Ser Leu Ile Phe Ser Gly  
20 25 30  
Asp Val Gly Pro Ser Ser Ser Ser Cys Thr Pro Ala Gly Tyr His Leu  
35 40 45  
Ser Ala Gln Leu Glu Asn Phe Arg Gly Gly Gly Gly Glu Met Ala Gly  
50 55 60  
Leu Val Ser Asn Asn Ser Asn Asn Ser Asp His Asn Lys Asn Cys Asn  
65 70 75 80  
Lys Gly Lys Gly Lys Arg Thr Ser Ala Met Gln Arg Ile Ala Phe His  
85 90 95  
Thr Arg Ser Asp Asp Asp Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys  
100 105 110  
Tyr Gly Gln Lys Ser Val Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr  
115 120 125  
Arg Cys Thr Tyr His Thr Cys Asn Val Lys Lys Gln Val Gln Arg Leu  
130 135 140  
Ala Lys Asp Pro Asn Val Val Val Thr Thr Tyr Glu Gly Val His Asn

(2) INFORMATION FOR SEQ ID NO:54:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1497914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1257

(D) OTHER INFORMATION: / Ceres Seq. ID 1497917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

(X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER						
aaagaaactc	aacttttttt	ctttattctt	aacatcaaaa	aactttatcg	atatctttac	60
aaccattaaa	caaaaaattt	ggccactaca	agttgaaaaa	gttttgatta	tatctaatacg	120
ctgaaatgga	ttacaaggta	tcaagaagtg	gggagatagt	agaaggagaa	gtagaagatt	180
cagaaaagat	tgatttacca	cctggtttca	gatttcaccc	aactgatgaa	gaacttataa	240
cacactatct	aagaccaaag	gttgtaaact	ctttttttct	tgctatagct	attgggtgaag	300
ttgatctcaa	caaagtcgag	ccttgggact	tgcttggaa	ggctaagctt	ggggaaaaag	360
agtggtaact	cttttgcgta	agagaccgaa	aatacccgac	tggtttaaga	acgaatcgtg	420
ctactaaaag	cggttattgg	aaagctacag	ggaaagataa	agagattctc	aaagggaaat	480
ctcttgttgg	tatgaagaaa	acattgggtt	tctacaaaag	aaagactcct	aaaggagtaa	540
aaacaaattg	ggtcatgcat	gagtatcgat	tagaaggcaa	atacggtatc	gataatctcc	600



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ctaaaaccgc taagaacgaa tgtgttatta gtcgtgtttt tcataaacgg actgatggta      660
cgaaggagca tatgtccgtt ggtttacctc cgctgatgga ttcttctcca tatctaaaga      720
gtagaggaca agactcttta gccgggacca cccttggtgg gttgttgtct cacgttacct      780
acttctccga ccaaacaacc gatgacaaga gtcttggtgg cgattttaaa actaccatgt      840
ttggttccgg atcgactaac tttttaccaa acatagggttc tctactagac ttcgatcctc      900
tgtttctaca aaacaattct tcagtactaa agatgttgct tgacaatgaa gaaacccaat      960
ttaagaagaa tcttcacaat tcaggttcat cagagagtga actaacagcg agttcttggc     1020
aaggtcaciaa ttcttatggg tccactgggc cagtgaatct tgattgcgtt tggaaattct     1080
gaatttgga aatcgaaaat ttggatgtta actagggggg atatatgggt tttaaaaaca     1140
gtgtatatat gcgttatgtg ttagctttag attctaggat atacaaagat gacactaata     1200
gattcttata acattttgta aaaaaaatc attgtagtga atactctctt gccattt

```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```

Met Asp Tyr Lys Val Ser Arg Ser Gly Glu Ile Val Glu Gly Glu Val
1      5      10      15
Glu Asp Ser Glu Lys Ile Asp Leu Pro Pro Gly Phe Arg Phe His Pro
20      25      30
Thr Asp Glu Glu Leu Ile Thr His Tyr Leu Arg Pro Lys Val Val Asn
35      40      45
Ser Phe Phe Ser Ala Ile Ala Ile Gly Glu Val Asp Leu Asn Lys Val
50      55      60
Glu Pro Trp Asp Leu Pro Trp Lys Ala Lys Leu Gly Glu Lys Glu Trp
65      70      75      80
Tyr Phe Phe Cys Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr
85      90      95
Asn Arg Ala Thr Lys Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys
100     105     110
Glu Ile Phe Lys Gly Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val
115     120     125
Phe Tyr Lys Gly Arg Ala Pro Lys Gly Val Lys Thr Asn Trp Val Met
130     135     140
His Glu Tyr Arg Leu Glu Gly Lys Tyr Gly Ile Asp Asn Leu Pro Lys
145     150     155     160
Thr Ala Lys Asn Glu Cys Val Ile Ser Arg Val Phe His Lys Arg Thr
165     170     175
Asp Gly Thr Lys Glu His Met Ser Val Gly Leu Pro Pro Leu Met Asp
180     185     190
Ser Ser Pro Tyr Leu Lys Ser Arg Gly Gln Asp Ser Leu Ala Gly Thr
195     200     205
Thr Leu Gly Gly Leu Leu Ser His Val Thr Tyr Phe Ser Asp Gln Thr
210     215     220
Thr Asp Asp Lys Ser Leu Val Ala Asp Phe Lys Thr Thr Met Phe Gly
225     230     235     240
Ser Gly Ser Thr Asn Phe Leu Pro Asn Ile Gly Ser Leu Leu Asp Phe
245     250     255
Asp Pro Leu Phe Leu Gln Asn Asn Ser Ser Val Leu Lys Met Leu Leu
260     265     270
Asp Asn Glu Glu Thr Gln Phe Lys Lys Asn Leu His Asn Ser Gly Ser
275     280     285
Ser Glu Ser Glu Leu Thr Ala Ser Ser Trp Gln Gly His Asn Ser Tyr
290     295     300

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Gly Ser Thr Gly Pro Val Asn Leu Asp Cys Val Trp Lys Phe  
305 310 315

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Lys	Gly	Arg	Ala	Pro	Lys	Gly	Val
1				5				10						15	
Lys	Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Glu	Gly	Lys	Tyr	Gly
			20				25						30		
Ile	Asp	Asn	Leu	Pro	Lys	Thr	Ala	Lys	Asn	Glu	Cys	Val	Ile	Ser	Arg
		35				40						45			
Val	Phe	His	Lys	Arg	Thr	Asp	Gly	Thr	Lys	Glu	His	Met	Ser	Val	Gly
	50				55						60				
Leu	Pro	Pro	Leu	Met	Asp	Ser	Ser	Pro	Tyr	Leu	Lys	Ser	Arg	Gly	Gln
65					70				75					80	
Asp	Ser	Leu	Ala	Gly	Thr	Thr	Leu	Gly	Gly	Leu	Leu	Ser	His	Val	Thr
			85					90						95	
Tyr	Phe	Ser	Asp	Gln	Thr	Thr	Asp	Asp	Lys	Ser	Leu	Val	Ala	Asp	Phe
			100				105						110		
Lys	Thr	Thr	Met	Phe	Gly	Ser	Gly	Ser	Thr	Asn	Phe	Leu	Pro	Asn	Ile
		115					120					125			
Gly	Ser	Leu	Leu	Asp	Phe	Asp	Pro	Leu	Phe	Leu	Gln	Asn	Asn	Ser	Ser
		130				135					140				
Val	Leu	Lys	Met	Leu	Leu	Asp	Asn	Glu	Glu	Thr	Gln	Phe	Lys	Lys	Asn
145					150				155						160
Leu	His	Asn	Ser	Gly	Ser	Ser	Glu	Ser	Glu	Leu	Thr	Ala	Ser	Ser	Trp
			165						170					175	
Gln	Gly	His	Asn	Ser	Tyr	Gly	Ser	Thr	Gly	Pro	Val	Asn	Leu	Asp	Cys
			180					185					190		
Val	Trp	Lys	Phe												
			195												

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	His	Glu	Tyr	Arg	Leu	Glu	Gly	Lys	Tyr	Gly	Ile	Asp	Asn	Leu	Pro
1				5				10						15	
Lys	Thr	Ala	Lys	Asn	Glu	Cys	Val	Ile	Ser	Arg	Val	Phe	His	Lys	Arg
		20						25					30		
Thr	Asp	Gly	Thr	Lys	Glu	His	Met	Ser	Val	Gly	Leu	Pro	Pro	Leu	Met
		35				40						45			
Asp	Ser	Ser	Pro	Tyr	Leu	Lys	Ser	Arg	Gly	Gln	Asp	Ser	Leu	Ala	Gly
	50					55				60					
Thr	Thr	Leu	Gly	Gly	Leu	Leu	Ser	His	Val	Thr	Phe	Ser	Asp	Gln	

65					70					75					80
Thr	Thr	Asp	Asp	Lys	Ser	Leu	Val	Ala	Asp	Phe	Lys	Thr	Thr	Met	Phe
				85					90					95	
Gly	Ser	Gly	Ser	Thr	Asn	Phe	Leu	Pro	Asn	Ile	Gly	Ser	Leu	Leu	Asp
				100				105					110		
Phe	Asp	Pro	Leu	Phe	Leu	Gln	Asn	Asn	Ser	Ser	Val	Leu	Lys	Met	Leu
				115				120				125			
Leu	Asp	Asn	Glu	Glu	Thr	Gln	Phe	Lys	Lys	Asn	Leu	His	Asn	Ser	Gly
				130			135				140				
Ser	Ser	Glu	Ser	Glu	Leu	Thr	Ala	Ser	Ser	Trp	Gln	Gly	His	Asn	Ser
145					150					155				160	
Tyr	Gly	Ser	Thr	Gly	Pro	Val	Asn	Leu	Asp	Cys	Val	Trp	Lys	Phe	
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

aaccaaaca	aaacaaaaca	aaaaaaacac	gagtgggaagc	ttttaaacaa	aattagaaaa	60
agagagagag	aatggcgac	gtcgggaaca	tacgtgacgg	aggtgccgct	aaaaggaacg	120
gtggagaaac	acttcaagag	gtacaggaac	gagaactatc	tcttccctga	cactatcggc	180
caccacatcc	aaagtgttac	tgttcacgat	ggcgaatggg	acactcaagg	aggcatcaag	240
atttggaact	acacactcgg	agatggaaag	gaggaggtat	tcaaggagag	gagagagata	300
gacgatgaca	ataagatagt	aaaggttgta	ggattggaag	gtcacgtgat	ggagcagttc	360
aaggtgtatg	agattgactt	ccaattttatt	cccaagtctg	agaagattg	cgtctgcaaa	420
atcactatga	tatgggagaa	gcgcaacgat	gatttccccg	aaccaagcag	ctacatgcaa	480
ctcctcaaga	gtatggttat	tgatatggag	gaccacgtcc	ttaaagctta	atcaatatca	540
caaccaccac	catcatcaca	accaccatca	tcatcatcct	atatgtttat	taaattgttt	600
tcatttatat	ataatagact	agataagaac	ctgtataatg	tgcgggataa	aatgattgaa	660
ataaattatt	atgcgtaaac	ttattgtatg	agatatcata	tatgttttga	tacaagaaaa	720
tatgtaatta	aagtbttttg	ttttattt				

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asn	Gln	Asn	Lys	Thr	Lys	Gln	Lys	Lys	His	Glu	Trp	Lys	Leu	Leu	Asn
1			5					10						15	
Lys	Ile	Arg	Lys	Arg	Glu	Arg	Glu	Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val
			20					25					30		
Thr	Glu	Val	Pro	Leu	Lys	Gly	Thr	Val	Glu	Lys	His	Phe	Lys	Arg	Tyr
			35				40					45			
Arg	Asn	Glu	Asn	Tyr	Leu	Phe	Pro	Asp	Thr	Ile	Gly	His	His	Ile	Gln
			50			55				60					
Ser	Val	Thr	Val	His	Asp	Gly	Glu	Trp	Asp	Thr	Gln	Gly	Gly	Ile	Lys
65				70				75						80	
Ile	Trp	Asn	Tyr	Thr	Leu	Gly	Asp	Gly	Lys	Glu	Glu	Val	Phe	Lys	Glu

				85					90					95		
Arg	Arg	Glu	Ile	Asp	Asp	Asp	Asn	Lys	Ile	Val	Lys	Val	Val	Gly	Leu	
			100					105						110		
Glu	Gly	His	Val	Met	Glu	Gln	Phe	Lys	Val	Tyr	Glu	Ile	Asp	Phe	Gln	
		115					120						125			
Phe	Ile	Pro	Lys	Ser	Glu	Glu	Asp	Cys	Val	Cys	Lys	Ile	Thr	Met	Ile	
	130					135					140					
Trp	Glu	Lys	Arg	Asn	Asp	Phe	Pro	Glu	Pro	Ser	Ser	Tyr	Met	Gln		
145				150						155				160		
Leu	Leu	Lys	Ser	Met	Val	Ile	Asp	Met	Glu	Asp	His	Val	Leu	Lys	Ala	
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..152

- (D) OTHER INFORMATION: / Ceres Seq. ID 1497926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val	Thr	Glu	Val	Pro	Leu	Lys	Gly	Thr	
1			5						10					15		
Val	Glu	Lys	His	Phe	Lys	Arg	Tyr	Arg	Asn	Glu	Asn	Tyr	Leu	Phe	Pro	
			20					25					30			
Asp	Thr	Ile	Gly	His	His	Ile	Gln	Ser	Val	Thr	Val	His	Asp	Gly	Glu	
		35					40					45				
Trp	Asp	Thr	Gln	Gly	Gly	Ile	Lys	Ile	Trp	Asn	Tyr	Thr	Leu	Gly	Asp	
	50					55					60					
Gly	Lys	Glu	Glu	Val	Phe	Lys	Glu	Arg	Arg	Glu	Ile	Asp	Asp	Asp	Asn	
65				70						75					80	
Lys	Ile	Val	Lys	Val	Val	Gly	Leu	Glu	Gly	His	Val	Met	Glu	Gln	Phe	
				85					90					95		
Lys	Val	Tyr	Glu	Ile	Asp	Phe	Gln	Phe	Ile	Pro	Lys	Ser	Glu	Glu	Asp	
		100						105					110			
Cys	Val	Cys	Lys	Ile	Thr	Met	Ile	Trp	Glu	Lys	Arg	Asn	Asp	Asp	Phe	
	115					120						125				
Pro	Glu	Pro	Ser	Ser	Tyr	Met	Gln	Leu	Leu	Lys	Ser	Met	Val	Ile	Asp	
	130					135					140					
Met	Glu	Asp	His	Val	Leu	Lys	Ala									
145				150												

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..591

- (D) OTHER INFORMATION: / Ceres Seq. ID 1497927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

gtgattcag	tttggtttt	ggaaccta	attctctc	taagattc	agatgag	ta	60
ctatgaa	atttgccgc	gaatgta	ataatc	ttctgt	atcc	taaggagg	120
acatcct	cctctatg	ctgcgt	gcgtaat	gtgatc	accagga	gtagctg	180
gtacaga	aaacgag	gttcat	cactctg	taagtg	agcgaac	tcagatc	240

```
cttctgacbb tactcttccc sgaaccaagg ctgtgcgttg ctctaagtgt cagcataggg      300
aggccgtttt cttccaggct acggttagag gtgaagaagg aatgacactg ttctttgtct      360
gttgcaaccc gaattgtggt catcgctgga gagaataaag agcttttcgg tttcaattgg      420
tgagttctta agagttttag gagttgatgt agttaccagt aagtgtataa tgtggaatga      480
cgggaacaac cttctgcccc agtcagagac aaatccgtat tcatgtaatc tgttatgaaa      540
ccataatctc aacttctggt tcaccaaaca taaagattgg aacttgtttc t
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1497928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
Asp Ser Val Leu Leu Glu Pro Asn Ser Leu Ser Arg Asp Ser Ala
1           5           10           15
Lys Met Ser Thr Met Lys Phe Cys Arg Glu Cys Asn Asn Ile Leu Tyr
          20           25           30
Pro Lys Glu Asp Lys Glu Gln Lys Ile Leu Leu Tyr Ala Cys Arg Asn
          35           40           45
Cys Asp His Gln Glu Val Ala Asp Asn Ser Cys Val Tyr Arg Asn Glu
          50           55           60
Val His His Ser Val Ser Glu Arg Thr Gln Ile Leu Thr Asp Val Ala
          65           70           75           80
Ser Asp Xaa Thr Leu Pro Xaa Thr Lys Ala Val Arg Cys Ser Lys Cys
          85           90           95
Gln His Arg Glu Ala Val Phe Phe Gln Ala Thr Val Arg Gly Glu Glu
          100          105          110
Gly Met Thr Leu Phe Phe Val Cys Asn Pro Asn Cys Gly His Arg
          115          120          125
Trp Arg Glu
          130
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1497929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Met Ser Thr Met Lys Phe Cys Arg Glu Cys Asn Asn Ile Leu Tyr Pro
1           5           10           15
Lys Glu Asp Lys Glu Gln Lys Ile Leu Leu Tyr Ala Cys Arg Asn Cys
          20           25           30
Asp His Gln Glu Val Ala Asp Asn Ser Cys Val Tyr Arg Asn Glu Val
          35           40           45
His His Ser Val Ser Glu Arg Thr Gln Ile Leu Thr Asp Val Ala Ser
          50           55           60
Asp Xaa Thr Leu Pro Xaa Thr Lys Ala Val Arg Cys Ser Lys Cys Gln
          65           70           75           80
His Arg Glu Ala Val Phe Phe Gln Ala Thr Val Arg Gly Glu Glu Gly
          85           90           95
Met Thr Leu Phe Phe Val Cys Cys Asn Pro Asn Cys Gly His Arg Trp
```

Arg Glu 100 105 110

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Lys	Phe	Cys	Arg	Glu	Cys	Asn	Asn	Ile	Leu	Tyr	Pro	Lys	Glu	Asp
1			5					10						15	
Lys	Glu	Gln	Lys	Ile	Leu	Leu	Tyr	Ala	Cys	Arg	Asn	Cys	Asp	His	Gln
			20					25					30		
Glu	Val	Ala	Asp	Asn	Ser	Cys	Val	Tyr	Arg	Asn	Glu	Val	His	His	Ser
			35					40					45		
Val	Ser	Glu	Arg	Thr	Gln	Ile	Leu	Thr	Asp	Val	Ala	Ser	Asp	Xaa	Thr
			50				55				60				
Leu	Pro	Xaa	Thr	Lys	Ala	Val	Arg	Cys	Ser	Lys	Cys	Gln	His	Arg	Glu
65					70				75						80
Ala	Val	Phe	Phe	Gln	Ala	Thr	Val	Arg	Gly	Glu	Glu	Gly	Met	Thr	Leu
				85					90					95	
Phe	Phe	Val	Cys	Cys	Asn	Pro	Asn	Cys	Gly	His	Arg	Trp	Arg	Glu	
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ccttggttag	ccatgggaag	catctctcct	cgttccatgt	tcgatgagct	gaagaaaaca	60
atctccgcat	caaccacctc	cacaactcca	aggaacggac	cgggagatac	aggactcaac	120
tggtaaatgt	atgagttgct	atggagggat	ttcttcaggt	ttataaccaa	gaaatacagc	180
tcagcgaaga	cgcaggtcga	ggctgggtccg	gctacagcct	gtaccgggtgc	ctttgcttaa	240
acatttgaaa	actttcaggt	gaccggaaaa	gttagaagcg	acctgtttct	ttgccctact	300
ctgggtgatg	gtggattaat	ttgctatccg	gacaggactt	tactgctctc	ttttgaaact	360
tgagtgtcag	gagaataaaa	tctaagcttc	tttttttggc	tcaatcaagt	tgcccgttcc	420
ctgttctaaa	catttcggat	actcattcca	taaaaagtct	ctacaatttg	agacgctctc	480
ctttgtggtt	aagacttgag	aatgtatctt	agaaartaay	cgaagtmgtt	gtgtctatga	540
atattaaatt	caggaatatt	aagatgtc				

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1497932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
Pro Trp Leu Ala Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu
1          5          10          15
Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn
20          25          30
Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp
35          40          45
Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr
50          55          60
Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1497933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu Leu Lys Lys Thr
1          5          10          15
Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn Gly Pro Gly Asp
20          25          30
Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp Arg Asp Phe Phe
35          40          45
Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr Gln Val Glu Ala
50          55          60
Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1497934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
Met Phe Asp Glu Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Ser Thr
1          5          10          15
Thr Pro Arg Asn Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr
20          25          30
Glu Leu Leu Trp Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser
35          40          45
Ser Ala Lys Thr Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly
50          55          60
Ala Phe Ala
65
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1012  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

acttcagcaa	aaccactaca	cctttcttat	ctctcagatt	ttctcaagaa	gattgtgtgg	60
aagatgatga	gacggaagat	ttttctcttt	ggtgattcca	tcactgaaga	atccttttagt	120
gacggtggct	ggggtgcttc	tctcgccgat	cctctccgcc	gcaaggctga	tatggtgcta	180
cgaggataca	gtggatataa	cacgaggtgg	gcactgaaag	tggtggagag	agtttttccg	240
gtggcagaag	aagacggcgg	agattctccg	gcagctgtga	ctgttttctt	tggagcgaac	300
gacgcgtgtc	ttccggagag	atgctcgggg	tttcagcatg	tgccacttca	cgagtacaag	360
cagaatcttc	gctctattgt	ttcgtttctc	aagaatcggt	ggccacaaac	ggccattatt	420
cttataactc	cgcctccaat	agacgaagag	gcccgcctca	gatatcctta	tatcgaaaac	480
acaacggggg	tgccggaaaag	aacgaatgaa	gtagccggac	tatacgcaaa	agcatgtata	540
gcagtagctg	aggaatgtca	aatttcggtc	actgatcttt	ggtccaaaat	gcagcaaaakt	600
scaaattggs	aaacagaatg	tctatgggac	gggttacatt	tgagtcgggt	cggttaacaaa	660
gtattgtttg	aagaagtagc	aaagaagcct	aaagaagaag	gcattggagc	tgaggactta	720
gctgtggatc	ttccccttat	agaagatggt	gaccctaagg	atcctctcaa	atcctttgat	780
gagttttgat	gcttttatatt	actaccatgc	agtttggttc	ttctatcttt	gattacttct	840
taatttcgat	attaatttag	ggaatgtgac	attattaggc	actttgtgag	aatctttttg	900
tgagaatctt	tttacgtttg	aggcacttgt	gagagagagg	gcactttgcc	atcttttttt	960
agaggagatt	gaaccaat	gtccctgaag	tgatgaaaac	acaataat	tt	

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 262 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..262  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Thr	Ser	Ala	Lys	Pro	Leu	His	Leu	Ser	Tyr	Leu	Ser	Asp	Phe	Leu	Lys
1				5					10					15	
Lys	Ile	Val	Trp	Lys	Met	Met	Arg	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp
				20					25					30	
Ser	Ile	Thr	Glu	Glu	Ser	Phe	Ser	Asp	Gly	Gly	Trp	Gly	Ala	Ser	Leu
				35					40					45	
Ala	Asp	Leu	Leu	Arg	Arg	Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser
				50					55					60	
Gly	Tyr	Asn	Thr	Arg	Trp	Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro
				65					70					75	80
Val	Ala	Glu	Glu	Asp	Gly	Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe
				85					90					95	
Phe	Gly	Ala	Asn	Asp	Ala	Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln
				100					105					110	
His	Val	Pro	Leu	His	Glu	Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser
				115					120					125	
Phe	Leu	Lys	Asn	Arg	Trp	Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro
				130					135					140	
Pro	Pro	Ile	Asp	Glu	Glu	Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn
				145					150					155	160
Thr	Thr	Gly	Leu	Pro	Glu	Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala
				165					170					175	
Lys	Ala	Cys	Ile	Ala	Val	Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp
				180					185					190	
Leu	Trp	Ser	Lys	Met	Gln	Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu



	195		200		205										
Trp	Asp	Gly	Leu	His	Leu	Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu
	210					215					220				
Glu	Val	Ala	Lys	Lys	Leu	Lys	Glu	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu
225					230					235				240	
Ala	Val	Asp	Leu	Pro	Leu	Ile	Glu	Asp	Val	Asp	Pro	Lys	Asp	Pro	Leu
			245						250					255	
Lys	Ser	Phe	Asp	Glu	Phe										
	260														

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..241

- (D) OTHER INFORMATION: / Ceres Seq. ID 1497941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Met	Arg	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp	Ser	Ile	Thr	Glu	Glu
1				5					10					15	
Ser	Phe	Ser	Asp	Gly	Gly	Trp	Gly	Ala	Ser	Leu	Ala	Asp	Leu	Leu	Arg
			20					25					30		
Arg	Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser	Gly	Tyr	Asn	Thr	Arg
		35					40					45			
Trp	Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro	Val	Ala	Glu	Glu	Asp
	50					55					60				
Gly	Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe	Phe	Gly	Ala	Asn	Asp
65					70					75				80	
Ala	Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln	His	Val	Pro	Leu	His
				85					90					95	
Glu	Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser	Phe	Leu	Lys	Asn	Arg
		100						105					110		
Trp	Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro	Pro	Pro	Ile	Asp	Glu
		115					120						125		
Glu	Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn	Thr	Thr	Gly	Leu	Pro
	130					135					140				
Glu	Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala	Lys	Ala	Cys	Ile	Ala
145					150					155				160	
Val	Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp	Leu	Trp	Ser	Lys	Met
				165					170					175	
Gln	Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu	Trp	Asp	Gly	Leu	His
		180					185						190		
Leu	Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu	Glu	Val	Ala	Lys	Lys
	195					200						205			
Leu	Lys	Glu	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu	Ala	Val	Asp	Leu	Pro
	210					215					220				
Leu	Ile	Glu	Asp	Val	Asp	Pro	Lys	Asp	Pro	Leu	Lys	Ser	Phe	Asp	Glu
225					230					235				240	
Phe															

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1497942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
Met Arg Arg Lys Ile Phe Leu Phe Gly Asp Ser Ile Thr Glu Glu Ser
1          5          10          15
Phe Ser Asp Gly Gly Trp Gly Ala Ser Leu Ala Asp Leu Leu Arg Arg
20          25          30
Lys Ala Asp Met Val Leu Arg Gly Tyr Ser Gly Tyr Asn Thr Arg Trp
35          40          45
Ala Leu Lys Val Val Glu Arg Val Phe Pro Val Ala Glu Glu Asp Gly
50          55          60
Gly Asp Ser Pro Ala Ala Val Thr Val Phe Phe Gly Ala Asn Asp Ala
65          70          75          80
Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln His Val Pro Leu His Glu
85          90          95
Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser Phe Leu Lys Asn Arg Trp
100         105         110
Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu
115         120         125
Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn Thr Thr Gly Leu Pro Glu
130         135         140
Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala Lys Ala Cys Ile Ala Val
145         150         155         160
Ala Glu Glu Cys Gln Ile Ser Val Thr Asp Leu Trp Ser Lys Met Gln
165         170         175
Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu Trp Asp Gly Leu His Leu
180         185         190
Ser Arg Val Gly Asn Lys Val Leu Phe Glu Glu Val Ala Lys Lys Leu
195         200         205
Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu Ala Val Asp Leu Pro Leu
210         215         220
Ile Glu Asp Val Asp Pro Lys Asp Pro Leu Lys Ser Phe Asp Glu Phe
225         230         235         240
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1380

(D) OTHER INFORMATION: / Ceres Seq. ID 1497943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
attttattcc tttctccgct ataaaaagcg atttttctat tgtagctcga tttgcgggaa      60
aatcttgcac ctgcctcaga aaatttttctg gggagctttc accaattagt tcttctcgtc      120
tctctctctc tctttggtta atgtttctac agattctctc ctcttaattc agagacgaca      180
aaacgctata aacaacattt ttacagtttg gaggaggaag gagaaatgat aggtttatta      240
actgagagta gcagcagtcg tatggttgga aatgtggatg ggttgatgag tccgataccg      300
atgtctccgg ttaatgcgga ggttgaggag atgagatcag agtcgccggt gggttaatgat      360
aaggcggttag atattttctga tgatgatcat gatgatgaga atgaaccgct tattgtttct      420
ggtgaatgtc gtatttggtc tgatgagtct cctgttgaga atcttgagag cccttggtgct      480
tgcagtggca gcctaaagta tgctcataga aaatgtgttc agcgttggtg caatgaaaag      540
aaaaacatta tatgcgagat ttgtcaccag ccttatcaac ctggatatac cgctccacca      600
cctccacttc agcctgaaga aacaactatt gacattggtg gaggatggac aatctcaggt      660
ttggatgtgc atgatcctcg tctccttgca attgctgaag ctgaacgtcg gtatttagag      720
tctgaatatg tggaatatac agcttcaagt gcaagcgggg ccgcattctg tcgctcagct      780
```



(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Val	Val	Asn	Val	Asp	Gly	Leu	Met	Arg	Pro	Ile	Pro	Met	Ser	Pro
1			5						10					15	
Val	Asn	Ala	Glu	Val	Glu	Glu	Met	Arg	Ser	Glu	Ser	Pro	Val	Val	Asn
			20						25					30	
Asp	Lys	Ala	Leu	Asp	Ile	Ser	Asp	Asp	Asp	His	Asp	Asp	Glu	Asn	Glu
			35						40					45	
Pro	Leu	Ile	Val	Ser	Gly	Glu	Cys	Arg	Ile	Cys	Ser	Asp	Glu	Ser	Pro
			50						55					60	
Val	Glu	Asn	Leu	Glu	Ser	Pro	Cys	Ala	Cys	Ser	Gly	Ser	Leu	Lys	Tyr
65															80
Ala	His	Arg	Lys	Cys	Val	Gln	Arg	Trp	Cys	Asn	Glu	Lys	Lys	Asn	Ile
															95
Ile	Cys	Glu	Ile	Cys	His	Gln	Pro	Tyr	Gln	Pro	Gly	Tyr	Thr	Ala	Pro
															110
Pro	Pro	Pro	Leu	Gln	Pro	Glu	Glu	Thr	Thr	Ile	Asp	Ile	Gly	Gly	Gly
															125
Trp	Thr	Ile	Ser	Gly	Leu	Asp	Val	His	Asp	Pro	Arg	Leu	Leu	Ala	Ile
															140
Ala	Glu	Ala	Glu	Arg	Arg	Tyr	Leu	Glu	Ser	Glu	Tyr	Val	Glu	Tyr	Thr
145															160
Ala	Ser	Ser	Ala	Ser	Gly	Ala	Ala	Phe	Cys	Arg	Ser	Ala	Ala	Leu	Ile
															175
Leu	Met	Ala	Leu	Leu	Leu	Leu	Arg	His	Ala	Leu	Thr	Ile	Thr	Asp	Asp
															190
Thr	Asp	Gly	Glu	Glu	Asp	Asp	Pro	Ser	Ser	Ile	Leu	Ser	Leu	Val	Leu
															205
Leu	Arg	Ala	Ala	Gly	Phe	Leu	Leu	Pro	Cys	Tyr	Ile	Met	Ala	Xaa	Ala
															220
Ile	Ser	Ile	Leu	Gln	Arg	Arg	Arg	Gln	Arg	Gln	Glu	Ala	Ala	Ala	Leu
225															240
Ala	Thr	Gln	Phe	Ala	Phe	Val	Leu	Gln	Ser	Gly	Gln	Pro	Arg	Thr	Val
															255
His	Phe	Thr	Val	Ser	Pro	Gly	Ile	Ser	Ser	Ser	Ser	Val	Ala	His	Ala
															270
Thr	Thr	Ser	Thr	Gln	Gln	Gln	His	Asp	Asp	Pro	Val				
															280

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Arg Pro Ile Pro Met Ser Pro Val Asn Ala Glu Val Glu Glu Met

1	5	10	15
Arg Ser Glu Ser Pro Val Val Asn Asp Lys Ala Leu Asp Ile Ser Asp			
20	25	30	
Asp Asp His Asp Asp Glu Asn Glu Pro Leu Ile Val Ser Gly Glu Cys			
35	40	45	
Arg Ile Cys Ser Asp Glu Ser Pro Val Glu Asn Leu Glu Ser Pro Cys			
50	55	60	
Ala Cys Ser Gly Ser Leu Lys Tyr Ala His Arg Lys Cys Val Gln Arg			
65	70	75	80
Trp Cys Asn Glu Lys Lys Asn Ile Ile Cys Glu Ile Cys His Gln Pro			
85	90	95	
Tyr Gln Pro Gly Tyr Thr Ala Pro Pro Pro Pro Leu Gln Pro Glu Glu			
100	105	110	
Thr Thr Ile Asp Ile Gly Gly Gly Trp Thr Ile Ser Gly Leu Asp Val			
115	120	125	
His Asp Pro Arg Leu Leu Ala Ile Ala Glu Ala Glu Arg Arg Tyr Leu			
130	135	140	
Glu Ser Glu Tyr Val Glu Tyr Thr Ala Ser Ser Ala Ser Gly Ala Ala			
145	150	155	160
Phe Cys Arg Ser Ala Ala Leu Ile Leu Met Ala Leu Leu Leu Leu Arg			
165	170	175	
His Ala Leu Thr Ile Thr Asp Asp Thr Asp Gly Glu Glu Asp Asp Pro			
180	185	190	
Ser Ser Ile Leu Ser Leu Val Leu Leu Arg Ala Ala Gly Phe Leu Leu			
195	200	205	
Pro Cys Tyr Ile Met Ala Xaa Ala Ile Ser Ile Leu Gln Arg Arg Arg			
210	215	220	
Gln Arg Gln Glu Ala Ala Ala Leu Ala Thr Gln Phe Ala Phe Val Leu			
225	230	235	240
Gln Ser Gly Gln Pro Arg Thr Val His Phe Thr Val Ser Pro Gly Ile			
245	250	255	
Ser Ser Ser Ser Val Ala His Ala Thr Thr Ser Thr Gln Gln Gln His			
260	265	270	
Asp Asp Pro Val			
275			

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

aaaatttcgc aaactaat	tttcactttc	ttcttctgtg	atctctctga	aagcttctct	60
tcttcttctc accatgtctg	gttatcctcc	atcaagccaa	ggttacggtt	acggcggtaa	120
tccaccacct cctcagccac	cgtacggatc	aaccggcaat	aacctcctc	cgtgcggatc	180
atccggcagc aatcctcctc	ctccgtacgg	atcatcagcc	tcctcaccgt	acgcagttcc	240
ctacggagct cagcccgtc	cttacggtgc	accaccgtca	gcaccgtacg	cgtctcctcc	300
aggagaccat aataagccgc	acaaagagaa	acctcaccgg	gcctcctacg	gatctccatc	360
tcccgggtggc tacggtgctc	atccatcgtc	tggaccttcc	gactacggtg	gttacggagg	420
agcgccgcag cagtctggac	atggaggagg	ttacggagga	gcgccgcagc	agtctggaca	480
tggaggaggt tacggagctc	ctcctccgca	agcttcttat	ggaagtccgt	ttgcgtctct	540
ggttccgctc gcgtttcctc	ccggaacaga	tccgaacatt	gtggcttggt	tccaagctgc	600
ggatcgggac aatagtggt	tcatcgatga	taaggagctt	caaggagctc	tatcttcgta	660
taatcagagc ttcagcataa	gaactgttca	tctccttatg	tatctattca	ccaacagcaa	720
tgtcaggaag attggaccaa	aagagtttac	ttcacttttc	tkkagtcttc	agaattggag	780
gtctatcttt gagaggtttg	ataaggacag	aagcggtaga	atagatacaa	acgagctgag	840

```
agatgcactc atgagccttg ggttttctgt gtctcctgtg attttgatc tgctggtttc 900
aaagtttgac aaaagcggag gcaggaacag ggctatcgaa tatgacaatt tcatcgagt 960
ttgtttgact gtaaaggggc tcaccgagaa gttcaaggag aaggatacgg cgttatcagg 1020
ctcagctact ttcaattacg agaacttcat gctcactgtt ttaccattcc tcgtcgcttg 1080
agtgattgtt tttttttttt ttgttgacca aasagattgt tttctaactc tattttcttt 1140
gtgagctttt ggatatttta ttgttgtct tttt
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1497948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Lys Phe Arg Lys Leu Ile Phe Ser Leu Ser Ser Ser Leu Ile Ser Leu
1      5      10      15
Lys Ala Ser Leu Leu Leu Thr Met Ser Gly Tyr Pro Pro Ser Ser
20      25      30
Gln Gly Tyr Gly Tyr Gly Gly Asn Pro Pro Pro Pro Gln Pro Pro Tyr
35      40      45
Gly Ser Thr Gly Asn Asn Pro Pro Pro Cys Gly Ser Ser Gly Ser Asn
50      55      60
Pro Pro Pro Pro Tyr Gly Ser Ser Ala Ser Ser Pro Tyr Ala Val Pro
65      70      75      80
Tyr Gly Ala Gln Pro Ala Pro Tyr Gly Ala Pro Pro Ser Ala Pro Tyr
85      90      95
Ala Ser Pro Pro Gly Asp His Asn Lys Pro His Lys Glu Lys Pro His
100     105     110
Gly Ala Ser Tyr Gly Ser Pro Ser Pro Gly Gly Tyr Gly Ala His Pro
115     120     125
Ser Ser Gly Pro Ser Asp Tyr Gly Gly Tyr Gly Gly Ala Pro Gln Gln
130     135     140
Ser Gly His Gly Gly Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His
145     150     155     160
Gly Gly Gly Tyr Gly Ala Pro Pro Pro Gln Ala Ser Tyr Gly Ser Pro
165     170     175
Phe Ala Ser Leu Val Pro Ser Ala Phe Pro Pro Gly Thr Asp Pro Asn
180     185     190
Ile Val Ala Cys Phe Gln Ala Ala Asp Arg Asp Asn Ser Gly Phe Ile
195     200     205
Asp Asp Lys Glu Leu Gln Gly Ala Leu Ser Ser Tyr Asn Gln Ser Phe
210     215     220
Ser Ile Arg Thr Val His Leu Leu Met Tyr Leu Phe Thr Asn Ser Asn
225     230     235     240
Val Arg Lys Ile Gly Pro Lys Glu Phe Thr Ser Leu Phe Xaa Ser Leu
245     250     255
Gln Asn Trp Arg Ser Ile Phe Glu Arg Phe Asp Lys Asp Arg Ser Gly
260     265     270
Arg Ile Asp Thr Asn Glu Leu Arg Asp Ala Leu Met Ser Leu Gly Phe
275     280     285
Ser Val Ser Pro Val Ile Leu Asp Leu Leu Val Ser Lys Phe Asp Lys
290     295     300
Ser Gly Gly Arg Asn Arg Ala Ile Glu Tyr Asp Asn Phe Ile Glu Cys
305     310     315     320
Cys Leu Thr Val Lys Gly Leu Thr Glu Lys Phe Lys Glu Lys Asp Thr
325     330     335
Ala Leu Ser Gly Ser Ala Thr Phe Asn Tyr Glu Asn Phe Met Leu Thr
```

340 345 350  
Val Leu Pro Phe Leu Val Ala  
355  
(2) INFORMATION FOR SEQ ID NO:80:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..335  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497949  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
Met Ser Gly Tyr Pro Pro Ser Ser Gln Gly Tyr Gly Tyr Gly Asn  
1 5 10 15  
Pro Pro Pro Pro Gln Pro Pro Tyr Gly Ser Thr Gly Asn Asn Pro Pro  
20 25 30  
Pro Cys Gly Ser Ser Gly Ser Asn Pro Pro Pro Pro Tyr Gly Ser Ser  
35 40 45  
Ala Ser Ser Pro Tyr Ala Val Pro Tyr Gly Ala Gln Pro Ala Pro Tyr  
50 55 60  
Gly Ala Pro Pro Ser Ala Pro Tyr Ala Ser Pro Pro Gly Asp His Asn  
65 70 75 80  
Lys Pro His Lys Gly Lys Pro His Gly Ala Ser Tyr Gly Ser Pro Ser  
85 90 95  
Pro Gly Gly Tyr Gly Ala His Pro Ser Ser Gly Pro Ser Asp Tyr Gly  
100 105 110  
Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His Gly Gly Tyr Gly Ala Pro Pro  
115 120 125  
Gly Ala Pro Gln Gln Ser Gly His Gly Gly Gly Tyr Gly Ala Pro Pro  
130 135 140  
Pro Gln Ala Ser Tyr Gly Ser Pro Phe Ala Ser Leu Val Pro Ser Ala  
145 150 155 160  
Phe Pro Pro Gly Thr Asp Pro Asn Ile Val Ala Cys Phe Gln Ala Ala  
165 170 175  
Asp Arg Asp Asn Ser Gly Phe Ile Asp Asp Lys Glu Leu Gln Gly Ala  
180 185 190  
Leu Ser Ser Tyr Asn Gln Ser Phe Ser Ile Arg Thr Val His Leu Leu  
195 200 205  
Met Tyr Leu Phe Thr Asn Ser Asn Val Arg Lys Ile Gly Pro Lys Glu  
210 215 220  
Phe Thr Ser Leu Phe Xaa Ser Leu Gln Asn Trp Arg Ser Ile Phe Glu  
225 230 235 240  
Arg Phe Asp Lys Asp Arg Ser Gly Arg Ile Asp Thr Asn Glu Leu Arg  
245 250 255  
Asp Ala Leu Met Ser Leu Gly Phe Ser Val Ser Pro Val Ile Leu Asp  
260 265 270  
Leu Leu Val Ser Lys Phe Asp Lys Ser Gly Gly Arg Asn Arg Ala Ile  
275 280 285  
Glu Tyr Asp Asn Phe Ile Glu Cys Cys Leu Thr Val Lys Gly Leu Thr  
290 295 300  
Glu Lys Phe Lys Glu Lys Asp Thr Ala Leu Ser Gly Ser Ala Thr Phe  
305 310 315 320  
Asn Tyr Glu Asn Phe Met Leu Thr Val Leu Pro Phe Leu Val Ala  
325 330 335

(2) INFORMATION FOR SEQ ID NO:81:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 748 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..748
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

attagtcatt	actcctcccg	gcgctccat	cgccgtctct	atctaatttc	gtcctgcgtc	60
gaccttgta	gctacttcag	tttccggcca	tcacgcagct	ccagttgtat	gttttgtggg	120
ttatacaaa	atgacaacaa	tcgaaaccgg	tcagaaaact	caaaagtctt	ctccttccgg	180
ttctgctact	accgctactg	gtacactcaa	gcagtcacat	gcacgtgtta	aaaggtgggg	240
agggagacac	ccgtttgtaa	gatatggact	tccgatgata	tctctcactg	tatttgagc	300
cctaggactc	ggccaactac	ttcaaggcag	taaggatatt	gcaaaggtaa	aagatgacca	360
agaatgggag	attatagaaa	caagaaaggc	actttcgaga	acaggacctg	tcgatgccta	420
taaacctaaa	aacacatcca	ttgaagatga	gctcaaggct	atgcaagaga	aggtggacat	480
aaacacgtac	gagtacaaga	aaattccaaa	gctaaacgaa	agcaagtoga	gttaagaaga	540
gtctttgtat	aagattagtc	tttctagatg	tgtttcagtt	ttaaagtact	cttcagttca	600
cataatcgcc	caagtacaaa	ttccagtaag	ttctgtctgg	gcttcctaaa	accaagaaca	660
acgagggact	tgccaattgk	tgataatata	tggtgtcgtg	ttgatttacg	acgtccaaat	720
agatctgaaa	gaggctttat	aaccagtt				

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..76
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ile	Ser	His	Tyr	Ser	Ser	Arg	Arg	Leu	His	Arg	Arg	Leu	Tyr	Leu	Ile
1				5				10						15	
Ser	Ser	Cys	Val	Asp	Leu	Val	Ser	Tyr	Phe	Ser	Phe	Arg	Pro	Ser	Arg
			20					25					30		
Ser	Ser	Ser	Cys	Met	Phe	Cys	Gly	Leu	Tyr	Lys	Asp	Asp	Asn	Asn	Arg
			35				40					45			
Asn	Arg	Ser	Glu	Asn	Ser	Lys	Val	Phe	Ser	Phe	Arg	Phe	Cys	Tyr	Tyr
			50			55					60				
Arg	Tyr	Trp	Tyr	Thr	Gln	Ala	Val	Ile	Ser	Ile	Val				
65				70				75							

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..134
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met	Thr	Thr	Ile	Glu	Thr	Gly	Gln	Lys	Thr	Gln	Lys	Ser	Ser	Pro	Ser
1				5				10						15	
Gly	Ser	Ala	Thr	Thr	Ala	Thr	Gly	Thr	Leu	Lys	Gln	Ser	Ser	Ala	Ser
			20				25					30			
Phe	Lys	Arg	Trp	Gly	Gly	Arg	His	Pro	Phe	Val	Arg	Tyr	Gly	Leu	Pro
			35			40						45			



Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu  
50 55 60  
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu  
65 70 75 80  
Ile Ile Glu Thr Arg Lys Ala Leu Ser Arg Thr Gly Pro Val Asp Ala  
85 90 95  
Tyr Lys Pro Lys Asn Thr Ser Ile Glu Asp Glu Leu Lys Ala Met Gln  
100 105 110  
Glu Lys Val Asp Ile Asn Thr Tyr Glu Tyr Lys Lys Ile Pro Lys Leu  
115 120 125  
Asn Glu Ser Lys Ser Ser  
130

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu  
1 5 10 15  
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu  
20 25 30  
Ile Ile Glu Thr Arg Lys Ala Leu Ser Arg Thr Gly Pro Val Asp Ala  
35 40 45  
Tyr Lys Pro Lys Asn Thr Ser Ile Glu Asp Glu Leu Lys Ala Met Gln  
50 55 60  
Glu Lys Val Asp Ile Asn Thr Tyr Glu Tyr Lys Lys Ile Pro Lys Leu  
65 70 75 80  
Asn Glu Ser Lys Ser Ser  
85

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

attcaccaga gaaatgggtcg tcgctgacta ctaaccagag ccatcggtgg ttgatttcgc 60  
gatttcgagc tccatttccta ctgtctcac cttaatctcc ggcgatcgaa tttcacggtt 120  
ccggttaatc aatctctccg tggccatgga caaagaagtt acaaagattg aaagtgatga 180  
cacttcacgc gtggagatca aagtgttgtt attcgccaga gcacgagagc tcacaggtgt 240  
gcctgatcta aactgaaga tgscatgagg tagtacaaca cagaaatgcc tggatgagtt 300  
ggtgcttaag tttccaagct tggaagaggt acgtagctgt gttgttctcg ctttgaacga 360  
ggaatataca accgattccg ccattgttca acatagagat gagttagcca tcatacctcc 420  
gataagcggc ggctaatagca tcgacacttc ttaaattccct ttaactcggg gattgtatct 480  
cattggcgat gatccaaaat gtaacttttg tcataataac acagaaaatat ctgtctttta 540  
taatggaaag aaaatgttac atc

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497958  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:  
Ser Pro Glu Lys Trp Ser Ser Leu Thr Thr Asn Gln Ser His Arg Trp  
1 5 10 15  
Leu Ile Ser Arg Phe Arg Ala Pro Phe Leu Leu Val Ser Pro  
20 25 30

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..40  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497959  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:  
Met Asp Lys Glu Val Thr Lys Ile Glu Ser Asp Asp Thr Ser Ser Val  
1 5 10 15  
Glu Ile Lys Val Leu Leu Phe Ala Arg Ala Arg Glu Leu Thr Gly Val  
20 25 30  
Pro Asp Leu Thr Leu Lys Met Xaa  
35 40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 933 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..933  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497963  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:  
acaattcaga tttcaatttc tcmaaaatasc ttaaaaactt tchctcaatt ctctckaggc 60  
ttcgtgrtca ggtatgcaga tctttygtya agacgtctsa cyggaaarac tatcacyyts 120  
gaggtggava gytctgacac catygayaac gtkaargcca agatccagga yaargarggt 180  
atyccwccgg aycagcagag gmttgatctt cgcyygaaag caasttggar gatggmagma 240  
ckttggctga ytacaacaty cagaaggagt ccacacttca cttggtcttg cgtctgcgtg 300  
gaggtatgca gatcttcgk aagactctva ccggaaagac catcactytk gaggtrgaga 360  
gctctgacac cattgacaac gtgaaggcca agatccagga taaggaaggt atccctccgg 420  
accagcagag gttgatcttt gccggaaaac aattggagga yggcagaact ttrgcggatt 480  
acaacatcca gaaggagtct acccttcact tggctcttgcg tctbcgtgga ggtatgcaga 540  
tcttgyttaa gactttgacc ggvaagacca tcaactcttga agtggagagc tcygacacca 600  
ttgacaacgt gaaggcyaag atccaggaya aggaaggwat ccctccggac cagcagasgt 660  
ctsatctts gkgaagca gcttgaggat ggacgtacat tggccgacta caacatccag 720  
aaggagtcta cccttcactt ggtccctcgt cttcgtggag gtttctaaat ctcgctctctg 780  
ttatgcttta agaagttcaa tgtctcgttt ctgttaaaac tttggtggct tgtgttttgg 840  
ggccttgtat aatcccctga tgaataattg ttccaactat gtttccattc ctgttatctc 900  
tttcttcta atgacaagtc gaacgtcttc ttt

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..127
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497964
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Thr Ile Gln Ile Ser Xaa Lys Xaa Leu Lys Thr Phe Xaa Gln  
1 5 10 15  
Phe Ser Xaa Gly Phe Val Xaa Arg Tyr Ala Asp Leu Xaa Xaa Arg Arg  
20 25 30  
Xaa Xaa Gly Xaa Thr Ile Xaa Xaa Glu Val Xaa Xaa Ser Asp Thr Xaa  
35 40 45  
Xaa Asn Xaa Xaa Ala Lys Ile Gln Xaa Xaa Xaa Gly Xaa Xaa Pro Xaa  
50 55 60  
Gln Gln Arg Xaa Asp Leu Arg Xaa Lys Ala Xaa Trp Xaa Met Xaa Xaa  
65 70 75 80  
Xaa Trp Leu Xaa Thr Thr Xaa Arg Arg Ser Pro His Phe Thr Trp Ser  
85 90 95  
Cys Val Cys Val Glu Val Cys Arg Ser Ser Xaa Arg Leu Xaa Pro Glu  
100 105 110  
Arg Pro Ser Xaa Xaa Arg Xaa Arg Ala Leu Thr Pro Leu Thr Thr  
115 120 125

- (2) INFORMATION FOR SEQ ID NO:90:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..126
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1497965
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Gln Ile Phe Xaa Lys Thr Xaa Thr Gly Lys Thr Ile Thr Xaa Glu  
1 5 10 15  
Xaa Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Xaa Gly Arg Thr Xaa Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Xaa Arg Gly Gly Met Gln Ile Xaa  
65 70 75 80  
Val Lys Thr Leu Thr Xaa Lys Thr Ile Thr Leu Glu Val Glu Ser Xaa  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Xaa Lys Ile Gln Xaa Lys Glu Xaa Ile  
100 105 110  
Pro Pro Asp Gln Gln Xaa Ser Xaa Leu Xaa Xaa Lys Ala Ala  
115 120 125

- (2) INFORMATION FOR SEQ ID NO:91:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1251

(D) OTHER INFORMATION: / Ceres Seq. ID 1497966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

acgcaggcaa	atgtctcgta	atttaatcta	tagaagaaac	agagctctct	gttttgtttt	60
aatcttggtc	tgcttccctt	accggttttg	cgctagaaac	acgccggagg	cggancaatc	120
cacagcaaaa	gcaactcaaa	taatacacgt	cagcaattcc	acgtggcatg	atttctctcg	180
tctttagatg	gtccaaaatag	gtagccacgt	cagcggcgta	tcagagctca	aaagatacct	240
ccaccgattc	ggttacgtca	aggatggctc	cgaaatattt	tccgacgtgt	tcgatgggtc	300
tctggaatcg	gcaatctctc	tgtatcaaga	aaatctcggt	ttaccaataa	ccggaagact	360
cgacacgagt	acagttactc	tcatgtcggt	accgcgatgt	ggcgttagsg	atacgcacat	420
gaccatcaac	aacgatttcc	tccacacaac	ggcgcattat	acgtatttca	acggtaaacc	480
gaaatggaac	cgtgatacgc	taacctacgc	tatctccaaa	actcacaac	tcgattactt	540
gacgtcagaa	gacgtcaaaa	ccgttttccg	gcgagctttt	tcacagtggg	caagcgtgat	600
tccggtgagt	ttcgaggaag	tcgacgattt	cacgacggct	gatttaaaga	tcggattcta	660
cgctgggtgat	cacggtgacg	ggcttccggt	tgacgggtga	cttggaactt	tagcacacgc	720
ttttgcgccg	gagaacggga	ggcttcacct	cgacgcggcg	gagacgtgga	tcgtcgacga	780
tgacttgaaa	ggatcttcag	aggtggccgt	tgacttggag	tctgtggcga	ctcacgagat	840
cggtcacttg	ttgggattag	gacatagctc	gcaggagtcg	gcggttatgt	atccgagtct	900
ccgaccgagg	accaagaaa	ttgatcttac	ggttgatgac	gtggcagggtg	tacttaagct	960
atatggtccg	aatcctaaac	tacggttgga	ttcactaacg	cagtcggaag	attctattaa	1020
aaacggcacc	gtatcacata	gattcttgct	ggggaatttt	atcggttatg	ttctgttggt	1080
tgttggtttg	attcttttcc	tataggttta	taggcataaa	aaatactgtt	tttattcatt	1140
tatttttaat	taaagtgtaca	tatatttttc	aactatgtaa	atgtaaatat	atagttgaac	1200
aaaaaaagat	gtacatatat	agttaggctt	ataattaggt	ttatggtctt	g	

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1497967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Arg	Arg	Gln	Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu
1			5						10					15	
Cys	Phe	Val	Leu	Ile	Leu	Phe	Cys	Phe	Pro	Tyr	Arg	Phe	Gly	Ala	Arg
			20						25					30	
Asn	Thr	Pro	Glu	Ala	Xaa	Gln	Ser	Thr	Ala	Lys	Ala	Thr	Gln	Ile	Ile
			35						40					45	
His	Val	Ser	Asn	Ser	Thr	Trp	His	Asp	Phe	Ser	Arg	Leu	Val	Asp	Val
			50						55					60	
Gln	Ile	Gly	Ser	His	Val	Ser	Gly	Val	Ser	Glu	Leu	Lys	Arg	Tyr	Leu
			65						70					75	
His	Arg	Phe	Gly	Tyr	Val	Lys	Asp	Gly	Ser	Glu	Ile	Phe	Ser	Asp	Val
			85						90					95	
Phe	Asp	Gly	Pro	Leu	Glu	Ser	Ala	Ile	Ser	Leu	Tyr	Gln	Glu	Asn	Leu
			100						105					110	
Gly	Leu	Pro	Ile	Thr	Gly	Arg	Leu	Asp	Thr	Ser	Thr	Val	Thr	Leu	Met
			115						120					125	
Ser	Leu	Pro	Arg	Cys	Gly	Val	Xaa	Asp	Thr	His	Met	Thr	Ile	Asn	Asn
			130						135					140	
Asp	Phe	Leu	His	Thr	Thr	Ala	His	Tyr	Thr	Tyr	Phe	Asn	Gly	Lys	Pro
			145						150					155	
Lys	Trp	Asn	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Ile	Ser	Lys	Thr	His	Lys
			165						170					175	
Leu	Asp	Tyr	Leu	Thr	Ser	Glu	Asp	Val	Lys	Thr	Val	Phe	Arg	Arg	Ala

(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 100																
Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu	Cys	Phe	Val	
1				5					10					15		
Leu	Ile	Leu	Phe	Cys	Phe	Pro	Tyr	Arg	Phe	Gly	Ala	Arg	Asn	Thr	Pro	
			20					25					30			
Glu	Ala	Xaa	Gln	Ser	Thr	Ala	Lys	Ala	Thr	Gln	Ile	Ile	His	Val	Ser	
			35				40					45				
Asn	Ser	Thr	Trp	His	Asp	Phe	Ser	Arg	Leu	Val	Asp	Val	Gln	Ile	Gly	
			50			55					60					
Ser	His	Val	Ser	Gly	Val	Ser	Glu	Leu	Lys	Arg	Tyr	Leu	His	Arg	Phe	
65					70					75					80	
Gly	Tyr	Val	Lys	Asp	Gly	Ser	Glu	Ile	Phe	Ser	Asp	Val	Phe	Asp	Gly	
				85					90					95		
Pro	Leu	Glu	Ser	Ala	Ile	Ser	Leu	Tyr	Gln	Glu	Asn	Leu	Gly	Leu	Pro	
			100					105					110			
Ile	Thr	Gly	Arg	Leu	Asp	Thr	Ser	Thr	Val	Thr	Leu	Met	Ser	Leu	Pro	
			115				120					125				
Arg	Cys	Gly	Val	Xaa	Asp	Thr	His	Met	Thr	Ile	Asn	Asn	Asp	Phe	Leu	
			130			135					140					
His	Thr	Thr	Ala	His	Tyr	Thr	Tyr	Phe	Asn	Gly	Lys	Pro	Lys	Trp	Asn	
145					150					155					160	
Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Ile	Ser	Lys	Thr	His	Lys	Leu	Asp	Tyr	
				165					170					175		
Leu	Thr	Ser	Glu	Asp	Val	Lys	Thr	Val	Phe	Arg	Arg	Ala	Phe	Ser	Gln	
			180					185					190			
Trp	Ser	Ser	Val	Ile	Pro	Val	Ser	Phe	Glu	Glu	Val	Asp	Asp	Phe	Thr	
			195				200					205				

Thr	Ala	Asp	Leu	Lys	Ile	Gly	Phe	Tyr	Ala	Gly	Asp	His	Gly	Asp	Gly
210						215					220				
Leu	Pro	Phe	Asp	Gly	Val	Leu	Gly	Thr	Leu	Ala	His	Ala	Phe	Ala	Pro
225				230						235					240
Glu	Asn	Gly	Arg	Leu	His	Leu	Asp	Ala	Ala	Glu	Thr	Trp	Ile	Val	Asp
			245						250					255	
Asp	Asp	Leu	Lys	Gly	Ser	Ser	Glu	Val	Ala	Val	Asp	Leu	Glu	Ser	Val
		260					265					270			
Ala	Thr	His	Glu	Ile	Gly	His	Leu	Gly	Leu	Gly	His	Ser	Ser	Gln	
	275					280					285				
Glu	Ser	Ala	Val	Met	Tyr	Pro	Ser	Leu	Arg	Pro	Arg	Thr	Lys	Lys	Val
290					295					300					
Asp	Leu	Thr	Val	Asp	Asp	Val	Ala	Gly	Val	Leu	Lys	Leu	Tyr	Gly	Pro
305				310						315					320
Asn	Pro	Lys	Leu	Arg	Leu	Asp	Ser	Leu	Thr	Gln	Ser	Glu	Asp	Ser	Ile
			325						330					335	
Lys	Asn	Gly	Thr	Val	Ser	His	Arg	Phe	Leu	Ser	Gly	Asn	Phe	Ile	Gly
	340						345					350			
Tyr	Val	Leu	Val	Val	Gly	Leu	Ile	Leu	Phe	Leu					
	355				360										

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met	Ser	Leu	Pro	Arg	Cys	Gly	Val	Xaa	Asp	Thr	His	Met	Thr	Ile	Asn
1			5					10						15	
Asn	Asp	Phe	Leu	His	Thr	Thr	Ala	His	Tyr	Thr	Tyr	Phe	Asn	Gly	Lys
		20						25				30			
Pro	Lys	Trp	Asn	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Ile	Ser	Lys	Thr	His
		35					40					45			
Lys	Leu	Asp	Tyr	Leu	Thr	Ser	Glu	Asp	Val	Lys	Thr	Val	Phe	Arg	Arg
	50					55				60					
Ala	Phe	Ser	Gln	Trp	Ser	Ser	Val	Ile	Pro	Val	Ser	Phe	Glu	Glu	Val
65					70					75					80
Asp	Asp	Phe	Thr	Thr	Ala	Asp	Leu	Lys	Ile	Gly	Phe	Tyr	Ala	Gly	Asp
			85						90					95	
His	Gly	Asp	Gly	Leu	Pro	Phe	Asp	Gly	Val	Leu	Gly	Thr	Leu	Ala	His
	100							105					110		
Ala	Phe	Ala	Pro	Glu	Asn	Gly	Arg	Leu	His	Leu	Asp	Ala	Ala	Glu	Thr
	115						120					125			
Trp	Ile	Val	Asp	Asp	Asp	Leu	Lys	Gly	Ser	Ser	Glu	Val	Ala	Val	Asp
	130					135					140				
Leu	Glu	Ser	Val	Ala	Thr	His	Glu	Ile	Gly	His	Leu	Leu	Gly	Leu	Gly
145					150					155					160
His	Ser	Ser	Gln	Glu	Ser	Ala	Val	Met	Tyr	Pro	Ser	Leu	Arg	Pro	Arg
			165						170					175	
Thr	Lys	Lys	Val	Asp	Leu	Thr	Val	Asp	Asp	Val	Ala	Gly	Val	Leu	Lys
		180						185					190		
Leu	Tyr	Gly	Pro	Asn	Pro	Lys	Leu	Arg	Leu	Asp	Ser	Leu	Thr	Gln	Ser
	195					200						205			
Glu	Asp	Ser	Ile	Lys	Asn	Gly	Thr	Val	Ser	His	Arg	Phe	Leu	Ser	Gly
	210					215					220				
Asn	Phe	Ile	Gly	Tyr	Val	Leu	Leu	Val	Val	Gly	Leu	Ile	Leu	Phe	Leu

225

230

235

240

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1457
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
gattggtcaa aaaaatggaa gcggcgaaga aacagagtgt tacaaatcag cttctcgccg      60
tgaaatcagc ttccggcaag acttttagcc agttagccgc ggagacaggt ctaaccaacg      120
tatacgtagc tcagcttctc cgtcgtcaag ctacagctcaa accggacaca gtcccaaagc      180
ttaaggaagc tttaccagct ctgaccgatg aactaatcgg agatatgatg tctccaccgt      240
ggagatccta cgatccctaatt ctcatccaag aaccactat ctacagggtg aatgaagcag      300
tgatgcattt tggtagagagt ataaaggaga ttatcaatga agattttgga gatggcatca      360
tgtcggcgat agattttctat tgctctgtcg acaaaatcaa aggagtggat ggtaacaatc      420
gcggtggtgt gacgcttgat ggaaagtmtc tttcgcattc cgaacagagg acggagaata      480
tgggtctcaag gctaaatctc aagggaggta caagcgaatg ataagaaagc ctttacgtat      540
ccatgaaggc cttattgtaa gtggtaacgt tgtaatacct atgtgtttgt ttatctgtaa      600
tatatgcaac ttcagcatct agattaaaag ctgtttcagg ttgaataaca gtgaataaac      660
aaaacttata aaacctttct atgtttatct tcaaaaaaaaa aaaaaaaaaa cggcacgaga      720
agcttttttt tttttttttt tattaatatct ctcttttatg tgtttggttg ctttgacacg      780
ttgagaggct taacttggtg aaattagccc ctggtggtca ccttggtagg tttgtgattt      840
ggactaagtc tgcttttgag aagcttgaat ctatctatgg ctggtttgag aaaccatcag      900
agaagaagaa gggttacgtc ttgcctcgtg cgaagatggt gaatgctgat cttgctagga      960
ttattaactc cgatgaggta cagagtgtgg tgaaccgat taaggatggt tccaagagag      1020
cggttctgaa gaagaatcca ttgaagaacc ttaatgtgat gttcaagttg aatccttatg      1080
ctaagaccgc aaagagaatg tctctgttgg ctgaagcttc aagggttaag gctaagaagg      1140
agaagctcga gaagaagagg aaagtcgtca ctaaggagga ggccaagcg atcaaagcag      1200
caggcaaggc ttggtatcag actatgattt cagacagtga ctacaccgag ttcgataact      1260
tcaccaagtg gcttggcgct agtcagtaat gatgctctcg tcatcgcaaa gtctcttata      1320
tctaggcaaa gatttttggtt ttctgattta tgttcttcgt ttgtattgga tttatctggg      1380
attttatggt gttgagttgg taagacgatt ttaagaact atgatggtgt ttttcaaact      1440
cttttcaatc tgtttcc
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
Leu Val Lys Lys Met Glu Ala Ala Lys Lys Gln Ser Val Thr Asn Gln
1           5           10           15
Leu Leu Ala Val Lys Ser Ala Ser Gly Lys Thr Phe Ser Gln Leu Ala
20           25           30
Ala Glu Thr Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Arg Arg
35           40           45
Gln Ala Gln Leu Lys Pro Asp Thr Val Pro Lys Leu Lys Glu Ala Leu
50           55           60
Pro Ala Leu Thr Asp Glu Leu Ile Gly Asp Met Met Ser Pro Pro Trp
```

65					70					75					80
Arg	Ser	Tyr	Asp	Pro	Asn	Leu	Ile	Gln	Glu	Pro	Thr	Ile	Tyr	Arg	Leu
				85					90					95	
Asn	Glu	Ala	Val	Met	His	Phe	Gly	Glu	Ser	Ile	Lys	Glu	Ile	Ile	Asn
			100					105					110		
Glu	Asp	Phe	Gly	Asp	Gly	Ile	Met	Ser	Ala	Ile	Asp	Phe	Tyr	Cys	Ser
		115					120					125			
Val	Asp	Lys	Ile	Lys	Gly	Val	Asp	Gly	Asn	Asn	Arg	Val	Val	Val	Thr
	130						135				140				
Leu	Asp	Gly	Lys	Xaa	Leu	Ser	His	Ser	Glu	Gln	Arg	Thr	Glu	Asn	Met
145					150					155					160
Val	Ser	Arg	Leu	Asn	Leu	Lys	Gly	Gly	Thr	Ser	Glu				
				165					170						

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1497972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met	Glu	Ala	Ala	Lys	Lys	Gln	Ser	Val	Thr	Asn	Gln	Leu	Leu	Ala	Val
1				5					10					15	
Lys	Ser	Ala	Ser	Gly	Lys	Thr	Phe	Ser	Gln	Leu	Ala	Ala	Glu	Thr	Gly
			20					25					30		
Leu	Thr	Asn	Val	Tyr	Val	Ala	Gln	Leu	Leu	Arg	Arg	Gln	Ala	Gln	Leu
		35					40					45			
Lys	Pro	Asp	Thr	Val	Pro	Lys	Leu	Lys	Glu	Ala	Leu	Pro	Ala	Leu	Thr
	50					55					60				
Asp	Glu	Leu	Ile	Gly	Asp	Met	Met	Ser	Pro	Pro	Trp	Arg	Ser	Tyr	Asp
65					70				75					80	
Pro	Asn	Leu	Ile	Gln	Glu	Pro	Thr	Ile	Tyr	Arg	Leu	Asn	Glu	Ala	Val
			85						90					95	
Met	His	Phe	Gly	Glu	Ser	Ile	Lys	Glu	Ile	Ile	Asn	Glu	Asp	Phe	Gly
			100					105					110		
Asp	Gly	Ile	Met	Ser	Ala	Ile	Asp	Phe	Tyr	Cys	Ser	Val	Asp	Lys	Ile
	115						120					125			
Lys	Gly	Val	Asp	Gly	Asn	Asn	Arg	Val	Val	Val	Thr	Leu	Asp	Gly	Lys
	130						135				140				
Xaa	Leu	Ser	His	Ser	Glu	Gln	Arg	Thr	Glu	Asn	Met	Val	Ser	Arg	Leu
145					150					155					160
Asn	Leu	Lys	Gly	Gly	Thr	Ser	Glu								
				165											

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1497973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met	Val	Asn	Ala	Asp	Leu	Ala	Arg	Ile	Ile	Asn	Ser	Asp	Glu	Val	Gln
1				5					10					15	



Ser Val Val Asn Pro Ile Lys Asp Gly Ser Lys Arg Ala Val Leu Lys  
20 25 30  
Lys Asn Pro Leu Lys Asn Leu Asn Val Met Phe Lys Leu Asn Pro Tyr  
35 40 45  
Ala Lys Thr Ala Lys Arg Met Ser Leu Leu Ala Glu Ala Ser Arg Val  
50 55 60  
Lys Ala Lys Lys Glu Lys Leu Glu Lys Lys Arg Lys Val Val Thr Lys  
65 70 75 80  
Glu Glu Ala Gln Ala Ile Lys Ala Ala Gly Lys Ala Trp Tyr Gln Thr  
85 90 95  
Met Ile Ser Asp Ser Asp Tyr Thr Glu Phe Asp Asn Phe Thr Lys Trp  
100 105 110  
Leu Gly Ala Ser Gln  
115

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..732
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

agaaacagtt	ccgtgtaggc	aaccattagg	aaaaccctaa	ctaaattcca	ttattaattt	60
cttttataat	ccctttctct	tgacattgac	ttctctctct	cgattcttct	tctccagttt	120
caatcaaact	caatttcttc	tcaacgaacc	ctaatttcca	acaaatcgga	ttcagtttct	180
tcttcggaga	ctaattcgaa	cgcaatggct	aagagttcct	tcaagatctc	taaccctctc	240
gaggcaagga	tgagtgaatc	ttctcgaatc	agagagaagt	accctgacag	aattcccggtg	300
attgtggaga	aggctggaca	aagtgatgtt	cctgacattg	acaagaagaa	gtatcktgta	360
ccagctgata	taacagtggg	acaatttgta	tacgtgggtc	gtaaaagaat	caagcttgga	420
gctgagaaag	ctatttttgt	ctttgttaag	aacacattgc	ctccaactgc	tgcatgtgatg	480
tctgcgatct	atgaasaaca	caaagatgag	gatgggttcc	tctacatgac	ttacagtggg	540
gagaacactt	ttggatctct	taccgttgct	tgaataaaaa	tcgatctttg	gatgactttg	600
atgtacatac	ataaatcagg	aagataaaga	tgtacattgc	ttccttcttt	tctctggctt	660
ttacttttgc	tttggatgtt	tggatatctt	tccctttggg	tttattaatc	gtcagaaact	720
tctccttttc	tt					

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ala Lys Ser Ser Phe Lys Ile Ser Asn Pro Leu Glu Ala Arg Met  
1 5 10 15  
Ser Glu Ser Ser Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro Val  
20 25 30  
Ile Val Glu Lys Ala Gly Gln Ser Asp Val Pro Asp Ile Asp Lys Lys  
35 40 45  
Lys Tyr Xaa Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val  
50 55 60  
Val Arg Lys Arg Ile Lys Leu Gly Ala Glu Lys Ala Ile Phe Val Phe  
65 70 75 80

Val Lys Asn Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr  
                    85                    90                    95  
Glu Xaa His Lys Asp Glu Asp Gly Phe Leu Tyr Met Thr Tyr Ser Gly  
                    100                    105                    110  
Glu Asn Thr Phe Gly Ser Leu Thr Val Ala  
                    115                    120

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1497976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Glu Ser Ser Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro  
1                    5                    10                    15  
Val Ile Val Glu Lys Ala Gly Gln Ser Asp Val Pro Asp Ile Asp Lys  
                    20                    25                    30  
Lys Lys Tyr Xaa Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr  
                    35                    40                    45  
Val Val Arg Lys Arg Ile Lys Leu Gly Ala Glu Lys Ala Ile Phe Val  
                    50                    55                    60  
Phe Val Lys Asn Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile  
65                    70                    75                    80  
Tyr Glu Xaa His Lys Asp Glu Asp Gly Phe Leu Tyr Met Thr Tyr Ser  
                    85                    90                    95  
Gly Glu Asn Thr Phe Gly Ser Leu Thr Val Ala  
                    100                    105

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1497977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

taacattgtg gtacttaatg gagggaggat agtagaggaa ggtacacatg attcttttagc	60
agcaaaaaat gggttgtatg tacgtttgat gcaaccacac tttggtaaag gtctacgcca	120
acatcgactg atatagagtt ttgaggctcc atcaatgata atgatttttg catctctgat	180
caatgattct cggaggatt acaagatggt caaaaaaac cctatacaac cacgggtagt	240
tctctagcag atagggscgt tagatgtaga tttccatagt cttcgagctg cttattcttt	300
ttttggagac gaagcatcag aagtaggtca tggtcattgc ttcgttctcc aaagtatatc	360
gattttgtct attgaatctg aatatttttag gaggttggtg aatcattttg gaggctgttt	420
atttgccitt cctttatatg tgtctgtgct ggtttgttct tgcaaaaaca tggatgatgt	480
atgtaaagct taag	

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..44  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497978  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:  
Asn Ile Val Val Leu Asn Gly Gly Arg Ile Val Glu Glu Gly Thr His  
1 5 10 15  
Asp Ser Leu Ala Ala Lys Asn Gly Leu Tyr Val Arg Leu Met Gln Pro  
20 25 30  
His Phe Gly Lys Gly Leu Arg Gln His Arg Leu Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Ile Met Ile Leu Ala Ser Leu Ile Asn Asp Ser Pro Glu Asp Tyr  
1 5 10 15  
Lys Met Phe Lys Lys Asn Pro Ile Gln Pro Arg Val Val Leu  
20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1592  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

aagactctct	ctgctttcga	ccmaaaaacc	ttctcctctc	ctctgggaga	tctccatctt	60
cttcgcttct	tcgcttcccc	gcctgaaaca	attactcgat	ctcgccggcg	gaacaagctc	120
tccgtttctc	tttccggcag	atcgattctt	ccaattcctt	attcctttct	aggtcttcc	180
taagaaaccc	ttactttctt	caaaatctgc	atztatggcg	attagggtta	ccttcaccta	240
ctccagctat	gttgctagga	gcattgcttc	atccgccggg	actcgtgtcg	gtaccggcga	300
cgttagatca	tgcttcgaaa	catgggttcg	tcccaggttc	tgcgccaca	atcagatacc	360
agatattggt	gataaatctc	ccggatccaa	cacatgggg	ccaagctcag	gccctcgtgc	420
tcgaccagct	tcattcaatgt	atagcaccat	tgcgagggaa	atcctcgaag	aaggctgcaa	480
gagtcacttt	gtcttgggta	tgatctctct	catgaatttg	actggagctc	cacagttttc	540
gggtgtgacc	ggtctcggga	tctctccctt	taagacttct	tctgtcatcc	cgttccttag	600
gggttccaag	tggatgcctt	gtagtattcc	ggcgacgtta	tcaacggata	ttgctgaggt	660
tgatagagga	ggaaagggtct	gtgatccctaa	agtgaagttg	gagttgagtg	ataaagtctc	720
gaatggtgga	aacggatggg	ttaataagct	gttgaatatc	tgctcggagg	atgctaaggc	780
tgctttcacg	gcggttactt	tttctctcct	ttccgcatcg	gctttggccg	agccaaagtc	840
tataccttca	acatctatgc	ttcctactct	cgatgtgggt	gatcgtgtta	tagccgagaa	900
ggtctcatac	tttttcagga	agccagaggt	ttcagacata	ggtatcttca	aggctcctcc	960
tattttggtg	gaacatggtt	acagttgtgc	tgatgttttc	ataaaaagga	tagttgctag	1020
cgaagggtgac	tgggttgaag	tttgtgatgg	aaagctctta	gtaaatgaca	ctgttcaagc	1080
agaggatttt	gtcttagagc	caattgacta	tgaaatggaa	ccaatgtttg	tccctgaagg	1140
ttatgtcttc	gtcctaggag	acaaccgcaa	caaaagcttt	gattctcata	actgggggtcc	1200
acttccaata	aagaacatca	tagggagatc	tgtgtttcgc	tattggccac	caagcaaagt	1260
gtcagacata	atacaccatg	aacaagttag	ccaaaagaga	gctgttgatg	tatcttgacc	1320
aacgcagatg	gtatcttagg	attaagcaga	aaatttgatt	agatgagctg	tgccatgcca	1380

```
accatttttg cgctgaaggc aacagagcaa ttctttcttc ctgtctaggc ttgatggcgg 1440
acatggaatg cactgggaaa tccatataaa aagaacaaga aaattgatat ttttgctttg 1500
attttttttg atgtgttgaa acctaaatgc atccagtgtg attggcagta gctgtcaaac 1560
ataaaagggt aaactttctt ttttgagtat tt
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1497988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```
Met Ala Ile Arg Val Thr Phe Thr Tyr Ser Ser Tyr Val Ala Arg Ser
1      5      10      15
Ile Ala Ser Ser Ala Gly Thr Arg Val Gly Thr Gly Asp Val Arg Ser
20     25     30
Cys Phe Glu Thr Trp Val Arg Pro Arg Phe Cys Gly His Asn Gln Ile
35     40     45
Pro Asp Ile Val Asp Lys Ser Pro Gly Ser Asn Thr Trp Gly Pro Ser
50     55     60
Ser Gly Pro Arg Ala Arg Pro Ala Ser Ser Met Tyr Ser Thr Ile Ala
65     70     75     80
Arg Glu Ile Leu Glu Gly Cys Lys Ser Pro Leu Val Leu Gly Met
85     90     95
Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val Thr
100    105    110
Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe Leu
115    120    125
Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser Thr
130    135    140
Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys Val
145    150    155    160
Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp Val
165    170    175
Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe Thr
180    185    190
Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro Lys
195    200    205
Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp Arg
210    215    220
Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val Ser
225    230    235    240
Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly Tyr
245    250    255
Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly Asp
260    265    270
Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val Gln
275    280    285
Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro Met
290    295    300
Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn Lys
305    310    315    320
Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile Ile
325    330    335
Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp Ile
340    345    350
Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser
```

355 360 365

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1497989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Tyr	Ser	Thr	Ile	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Gly	Cys	Lys	Ser
1				5				10						15	
Pro	Leu	Val	Leu	Gly	Met	Ile	Ser	Leu	Met	Asn	Leu	Thr	Gly	Ala	Pro
			20					25					30		
Gln	Phe	Ser	Gly	Val	Thr	Gly	Leu	Gly	Ile	Ser	Pro	Phe	Lys	Thr	Ser
			35				40					45			
Ser	Val	Ile	Pro	Phe	Leu	Arg	Gly	Ser	Lys	Trp	Met	Pro	Cys	Ser	Ile
			50				55				60				
Pro	Ala	Thr	Leu	Ser	Thr	Asp	Ile	Ala	Glu	Val	Asp	Arg	Gly	Gly	Lys
65						70				75					80
Val	Cys	Asp	Pro	Lys	Val	Lys	Leu	Glu	Leu	Ser	Asp	Lys	Val	Ser	Asn
				85					90					95	
Gly	Gly	Asn	Gly	Trp	Val	Asn	Lys	Leu	Leu	Asn	Ile	Cys	Ser	Glu	Asp
			100					105					110		
Ala	Lys	Ala	Ala	Phe	Thr	Ala	Val	Thr	Phe	Ser	Leu	Leu	Phe	Arg	Ser
			115				120					125			
Ala	Leu	Ala	Glu	Pro	Lys	Ser	Ile	Pro	Ser	Thr	Ser	Met	Leu	Pro	Thr
			130				135					140			
Leu	Asp	Val	Gly	Asp	Arg	Val	Ile	Ala	Glu	Lys	Val	Ser	Tyr	Phe	Phe
145						150				155					160
Arg	Lys	Pro	Glu	Val	Ser	Asp	Ile	Val	Ile	Phe	Lys	Ala	Pro	Pro	Ile
				165					170					175	
Leu	Val	Glu	His	Gly	Tyr	Ser	Cys	Ala	Asp	Val	Phe	Ile	Lys	Arg	Ile
			180					185					190		
Val	Ala	Ser	Glu	Gly	Asp	Trp	Val	Glu	Val	Cys	Asp	Gly	Lys	Leu	Leu
			195				200					205			
Val	Asn	Asp	Thr	Val	Gln	Ala	Glu	Asp	Phe	Val	Leu	Glu	Pro	Ile	Asp
			210				215					220			
Tyr	Glu	Met	Glu	Pro	Met	Phe	Val	Pro	Glu	Gly	Tyr	Val	Phe	Val	Leu
225						230				235					240
Gly	Asp	Asn	Arg	Asn	Lys	Ser	Phe	Asp	Ser	His	Asn	Trp	Gly	Pro	Leu
				245					250					255	
Pro	Ile	Lys	Asn	Ile	Ile	Gly	Arg	Ser	Val	Phe	Arg	Tyr	Trp	Pro	Pro
			260					265					270		
Ser	Lys	Val	Ser	Asp	Ile	Ile	His	His	Glu	Gln	Val	Ser	Gln	Lys	Arg
			275				280						285		
Ala	Val	Asp	Val	Ser											
															290

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1497990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Ile	Ser	Leu	Met	Asn	Leu	Thr	Gly	Ala	Pro	Gln	Phe	Ser	Gly	Val
1				5				10						15	
Thr	Gly	Leu	Gly	Ile	Ser	Pro	Phe	Lys	Thr	Ser	Ser	Val	Ile	Pro	Phe
			20					25					30		
Leu	Arg	Gly	Ser	Lys	Trp	Met	Pro	Cys	Ser	Ile	Pro	Ala	Thr	Leu	Ser
		35				40					45				
Thr	Asp	Ile	Ala	Glu	Val	Asp	Arg	Gly	Gly	Lys	Val	Cys	Asp	Pro	Lys
	50					55					60				
Val	Lys	Leu	Glu	Leu	Ser	Asp	Lys	Val	Ser	Asn	Gly	Gly	Asn	Gly	Trp
65					70					75				80	
Val	Asn	Lys	Leu	Leu	Asn	Ile	Cys	Ser	Glu	Asp	Ala	Lys	Ala	Ala	Phe
			85						90					95	
Thr	Ala	Val	Thr	Phe	Ser	Leu	Leu	Phe	Arg	Ser	Ala	Leu	Ala	Glu	Pro
			100					105					110		
Lys	Ser	Ile	Pro	Ser	Thr	Ser	Met	Leu	Pro	Thr	Leu	Asp	Val	Gly	Asp
	115						120					125			
Arg	Val	Ile	Ala	Glu	Lys	Val	Ser	Tyr	Phe	Phe	Arg	Lys	Pro	Glu	Val
	130					135					140				
Ser	Asp	Ile	Val	Ile	Phe	Lys	Ala	Pro	Pro	Ile	Leu	Val	Glu	His	Gly
145					150					155				160	
Tyr	Ser	Cys	Ala	Asp	Val	Phe	Ile	Lys	Arg	Ile	Val	Ala	Ser	Glu	Gly
			165						170					175	
Asp	Trp	Val	Glu	Val	Cys	Asp	Gly	Lys	Leu	Leu	Val	Asn	Asp	Thr	Val
		180						185					190		
Gln	Ala	Glu	Asp	Phe	Val	Leu	Glu	Pro	Ile	Asp	Tyr	Glu	Met	Glu	Pro
	195							200				205			
Met	Phe	Val	Pro	Glu	Gly	Tyr	Val	Phe	Val	Leu	Gly	Asp	Asn	Arg	Asn
	210					215					220				
Lys	Ser	Phe	Asp	Ser	His	Asn	Trp	Gly	Pro	Leu	Pro	Ile	Lys	Asn	Ile
225					230					235				240	
Ile	Gly	Arg	Ser	Val	Phe	Arg	Tyr	Trp	Pro	Pro	Ser	Lys	Val	Ser	Asp
			245						250					255	
Ile	Ile	His	His	Glu	Gln	Val	Ser	Gln	Lys	Arg	Ala	Val	Asp	Val	Ser
			260					265						270	

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..591

(D) OTHER INFORMATION: / Ceres Seq. ID 1497991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

aatttcacat	ctttctcacc	caaattctact	cttaaccgta	cttcttcttc	tacagacatc	60
aattttctctc	gagataaact	aaattcttcgc	tgaaaaaatg	tcgggtcgtg	gaaaggagg	120
aaaaggtttg	ggtaaaggag	gagccaagcg	tcacaggaag	gttctgagag	acaacatcca	180
aggaatcacc	aagcctgcga	ttcgaagatt	ggctcgtaga	ggtggagtca	agcgtatcag	240
tggtctcatc	tacgaggaga	ctcgtggcgt	cctcaagatc	tttctcgaga	acgtgattcg	300
tgatgctgtc	acttacaccg	agcacgctag	gaggaagact	gtgaccgcca	tggatgttgt	360
ctacgctctc	aagaggcaag	gaaggactct	ttacggattc	ggtgggtaat	tagagttttt	420
cagatccgcg	tttgtgtttt	ctgggtttct	cacttaagcg	tctgcgtttt	acttttgtat	480
tgggtttggc	gtttagtagt	ttgcggtagc	gttcttggtta	tgtgtaatta	cgctttttct	540
tcttgcttca	gcagtttcg	ttgaaatata	aatcgaatca	agtttcactt	c	

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 103 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..103  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala
 1             5             10             15
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
          20          25          30
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
          35          40          45
Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu
          50          55          60
Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys
          65          70          75          80
Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg
          85          90          95
Thr Leu Tyr Gly Phe Gly Gly
          100
```

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1508 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1508  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
gcncnagncc nttncskggg nsggcnnkrr ksggrrrrrrk srsqkkkkkk gatcactttt      60
tttggtttct ttcgcgaagc caaaaaaaaaa caagacaaaa agaaataaac gacgaggctt      120
ttgtttatct tataaagctc ctccaccggt aaaagccttg gtcctcatga aaccgggaag      180
cccaagtact tacttccacc atcaaactcg caaaccattt gcaaccatcg atggtggtca      240
tgtcacgagt aagcttctac tcttctttct tgctactact gttagaggtc gttgtcgcta      300
gcagcgagtt tgatgatgag aagaacatcg ttcagtccaa ccacggctat aatcatgac      360
gtactcgcta gtgttttctt cgcacttgga tgtatctccg tctacatgag gaggtgtctc      420
cagcacgctc tggggatgga cagcggtggt ggtccaggaa actggcttaa cgtgaggcaa      480
acgacggagc ctgggctaga cgcgtctggt atagaaacgt ttccaacggt tccttactct      540
acagtgaaga cgttgaggat cggtaaagaa gctttggagt gtcccgtttg tctcaacgag      600
ttcgaggacg acgaaacgct gcgtttgatt cctcagtggt gtcacgtggt tcatcctggt      660
tgcattgatg cctggctccg ttctcagacc acatgtcctc tttgccgagc caatctcggt      720
cctgtaccgg gtgagctctg ttcttcggag ataccgggtt tagctagaga aaccggtcag      780
aactctctca gaacgccgat tgatgataac cggaaaaggg ttttaacttc acctgacgag      840
cgggttgatt actcagtggc ttggacgggt aaccaaagca tgccacgtaa atccatgtct      900
acaggttgga aactagctga attgtacagc ccggctagtt caccggggcca accggaggag      960
aatctcgacc ggtatacgct gaggttacca caagagatac atgaccagct tgtgaactcc      1020
agcctgggaa agcaagggtc aaaaggccaa ctggccttac ctcaagaaag gagctcggtt      1080
agaggggttc gaaccggaag cctagggact gaaaagaact atttctactt tgaacgggtt      1140
gatcaagacg gtcgggttga ccggagacca ttttctataa ctccctccata ccatacccggt      1200
tcgatacagt ctccggatga gattatcaac gctagtggta attatcagga tcgtgctggt      1260
tcacctaaag gtttgcttct agcaataagg tcaccggttg atcggttatt tactgggaag      1320
aaaaatgccg gtgagcggtc gtaccttcaa tccggcgatg cgagccctgt ctaggcgaat      1380
tactactatt ggggttatta agaataattct gaaataaaga aaatctgtat atgtattttc      1440
```

tttcttctag tttctttatg ttatatgaga aattcaattc cttcaccaat ataatgcac 1500  
tggtactg

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Met	Arg	Arg	Thr	Ser	Phe	Ser	Pro	Thr	Thr	Ala	Ile	Ile	Met	Ile
1				5					10					15	
Val	Leu	Val	Ser	Val	Phe	Phe	Ala	Leu	Gly	Cys	Ile	Ser	Val	Tyr	Met
			20					25					30		
Arg	Arg	Cys	Leu	Gln	His	Ala	Leu	Gly	Met	Asp	Ser	Gly	Gly	Gly	Pro
		35					40					45			
Gly	Asn	Trp	Leu	Asn	Val	Arg	Gln	Thr	Thr	Glu	Pro	Gly	Leu	Asp	Ala
	50					55					60				
Ser	Val	Ile	Glu	Thr	Phe	Pro	Thr	Phe	Pro	Tyr	Ser	Thr	Val	Lys	Thr
65					70					75				80	
Leu	Arg	Ile	Gly	Lys	Glu	Ala	Leu	Glu	Cys	Pro	Val	Cys	Leu	Asn	Glu
			85					90					95		
Phe	Glu	Asp	Asp	Glu	Thr	Leu	Arg	Leu	Ile	Pro	Gln	Cys	Cys	His	Val
		100					105					110			
Phe	His	Pro	Gly	Cys	Ile	Asp	Ala	Trp	Leu	Arg	Ser	Gln	Thr	Thr	Cys
		115					120					125			
Pro	Leu	Cys	Arg	Ala	Asn	Leu	Val	Pro	Val	Pro	Gly	Glu	Ser	Val	Ser
	130					135					140				
Ser	Glu	Ile	Pro	Gly	Leu	Ala	Arg	Glu	Thr	Gly	Gln	Asn	Ser	Leu	Arg
145					150					155				160	
Thr	Pro	Ile	Asp	Asp	Asn	Arg	Lys	Arg	Val	Leu	Thr	Ser	Pro	Asp	Glu
			165					170						175	
Arg	Leu	Ile	Asp	Ser	Val	Ala	Trp	Thr	Gly	Asn	Gln	Ser	Met	Pro	Arg
		180					185						190		
Lys	Ser	Met	Ser	Thr	Gly	Trp	Lys	Leu	Ala	Glu	Leu	Tyr	Ser	Pro	Ala
		195				200						205			
Ser	Ser	Pro	Gly	Gln	Pro	Glu	Glu	Asn	Leu	Asp	Arg	Tyr	Thr	Leu	Arg
	210					215					220				
Leu	Pro	Gln	Glu	Ile	His	Asp	Gln	Leu	Val	Asn	Ser	Ser	Leu	Gly	Lys
225					230					235				240	
Gln	Gly	Ser	Lys	Gly	Gln	Leu	Ala	Leu	Pro	Gln	Glu	Arg	Ser	Ser	Val
			245					250					255		
Arg	Gly	Phe	Arg	Thr	Gly	Ser	Leu	Gly	Thr	Glu	Lys	Asn	Tyr	Phe	Tyr
		260					265						270		
Phe	Glu	Arg	Phe	Asp	Gln	Asp	Gly	Arg	Leu	Asp	Arg	Arg	Pro	Phe	Ser
		275					280					285			
Ile	Thr	Pro	Pro	Tyr	His	Thr	Arg	Ser	Ile	Gln	Ser	Pro	Asp	Glu	Ile
	290					295					300				
Ile	Asn	Ala	Ser	Gly	Asn	Tyr	Gln	Asp	Arg	Ala	Gly	Ser	Pro	Lys	Gly
305					310					315				320	
Leu	Leu	Leu	Ala	Ile	Arg	Ser	Pro	Phe	Asp	Arg	Leu	Phe	Thr	Gly	Lys
			325					330					335		
Lys	Asn	Ala	Gly	Glu	Arg	Ser	Tyr	Leu	Gln	Ser	Gly	Asp	Ala	Ser	Pro
			340					345					350		
Val															

(2) INFORMATION FOR SEQ ID NO:113:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 352 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..352  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met	Arg	Arg	Thr	Ser	Phe	Ser	Pro	Thr	Thr	Ala	Ile	Ile	Met	Ile	Val
1				5				10					15		
Leu	Val	Ser	Val	Phe	Phe	Ala	Leu	Gly	Cys	Ile	Ser	Val	Tyr	Met	Arg
			20					25					30		
Arg	Cys	Leu	Gln	His	Ala	Leu	Gly	Met	Asp	Ser	Gly	Gly	Gly	Pro	Gly
		35					40					45			
Asn	Trp	Leu	Asn	Val	Arg	Gln	Thr	Thr	Glu	Pro	Gly	Leu	Asp	Ala	Ser
	50					55					60				
Val	Ile	Glu	Thr	Phe	Pro	Thr	Phe	Pro	Tyr	Ser	Thr	Val	Lys	Thr	Leu
65				70					75					80	
Arg	Ile	Gly	Lys	Glu	Ala	Leu	Glu	Cys	Pro	Val	Cys	Leu	Asn	Glu	Phe
			85					90						95	
Glu	Asp	Asp	Glu	Thr	Leu	Arg	Leu	Ile	Pro	Gln	Cys	Cys	His	Val	Phe
			100					105					110		
His	Pro	Gly	Cys	Ile	Asp	Ala	Trp	Leu	Arg	Ser	Gln	Thr	Thr	Cys	Pro
		115					120					125			
Leu	Cys	Arg	Ala	Asn	Leu	Val	Pro	Val	Pro	Gly	Glu	Ser	Val	Ser	Ser
		130				135						140			
Glu	Ile	Pro	Gly	Leu	Ala	Arg	Glu	Thr	Gly	Gln	Asn	Ser	Leu	Arg	Thr
145				150					155					160	
Pro	Ile	Asp	Asp	Asn	Arg	Lys	Arg	Val	Leu	Thr	Ser	Pro	Asp	Glu	Arg
			165					170						175	
Leu	Ile	Asp	Ser	Val	Ala	Trp	Thr	Gly	Asn	Gln	Ser	Met	Pro	Arg	Lys
		180					185						190		
Ser	Met	Ser	Thr	Gly	Trp	Lys	Leu	Ala	Glu	Leu	Tyr	Ser	Pro	Ala	Ser
		195				200						205			
Ser	Pro	Gly	Gln	Pro	Glu	Glu	Asn	Leu	Asp	Arg	Tyr	Thr	Leu	Arg	Leu
	210					215					220				
Pro	Gln	Glu	Ile	His	Asp	Gln	Leu	Val	Asn	Ser	Ser	Leu	Gly	Lys	Gln
225				230					235					240	
Gly	Ser	Lys	Gly	Gln	Leu	Ala	Leu	Pro	Gln	Glu	Arg	Ser	Ser	Val	Arg
			245						250					255	
Gly	Phe	Arg	Thr	Gly	Ser	Leu	Gly	Thr	Glu	Lys	Asn	Tyr	Phe	Tyr	Phe
		260					265						270		
Glu	Arg	Phe	Asp	Gln	Asp	Gly	Arg	Leu	Asp	Arg	Arg	Pro	Phe	Ser	Ile
		275				280						285			
Thr	Pro	Pro	Tyr	His	Thr	Arg	Ser	Ile	Gln	Ser	Pro	Asp	Glu	Ile	Ile
	290				295						300				
Asn	Ala	Ser	Gly	Asn	Tyr	Gln	Asp	Arg	Ala	Gly	Ser	Pro	Lys	Gly	Leu
305				310					315					320	
Leu	Leu	Ala	Ile	Arg	Ser	Pro	Phe	Asp	Arg	Leu	Phe	Thr	Gly	Lys	Lys
			325					330						335	
Asn	Ala	Gly	Glu	Arg	Ser	Tyr	Leu	Gln	Ser	Gly	Asp	Ala	Ser	Pro	Val
		340					345						350		

- (2) INFORMATION FOR SEQ ID NO:114:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 339 amino acids  
        (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..339  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497996  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Ile	Val	Leu	Val	Ser	Val	Phe	Phe	Ala	Leu	Gly	Cys	Ile	Ser	Val
1			5						10					15	
Tyr	Met	Arg	Arg	Cys	Leu	Gln	His	Ala	Leu	Gly	Met	Asp	Ser	Gly	Gly
			20					25					30		
Gly	Pro	Gly	Asn	Trp	Leu	Asn	Val	Arg	Gln	Thr	Thr	Glu	Pro	Gly	Leu
			35				40					45			
Asp	Ala	Ser	Val	Ile	Glu	Thr	Phe	Pro	Thr	Phe	Pro	Tyr	Ser	Thr	Val
	50					55					60				
Lys	Thr	Leu	Arg	Ile	Gly	Lys	Glu	Ala	Leu	Glu	Cys	Pro	Val	Cys	Leu
65					70					75				80	
Asn	Glu	Phe	Glu	Asp	Asp	Glu	Thr	Leu	Arg	Leu	Ile	Pro	Gln	Cys	Cys
				85					90					95	
His	Val	Phe	His	Pro	Gly	Cys	Ile	Asp	Ala	Trp	Leu	Arg	Ser	Gln	Thr
			100					105						110	
Thr	Cys	Pro	Leu	Cys	Arg	Ala	Asn	Leu	Val	Pro	Val	Pro	Gly	Glu	Ser
		115					120					125			
Val	Ser	Ser	Glu	Ile	Pro	Gly	Leu	Ala	Arg	Glu	Thr	Gly	Gln	Asn	Ser
	130					135						140			
Leu	Arg	Thr	Pro	Ile	Asp	Asn	Arg	Lys	Arg	Val	Leu	Thr	Ser	Pro	
145				150					155					160	
Asp	Glu	Arg	Leu	Ile	Asp	Ser	Val	Ala	Trp	Thr	Gly	Asn	Gln	Ser	Met
			165					170						175	
Pro	Arg	Lys	Ser	Met	Ser	Thr	Gly	Trp	Lys	Leu	Ala	Glu	Leu	Tyr	Ser
		180						185					190		
Pro	Ala	Ser	Ser	Pro	Gly	Gln	Pro	Glu	Glu	Asn	Leu	Asp	Arg	Tyr	Thr
	195					200						205			
Leu	Arg	Leu	Pro	Gln	Glu	Ile	His	Asp	Gln	Leu	Val	Asn	Ser	Ser	Leu
	210					215					220				
Gly	Lys	Gln	Gly	Ser	Lys	Gly	Gln	Leu	Ala	Leu	Pro	Gln	Glu	Arg	Ser
225					230					235				240	
Ser	Val	Arg	Gly	Phe	Arg	Thr	Gly	Ser	Leu	Gly	Thr	Glu	Lys	Asn	Tyr
			245						250					255	
Phe	Tyr	Phe	Glu	Arg	Phe	Asp	Gln	Asp	Gly	Arg	Leu	Asp	Arg	Arg	Pro
		260				265						270			
Phe	Ser	Ile	Thr	Pro	Pro	Tyr	His	Thr	Arg	Ser	Ile	Gln	Ser	Pro	Asp
	275					280						285			
Glu	Ile	Ile	Asn	Ala	Ser	Gly	Asn	Tyr	Gln	Asp	Arg	Ala	Gly	Ser	Pro
	290					295					300				
Lys	Gly	Leu	Leu	Leu	Ala	Ile	Arg	Ser	Pro	Phe	Asp	Arg	Leu	Phe	Thr
305					310					315				320	
Gly	Lys	Lys	Asn	Ala	Gly	Glu	Arg	Ser	Tyr	Leu	Gln	Ser	Gly	Asp	Ala
			325						330					335	
Ser	Pro	Val													

- (2) INFORMATION FOR SEQ ID NO:115:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 842 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -

(B) LOCATION: 1..842

(D) OTHER INFORMATION: / Ceres Seq. ID 1497997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ctacgattag	tttaatctct	cagtccaccg	gagagtgtaa	aaacagcgag	aaaatcgacg	60
tcgttcgac	gccgactgcg	agcgaagaag	aagatggctg	aagaagaagt	tgactacgta	120
ttcaaggttg	ttttgaacgg	agattcagcg	gttgggaagt	cacagctacg	ggctcggttc	180
acaagagacg	aattcagtat	ggattccaaa	gccacaattc	ggtgtcgatt	tcaataactcg	240
aacgctcgtt	attgacgata	agaacatcaa	agctcagatc	tgggacatcg	caggccagaa	300
acgacacaga	gctattacat	agcctacta	caaagggtgt	gttgggtgcaa	tgttagttaa	360
cgatatgaca	atacgtgaaa	gccttgagca	cattcctcag	tggttggaag	aactacgagt	420
gcacgcggat	aagaacattg	tcatcatctt	gattggtaac	aagacggatt	tagagaacca	480
gagatcgggt	cctgtggaag	atgccaaagg	atttgcagag	aaggaagggc	tttttttcct	540
tgagacttcv	gcactaaact	ccacaaatgt	cgagaactct	ttcaacactc	tcttgactga	600
gatcttcaac	aaggtgaaca	agaagaatct	cgctaagacc	accgtgtctt	gcagctcaca	660
agtcagtctt	ctaagaccac	cgtgtgttgc	agctcamtaa	gtcagtcttc	tcgatttggt	720
ccattacagt	ttagaatgaa	ataaaccatt	tcatatactt	caaaaatatt	gtttatatatt	780
ggtttttaga	tagtgagttt	tgtgtagtgt	acgttgattt	ttagaacaaa	atctttcatt	840
tt						

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1497998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met	Leu	Val	Tyr	Asp	Met	Thr	Ile	Arg	Glu	Ser	Phe	Glu	His	Ile	Pro
1			5						10					15	
Gln	Trp	Leu	Glu	Glu	Leu	Arg	Val	His	Ala	Asp	Lys	Asn	Ile	Val	Ile
		20						25					30		
Ile	Leu	Ile	Gly	Asn	Lys	Thr	Asp	Leu	Glu	Asn	Gln	Arg	Ser	Val	Pro
		35					40					45			
Val	Glu	Asp	Ala	Lys	Glu	Phe	Ala	Glu	Lys	Glu	Gly	Leu	Phe	Phe	Leu
		50				55					60				
Glu	Thr	Xaa	Ala	Leu	Asn	Ser	Thr	Asn	Val	Glu	Asn	Ser	Phe	Asn	Thr
		65			70					75				80	
Leu	Leu	Thr	Glu	Ile	Phe	Asn	Lys	Val	Asn	Lys	Lys	Asn	Leu	Ala	Lys
			85						90					95	
Thr	Thr	Val	Ser	Cys	Ser	Ser	Gln	Val	Ser	Leu	Leu	Arg	Pro	Pro	Cys
		100						105					110		
Val	Ala	Ala	Xaa												
		115													

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1497999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met	Thr	Ile	Arg	Glu	Ser	Phe	Glu	His	Ile	Pro	Gln	Trp	Leu	Glu	Glu
1				5						10				15	
Leu	Arg	Val	His	Ala	Asp	Lys	Asn	Ile	Val	Ile	Ile	Leu	Ile	Gly	Asn

	20		25		30										
Lys	Thr	Asp	Leu	Glu	Asn	Gln	Arg	Ser	Val	Pro	Val	Glu	Asp	Ala	Lys
	35						40					45			
Glu	Phe	Ala	Glu	Lys	Glu	Gly	Leu	Phe	Phe	Leu	Glu	Thr	Xaa	Ala	Leu
	50					55					60				
Asn	Ser	Thr	Asn	Val	Glu	Asn	Ser	Phe	Asn	Thr	Leu	Leu	Thr	Glu	Ile
65					70					75				80	
Phe	Asn	Lys	Val	Asn	Lys	Lys	Asn	Leu	Ala	Lys	Thr	Thr	Val	Ser	Cys
			85						90					95	
Ser	Ser	Gln	Val	Ser	Leu	Leu	Arg	Pro	Pro	Cys	Val	Ala	Ala	Xaa	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

taaaaaagg	tacaaaagg	gatgtcacag	cactaaagcc	cactataatg	acagctgttc	60
cagccattct	tgatcgtgtc	agggatgggt	tccgcaaaaa	ggttgatgca	aaggggcggat	120
tgtcaaagaa	attgtttgac	tttgcataatg	ctcggcgatt	atctgcaatc	aatgggaagt	180
ggtttggagc	ctgggggattg	gaaaagcttt	tgtgggatgt	gcttgtgttc	aggaaaattc	240
gtgcagtgtt	gggaggtcaa	attcgctatt	tgctctctgg	tggtgccct	ctttctgggtg	300
acactcagag	attcatatac	atctgcgttg	gggtccaat	cggtcaggga	tatgggctca	360
cagagacttg	tgctgggtgga	accttctctg	agtttgagga	cacatccgtt	ggccgagttg	420
gtgctccact	tccttgctcc	tttgtaaagc	tagtagactg	ggcggaaggt	gggtatctaa	480
ccagtataaa	gccaatgccc	cgtggtgaaa	ttgtaattgg	tggtcctaat	atcacgcttg	540
ggtatttcaa	aaatgaggag	aaaactaaag	aagtgtacaa	ggttgatgaa	aagggaatga	600
ggtgggttcta	cacaggagac	ataggacgat	ttcacctga	tggtgcctc	gagataatag	660
accgaaaaaa	ggatatacgtt	aaacttcagc	acggagaata	tgctccttg	ggcaaagtgtg	720
aagctgctct	aagtataagt	ccctatgttg	aaaacataat	ggttcatgct	gattcgttct	780
acagttactg	tgtggctctt	gtggctcgct	cccaacatac	agttgaaggt	tgggcttcaa	840
agsaaggaa	agastttgcc	aacttcgaag	aactgtgcac	gaaagagcaa	gccgtgaaag	900
aagtgtatgc	ttatcttgct	aaggcggcta	aacaatcacg	attggagaag	tttgagatac	960
cmgcaaagat	caaattgttg	gcattctccat	ggacgccaga	gtcaggatta	gtcacagcag	1020
ctctaaagct	taaaagagac	gtaattagga	gggaattctc	tgaagatctc	accaagtatt	1080
atgcctaaac	ttttcttctt	cccttacttt	gttttatctt	ttacgtctcg	atgcattcga	1140
aagacgcaac	agctgcacaa	aaacttaatt	ctaagaatag	tgtatctttt	ctctctgtga	1200
tgtctgtctt	ttcgtgcaaa	tgtatggggg	taactgtgac	gagactgaaa	gaaagaaagt	1260
tatgggtctt						

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..361
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Lys	Lys	Gly	Thr	Lys	Gly	Asp	Val	Thr	Ala	Leu	Lys	Pro	Thr	Ile	Met
1			5				10				15				
Thr	Ala	Val	Pro	Ala	Ile	Leu	Asp	Arg	Val	Arg	Asp	Gly	Val	Arg	Lys
		20					25					30			

Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe Ala  
35 40 45  
Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala Trp  
50 55 60  
Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile Arg  
65 70 75 80  
Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala Pro  
85 90 95  
Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala Pro  
100 105 110  
Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr Phe  
115 120 125  
Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu Pro  
130 135 140  
Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu Thr  
145 150 155 160  
Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn  
165 170 175  
Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr  
180 185 190  
Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly  
195 200 205  
Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp  
210 215 220  
Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu  
225 230 235 240  
Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala  
245 250 255  
Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His  
260 265 270  
Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe  
275 280 285  
Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr  
290 295 300  
Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa  
305 310 315 320  
Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu  
325 330 335  
Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe  
340 345 350  
Ser Glu Asp Leu Thr Lys Leu Tyr Ala  
355 360

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg  
1 5 10 15  
Lys Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe  
20 25 30  
Ala Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala  
35 40 45  
Trp Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile

<div>(X1) SEQUENCE DESCRIPTION: SEQ ID: 1</div>															
Met	Pro	Arg	Gly	Glu	Ile	Val	Ile	Gly	Gly	Ser	Asn	Ile	Thr	Leu	Gly
1				5					10					15	
Tyr	Phe	Lys	Asn	Glu	Glu	Lys	Thr	Lys	Glu	Val	Tyr	Lys	Val	Asp	Glu
			20					25					30		
Lys	Gly	Met	Arg	Trp	Phe	Tyr	Thr	Gly	Asp	Ile	Gly	Arg	Phe	His	Pro
		35					40					45			
Asp	Gly	Cys	Leu	Glu	Ile	Ile	Asp	Arg	Lys	Lys	Asp	Ile	Val	Lys	Leu
	50					55					60				
Gln	His	Gly	Glu	Tyr	Val	Ser	Leu	Gly	Lys	Val	Glu	Ala	Ala	Leu	Ser
65				70						75				80	
Ile	Ser	Pro	Tyr	Val	Glu	Asn	Ile	Met	Val	His	Ala	Asp	Ser	Phe	Tyr
				85					90					95	

Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His Thr Val Glu Gly  
100 105 110  
Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe Glu Glu Leu Cys  
115 120 125  
Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr Leu Val Lys Ala  
130 135 140  
Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa Ala Lys Ile Lys  
145 150 155 160  
Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala Ala  
165 170 175  
Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe Ser Glu Asp Leu  
180 185 190  
Thr Lys Leu Tyr Ala  
195

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..764
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

ctaatacgaaa aatcatcact ttcacaatct tcttcatcga tttctctctt ccaaatctcc	60
caaaagatgt cgaaccctag agttttcttc gacatgagtc tcagcggtag tcccatcgga	120
cggatcgaga tggagctttt cgctgataca accccaaaca cggcggagaa tttccgtgct	180
ctctgtaccg gcgagaaagg aatgggaaag ctaggtaagc cacttcactt caaaggatcg	240
atcttccacc gtgtgattcc cggattcatg tgtcaaggag gtgatttcac cgccaagaac	300
ggaaccggtg gtgaatcgat ctacgggtgct aagttcaagg acgagaactt tatcaagaag	360
catacaggag ctgggattct ctcaatggct aactctggtc ctaacactaa cggatctcag	420
ttcttcatct gtaccgataa gacgtcgtgg ttagatggta agcacgttgt gtttggaaca	480
gttgttaaag gcttggacgt cgtgaaggcg attgagaaaag ttggatctga ttctggaaaag	540
acttccaaaag tcgttaccat cactgattgt ggtcagcttt cttagatcta agtgagaaaag	600
tgagagactt tgatctttat gagtaataat ggtgtctttt gctttcggtt gttcttcctc	660
ttaccttaat ggattattct gtttaggggt tgagttttcg tttcagagtt tgtaacaaaa	720
cccttttgtg ttttctgggg tttgaaataa ttatgagctt actc	

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Leu Ile Glu Lys Ser Ser Leu Ser Gln Ser Ser Ser Ile Ser Leu  
1 5 10 15  
Phe Gln Ile Ser Gln Lys Met Ser Asn Pro Arg Val Phe Phe Asp Met  
20 25 30  
Ser Leu Ser Gly Thr Pro Ile Gly Arg Ile Glu Met Glu Leu Phe Ala  
35 40 45  
Asp Thr Thr Pro Asn Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly  
50 55 60  
Glu Lys Gly Met Gly Lys Leu Gly Lys Pro Leu His Phe Lys Gly Ser  
65 70 75 80

Ile	Phe	His	Arg	Val	Ile	Pro	Gly	Phe	Met	Cys	Gln	Gly	Gly	Asp	Phe
				85					90					95	
Thr	Ala	Lys	Asn	Gly	Thr	Gly	Gly	Glu	Ser	Ile	Tyr	Gly	Ala	Lys	Phe
			100					105					110		
Lys	Asp	Glu	Asn	Phe	Ile	Lys	Lys	His	Thr	Gly	Ala	Gly	Ile	Leu	Ser
		115					120					125			
Met	Ala	Asn	Ser	Gly	Pro	Asn	Thr	Asn	Gly	Ser	Gln	Phe	Phe	Ile	Cys
	130					135				140					
Thr	Asp	Lys	Thr	Ser	Trp	Leu	Asp	Gly	Lys	His	Val	Val	Phe	Gly	Gln
145					150					155					160
Val	Val	Lys	Gly	Leu	Asp	Val	Val	Lys	Ala	Ile	Glu	Lys	Val	Gly	Ser
			165					170						175	
Asp	Ser	Gly	Lys	Thr	Ser	Lys	Val	Val	Thr	Ile	Thr	Asp	Cys	Gly	Gln
			180					185					190		
Leu	Ser														

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1498008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met	Ser	Asn	Pro	Arg	Val	Phe	Phe	Asp	Met	Ser	Leu	Ser	Gly	Thr	Pro
1			5					10						15	
Ile	Gly	Arg	Ile	Glu	Met	Glu	Leu	Phe	Ala	Asp	Thr	Thr	Pro	Asn	Thr
			20					25					30		
Ala	Glu	Asn	Phe	Arg	Ala	Leu	Cys	Thr	Gly	Glu	Lys	Gly	Met	Gly	Lys
		35				40						45			
Leu	Gly	Lys	Pro	Leu	His	Phe	Lys	Gly	Ser	Ile	Phe	His	Arg	Val	Ile
	50				55					60					
Pro	Gly	Phe	Met	Cys	Gln	Gly	Gly	Asp	Phe	Thr	Ala	Lys	Asn	Gly	Thr
65				70				75						80	
Gly	Gly	Glu	Ser	Ile	Tyr	Gly	Ala	Lys	Phe	Lys	Asp	Glu	Asn	Phe	Ile
			85					90						95	
Lys	Lys	His	Thr	Gly	Ala	Gly	Ile	Leu	Ser	Met	Ala	Asn	Ser	Gly	Pro
			100				105						110		
Asn	Thr	Asn	Gly	Ser	Gln	Phe	Phe	Ile	Cys	Thr	Asp	Lys	Thr	Ser	Trp
		115				120						125			
Leu	Asp	Gly	Lys	His	Val	Val	Phe	Gly	Gln	Val	Val	Lys	Gly	Leu	Asp
	130					135					140				
Val	Val	Lys	Ala	Ile	Glu	Lys	Val	Gly	Ser	Asp	Ser	Gly	Lys	Thr	Ser
145					150					155					160
Lys	Val	Val	Thr	Ile	Thr	Asp	Cys	Gly	Gln	Leu	Ser				
					165					170					

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498009



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Ser Leu Ser Gly Thr Pro Ile Gly Arg Ile Glu Met Glu Leu Phe  
1 5 10 15  
Ala Asp Thr Thr Pro Asn Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr  
20 25 30  
Gly Glu Lys Gly Met Gly Lys Leu Gly Lys Pro Leu His Phe Lys Gly  
35 40 45  
Ser Ile Phe His Arg Val Ile Pro Gly Phe Met Cys Gln Gly Gly Asp  
50 55 60  
Phe Thr Ala Lys Asn Gly Thr Gly Gly Glu Ser Ile Tyr Gly Ala Lys  
65 70 75 80  
Phe Lys Asp Glu Asn Phe Ile Lys Lys His Thr Gly Ala Gly Ile Leu  
85 90 95  
Ser Met Ala Asn Ser Gly Pro Asn Thr Asn Gly Ser Gln Phe Phe Ile  
100 105 110  
Cys Thr Asp Lys Thr Ser Trp Leu Asp Gly Lys His Val Val Phe Gly  
115 120 125  
Gln Val Val Lys Gly Leu Asp Val Val Lys Ala Ile Glu Lys Val Gly  
130 135 140  
Ser Asp Ser Gly Lys Thr Ser Lys Val Val Thr Ile Thr Asp Cys Gly  
145 150 155 160  
Gln Leu Ser

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

aaccaaaga atcacgacat tgaatcttct ttcatctctc tcctcaagac atagtagcat 60  
aagamaatga agatatacat actaggatgg gtcttagtcc ttatcttcat ctctattacc 120  
attgttttoga gtgcaccagc acctaaacct cctaaacctta agcctgcacc agcacctaca 180  
cctcctaaac ctaagccccc accagcacct acacctccta aacctaaagg caaaccagca 240  
cctacacctc ctaaacctaa gccacacca gcacctacac ctccctaaacc taagcctgca 300  
ccagcaccag caccagcacc aacaccagca ccgaaacctta aacctgcacc taaaccagca 360  
ccaggtggag aagttgagga cgaaaccgag ttttagctacg agacgaaagg aaacaagggg 420  
ccagcgaaat ggggaacact acatgcagag tggaaaatgt gtggaatagg caaaatgcaa 480  
tctcctattg atcttcggga caaaaatgtg gtagttagta ataaatttgg attgcttcgt 540  
agccagtatc tgccttctaa taccaccatt aagaacagag gtcattgat catgttgaaa 600  
ttcaaaggag gcaataaagg tattggtgtc actatccgtg gtactagata tcaacttcaa 660  
caacttcatt ggcactctcc ttccgaacat acaatcaatg gcaaaagggt tgcgctagag 720  
gaacacttgg ttcatgagag taaagatava cgctacgctg ttgtcgcttt cttatacaat 780  
ctcggagcat ctgacccttt tctcttttctg ttggaaaaac aattgaagaa gataactgat 840  
acacatgcgt ccgaggaaca tgtcggaatc attgatccca aaaaactcag ttttgaatca 900  
aaacattatt atagatatcc cggatcactt actgctcctc catgttctga aaatgttatt 960  
tggtccgctt ccaaagagat tcgcactgtg tcaagtaaac aagtgaagct tctccgtgtg 1020  
gctgtacacg atgcttcaga ttcaaagtgc aggcgcttc aagcagtc aaagcgcaag 1080  
gtatatattt acaaaccaaa gggttaagtta atgaagaaat actgtaatat aagttcttac 1140  
tagtaatctt taattcttta tatatgtaca ttatgaattg tactactaaa tgatgttttt 1200  
agggataaac tgatgacttg gttttgttat t

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..358  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498011  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met	Lys	Ile	Ser	Ser	Leu	Gly	Trp	Val	Leu	Val	Leu	Ile	Phe	Ile	Ser
1			5					10						15	
Ile	Thr	Ile	Val	Ser	Ser	Ala	Pro	Ala	Pro	Lys	Pro	Pro	Lys	Pro	Lys
			20				25						30		
Pro	Ala	Pro	Ala	Pro	Thr	Pro	Pro	Lys	Pro	Lys	Pro	Thr	Pro	Ala	Pro
			35				40					45			
Thr	Pro	Pro	Lys	Pro	Lys	Pro	Lys	Pro	Ala	Pro	Thr	Pro	Pro	Lys	Pro
			50				55				60				
Lys	Pro	Thr	Pro	Ala	Pro	Thr	Pro	Pro	Lys	Pro	Lys	Pro	Ala	Pro	Ala
65					70					75					80
Pro	Ala	Pro	Ala	Pro	Thr	Pro	Ala	Pro	Lys	Pro	Lys	Pro	Ala	Pro	Lys
				85					90					95	
Pro	Ala	Pro	Gly	Gly	Glu	Val	Glu	Asp	Glu	Thr	Glu	Phe	Ser	Tyr	Glu
			100					105					110		
Thr	Lys	Gly	Asn	Lys	Gly	Pro	Ala	Lys	Trp	Gly	Thr	Leu	His	Ala	Glu
			115				120					125			
Trp	Lys	Met	Cys	Gly	Ile	Gly	Lys	Met	Gln	Ser	Pro	Ile	Asp	Leu	Arg
						135					140				
Asp	Lys	Asn	Val	Val	Val	Ser	Asn	Lys	Phe	Gly	Leu	Leu	Arg	Ser	Gln
145					150					155					160
Tyr	Leu	Pro	Ser	Asn	Thr	Thr	Ile	Lys	Asn	Arg	Gly	His	Asp	Ile	Met
				165					170					175	
Leu	Lys	Phe	Lys	Gly	Gly	Asn	Lys	Gly	Ile	Gly	Val	Thr	Ile	Arg	Gly
			180					185					190		
Thr	Arg	Tyr	Gln	Leu	Gln	Gln	Leu	His	Trp	His	Ser	Pro	Ser	Glu	His
			195				200					205			
Thr	Ile	Asn	Gly	Lys	Arg	Phe	Ala	Leu	Glu	Glu	His	Leu	Val	His	Glu
			210				215					220			
Ser	Lys	Asp	Xaa	Arg	Tyr	Ala	Val	Val	Ala	Phe	Leu	Tyr	Asn	Leu	Gly
225					230					235					240
Ala	Ser	Asp	Pro	Phe	Leu	Phe	Ser	Leu	Glu	Lys	Gln	Leu	Lys	Lys	Ile
				245					250					255	
Thr	Asp	Thr	His	Ala	Ser	Glu	Glu	His	Val	Gly	Ile	Ile	Asp	Pro	Lys
			260					265					270		
Lys	Leu	Ser	Phe	Glu	Ser	Lys	His	Tyr	Tyr	Arg	Tyr	Ser	Gly	Ser	Leu
			275				280					285			
Thr	Ala	Pro	Pro	Cys	Ser	Glu	Asn	Val	Ile	Trp	Ser	Val	Ser	Lys	Glu
					295						300				
Ile	Arg	Thr	Val	Ser	Ser	Lys	Gln	Val	Lys	Leu	Leu	Arg	Val	Ala	Val
305					310					315					320
His	Asp	Ala	Ser	Asp	Ser	Asn	Ala	Arg	Pro	Leu	Gln	Ala	Val	Asn	Lys
				325					330					335	
Arg	Lys	Val	Tyr	Leu	Tyr	Lys	Pro	Lys	Val	Lys	Leu	Met	Lys	Lys	Tyr
			340					345					350		
Cys	Asn	Ile	Ser	Ser	Tyr										
					355										

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 228 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..228  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp Lys
1          5          10          15
Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu
20          25          30
Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu Lys
35          40          45
Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr Arg
50          55          60
Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr Ile
65          70          75          80
Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser Lys
85          90          95
Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser
100          105          110
Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp
115          120          125
Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys Lys Leu
130          135          140
Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala
145          150          155          160
Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu Ile Arg
165          170          175
Thr Val Ser Ser Lys Gln Val Lys Leu Arg Val Ala Val His Asp
180          185          190
Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys Arg Lys
195          200          205
Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr Cys Asn
210          215          220
Ile Ser Ser Tyr
225
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..222  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
Met Gln Ser Pro Ile Asp Leu Arg Asp Lys Asn Val Val Val Ser Asn
1          5          10          15
Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu Pro Ser Asn Thr Thr Ile
20          25          30
Lys Asn Arg Gly His Asp Ile Met Leu Lys Phe Lys Gly Gly Asn Lys
35          40          45
Gly Ile Gly Val Thr Ile Arg Gly Thr Arg Tyr Gln Leu Gln Gln Leu
50          55          60
His Trp His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Ala
65          70          75          80
Leu Glu Glu His Leu Val His Glu Ser Lys Asp Xaa Arg Tyr Ala Val
85          90          95
Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser Asp Pro Phe Leu Phe Ser
100          105          110
Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp Thr His Ala Ser Glu Glu
```

115 120 125  
His Val Gly Ile Ile Asp Pro Lys Lys Leu Ser Phe Glu Ser Lys His  
130 135 140  
Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala Pro Pro Cys Ser Glu Asn  
145 150 155 160  
Val Ile Trp Ser Val Ser Lys Glu Ile Arg Thr Val Ser Ser Lys Gln  
165 170 175  
Val Lys Leu Leu Arg Val Ala Val His Asp Ala Ser Asp Ser Asn Ala  
180 185 190  
Arg Pro Leu Gln Ala Val Asn Lys Arg Lys Val Tyr Leu Tyr Lys Pro  
195 200 205  
Lys Val Lys Leu Met Lys Lys Tyr Cys Asn Ile Ser Ser Tyr  
210 215 220

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1084
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

aaatttcaac	ccctggttgc	tttgtttgat	ccctagattt	tcgccgtggt	atagaagaat	60
ctcatttttt	gccgtctgaa	tcgaaatttc	gtgtcgagaa	ctcctccact	cctccacttc	120
tcgttttttc	tttttaattt	attttactct	attgtgacca	ttttgagcgt	tattgagaac	180
tcaaagctca	agaatgcgtg	caccatcttt	gcttgacaaa	tgcttgccgg	gtttgctgcc	240
tcaagaccga	gsgggtgtgt	ctgcrttatc	agagaaggat	ttgcagcttc	caacaccagc	300
tgttgagatc	ataccttcta	agacagtagc	tcacacacag	tattcagggg	agaatctaga	360
tgcgctcggt	ttacaagttt	tcaagggaaa	agtaagtgtt	gctgatatca	ttgggctctc	420
tgggtcagaa	actgtctcct	taaaaaatga	aggttctttg	aaaagttggg	aaagctctgt	480
tgttcttggt	aatgtcctta	aaaacgagat	ccgtgatgga	cagcttagct	tcagggggcaa	540
aagggtcctc	gagctaggct	gtccatcacg	gatctcgttt	ttaaggacnt	taaagagwac	600
aagcaacttg	atgctgaaat	ccacaggaac	tacatctacg	gtggccatct	ctcaaactac	660
atgaagctgt	tggggggaaga	tgagccggag	aagttgcaaa	ctcacttcag	tgcttacatt	720
aagaaaggag	ttgaagctga	gagcatcgag	gagatgtaca	agaaggttca	cgcagctatc	780
cgagcagaac	ccaaccataa	gaaaaccgag	aaatctgctc	ccamsgaaca	caagaggtag	840
aacttgaaga	aactgactta	cgaagagagg	aagaacaagt	tgatcgagag	agtgaaggca	900
ttaaaccggag	caggtggtga	tgatgatgat	gaggatgatg	aagagtaaata	caccaatcaa	960
gccttctttg	tctcatgcct	ctagtagctt	tttacttatt	tattttcaga	ctaaaacact	1020
cagtttttgt	tttcacattt	tagttgcgtt	tgaagatttt	gaattcgagg	atatgttttg	1080
tttg						

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Arg Ala Pro Ser Leu Leu Ala Gln Cys Leu Pro Gly Leu Leu Pro  
1 5 10 15  
Gln Asp Arg Xaa Gly Val Ser Xaa Leu Ser Glu Lys Asp Leu Gln Leu  
20 25 30  
Pro Thr Pro Ala Val Glu Ile Ile Pro Ser Lys Thr Val Ala His His

35 40 45  
Arg Tyr Ser Gly Glu Asn Leu Asp Ala Leu Gly Leu Gln Val Phe Lys  
50 55 60  
Gly Lys Val Ser Val Ala Asp Ile Ile Gly Leu Ser Gly Ser Glu Thr  
65 70 75 80  
Ala Pro Leu Lys Asn Glu Gly Ser Leu Lys Ser Trp Glu Ser Ser Val  
85 90 95  
Val Leu Val Asn Val Leu Lys Asn Glu Ile Arg Asp Gly Gln Leu Ser  
100 105 110  
Phe Arg Gly Lys Arg Val Leu Glu Gly Cys Pro Ser Arg Ile Ser  
115 120 125  
Phe Leu Arg Xaa Leu Lys Xaa Thr Ser Asn Leu Met Leu Lys Ser Thr  
130 135 140  
Gly Thr Thr Ser Thr Val Ala Ile Ser Gln Thr Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe  
1 5 10 15  
Ser Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Met  
20 25 30  
Tyr Lys Lys Val His Ala Ala Ile Arg Ala Glu Pro Asn His Lys Lys  
35 40 45  
Thr Glu Lys Ser Ala Pro Xaa Glu His Lys Arg Tyr Asn Leu Lys Lys  
50 55 60  
Leu Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Lys Ala  
65 70 75 80  
Leu Asn Gly Ala Gly Gly Asp Asp Asp Asp Glu Asp Asp Glu Glu  
85 90 95

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..656

(D) OTHER INFORMATION: / Ceres Seq. ID 1498028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

attaaatcct aaaatccatt attgattgaa tcttcgagtt accaacaaaa aaaaaactct 60  
cctttatttc agttttcttt tacaaacat aatcttctct ttgattccat cttgtgaacc 120  
accggcataa gaaaatatga caattgcttt aacgatcgga ggaaacgggt tttcgggtct 180  
accaggatcg tcgttttcoat catcatcttc gtcgtttcga ttaaaaaaca gcagaagaaa 240  
gaacacgaag atgctcaaca gatcaaaagt cgtttgttct tcttcatctt ctgtaatgga 300  
tccgthtaag actcttaaga tccgacccga ttcattctgaa tacgaggtca agaaagcttt 360  
cagacaactc gctaaaaagg tttgaccttt tgtttagctc aatcatctta gatctgggtt 420  
tttaaaattt gacatctttc tgatcgattt tgttttgatt gttgcagtat catcctgatg 480  
tttgtagagg aagcaattgt ggggtacagt ttcagacaat taacgaagct tacgatgtaa 540  
gcgtgtgttt atgaaagcta actatgcttt ttggttaact taaaacagat tgaaattcgc 600

ttttgtaatg aaaattgata tctttgtttt ttttcctttg aagattgtgt tgaagc

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Thr	Ile	Ala	Leu	Thr	Ile	Gly	Gly	Asn	Gly	Phe	Ser	Gly	Leu	Pro
1				5					10					15	
Gly	Ser	Ser	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Arg	Leu	Lys	Asn	Ser
			20					25					30		
Arg	Arg	Lys	Asn	Thr	Lys	Met	Leu	Asn	Arg	Ser	Lys	Val	Val	Cys	Ser
		35					40					45			
Ser	Ser	Ser	Ser	Val	Met	Asp	Pro	Xaa	Lys	Thr	Leu	Lys	Ile	Arg	Pro
		50				55					60				
Asp	Ser	Ser	Glu	Tyr	Glu	Val	Lys	Lys	Ala	Phe	Arg	Gln	Leu	Ala	Lys
65					70					75					80
Lys	Val														

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Leu	Asn	Arg	Ser	Lys	Val	Val	Cys	Ser	Ser	Ser	Ser	Ser	Val	Met
1				5					10					15	
Asp	Pro	Xaa	Lys	Thr	Leu	Lys	Ile	Arg	Pro	Asp	Ser	Ser	Glu	Tyr	Glu
			20					25					30		
Val	Lys	Lys	Ala	Phe	Arg	Gln	Leu	Ala	Lys	Lys	Val				
		35					40								

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

actcaccaaaa	gcatacacata	acactcacac	acacactttc	tcttctctta	ttttctcagt	60
tcttttaact	cttttctcta	cctatatcca	aatggccacc	gtcgagggtg	aacaagtgc	120
tccagtagca	gctgagaaca	tcgagggtgc	accaccaaa	gctgtggagt	cggaggaagt	180
caccaccgtc	tccgagtctc	ttccagctcc	ggtaacagaa	tctcaagcgc	ctgtcgaagt	240
aacaactaaa	gatttggtcg	tggaagagac	agagaaacca	atcgaagaaa	cagaggaagc	300
tcaagttgaa	actccggagg	ttgtggagat	caagaaagat	gaagaagctc	cggttgaaac	360

tccgggtgggt	gtggaggatg	agagcaaaac	agaggaagtt	gtagaggcga	agaaagagga	420
agaagtagaa	gaaaagaaga	cagaggaagc	tccagtgggt	gtggagggaag	agaagaagcc	480
agaggcagag	gaggagaaac	ccgccgtggt	tacctccccg	gctcaagcca	ccatggtcgc	540
tccattcacc	ggcttgaagt	catccgcttc	tttcccggtc	acccgcaagg	ccaacaacga	600
cattacttcc	atcacaagca	acggaggaag	agtttagctgc	atgaagggtgt	ggccaccaat	660
cggaaagaag	aagtttagac	tctatcttac	ctccctgacc	ttagtgacgt	tgaattggct	720
aaggaagttg	actaccttct	ccgcaacaag	tggattcctt	gtgttgaatt	cgagttggag	780
cacggatttg	tgtaccgtga	gcacggaaac	actcccggat	actatgatgg	acggtactgg	840
acaatgtgga	agcttccatt	gttcggatgc	accgactccg	ctcaagtgtt	gaaggaagtt	900
gaagaatgca	agaaggagta	ccctggcgcc	ttcattagga	tcatacgatt	cgacaacacc	960
cgtcaagtcc	aatgcatcag	tttcattgcc	tacaagcccc	caagcttcac	cgaagcttaa	1020
tcccctttct	ggaatattca	gcgttgatta	ttctggaacc	cattttctatg	tgggtcaatgc	1080
aaatttaaga	aattattttgc	cgacttaaaa	gttgaggaac	tattgtttga	aagtc	

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Leu	Thr	Lys	Ala	Ser	His	Asn	Thr	His	Thr	His	Thr	Phe	Ser	Ser	Leu
1				5					10					15	
Ile	Phe	Ser	Val	Leu	Leu	Thr	Leu	Phe	Ser	Thr	Tyr	Ile	Gln	Met	Ala
			20					25					30		
Thr	Val	Glu	Val	Glu	Gln	Val	Thr	Pro	Val	Ala	Ala	Glu	Asn	Ile	Glu
			35				40					45			
Val	Pro	Pro	Pro	Lys	Ala	Val	Glu	Ser	Glu	Glu	Val	Thr	Thr	Val	Ser
			50			55					60				
Glu	Ser	Leu	Pro	Ala	Pro	Val	Thr	Glu	Ser	Gln	Ala	Pro	Val	Glu	Val
65					70					75				80	
Thr	Thr	Lys	Asp	Leu	Val	Val	Glu	Glu	Thr	Glu	Lys	Pro	Ile	Glu	Glu
				85					90					95	
Thr	Glu	Glu	Ala	Gln	Val	Glu	Thr	Pro	Glu	Val	Val	Glu	Ile	Lys	Lys
			100					105					110		
Asp	Glu	Glu	Ala	Pro	Val	Glu	Thr	Pro	Val	Val	Val	Glu	Asp	Glu	Ser
			115				120					125			
Lys	Thr	Glu	Glu	Val	Val	Glu	Ala	Lys	Lys	Glu	Glu	Glu	Val	Glu	Glu
			130			135					140				
Lys	Lys	Thr	Glu	Glu	Ala	Pro	Val	Val	Val	Glu	Glu	Glu	Lys	Lys	Pro
145					150					155				160	
Glu	Ala	Glu	Glu	Glu	Lys	Pro	Ala	Val	Val	Thr	Ser	Pro	Ala	Gln	Ala
				165					170					175	
Thr	Met	Val	Ala	Pro	Phe	Thr	Gly	Leu	Lys	Ser	Ser	Ala	Ser	Phe	Pro
			180					185					190		
Val	Thr	Arg	Lys	Ala	Asn	Asn	Asp	Ile	Thr	Ser	Ile	Thr	Ser	Asn	Gly
			195				200					205			
Gly	Arg	Val	Ser	Cys	Met	Lys	Val	Trp	Pro	Pro	Ile	Gly	Lys	Lys	Lys
			210			215					220				
Phe	Arg	Leu	Tyr	Leu	Thr	Ser	Leu	Thr	Leu	Val	Thr	Leu	Asn	Trp	Leu
225					230					235				240	
Arg	Lys	Leu	Thr	Thr	Phe	Ser	Ala	Thr	Ser	Gly	Phe	Leu	Val	Leu	Asn
				245					250					255	
Ser	Ser	Trp	Ser	Thr	Asp	Leu	Cys	Thr	Val	Ser	Thr	Glu	Thr	Leu	Pro
			260					265					270		
Asp	Thr	Met	Met	Asp	Gly	Thr	Gly	Gln	Cys	Gly	Ser	Phe	His	Cys	Ser
			275				280					285			

Asp Ala Pro Thr Pro Leu Lys Cys  
290 295

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn
1          5          10          15
Ile Glu Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr
          20          25          30
Val Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val
          35          40          45
Glu Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile
          50          55          60
Glu Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile
65          70          75          80
Lys Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp
          85          90          95
Glu Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val
          100          105          110
Glu Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys
          115          120          125
Lys Pro Glu Ala Glu Glu Glu Lys Pro Ala Val Val Thr Ser Pro Ala
          130          135          140
Gln Ala Thr Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ser Ala Ser
145          150          155          160
Phe Pro Val Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
          165          170          175
Asn Gly Gly Arg Val Ser Cys Met Lys Val Trp Pro Pro Ile Gly Lys
          180          185          190
Lys Lys Phe Arg Leu Tyr Leu Thr Ser Leu Thr Leu Val Thr Leu Asn
          195          200          205
Trp Leu Arg Lys Leu Thr Thr Phe Ser Ala Thr Ser Gly Phe Leu Val
          210          215          220
Leu Asn Ser Ser Trp Ser Thr Asp Leu Cys Thr Val Ser Thr Glu Thr
225          230          235          240
Leu Pro Asp Thr Met Met Asp Gly Thr Gly Gln Cys Gly Ser Phe His
          245          250          255
Cys Ser Asp Ala Pro Thr Pro Leu Lys Cys
260          265

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

gctcattagg gtttctcatc tacgacggcg tgggtgttcct ctttctgtct ctgaaaaatg



```
gcgaagagaa cgaagaaggt tggaatcgtc ggcaaatacg gaacacgtta tggcgaggt 120
atcaggaagc agattaagaa gatggaggtc agccagcaca gcaagtactt ctgtgagttg 180
tatctggggg tgcaaggatt gtggcaaggt caaggcaggt ggtgcttaca caatgaacac 240
cgccagtgcg gtcactgtta gaagcacgat cagaagggtg agggagcaga tcgaggggta 300
aaagtctgct ggctttttat atttggtttc cttggtttga caattttaagt ttgcaaact 360
ctatgcttgt gatittgaat caagacttat acattgagca gtttaagcag gtttttattt 420
tttggtg
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
Leu Ile Arg Val Ser His Leu Arg Arg Gly Val Pro Pro Ser Cys
1           5           10           15
Ser Glu Lys Trp Arg Arg Glu Arg Arg Arg Leu Glu Ser Ser Ala Asn
          20           25           30
Thr Glu His Val Met Val Arg Val Ser Gly Ser Arg Leu Arg Arg Trp
          35           40           45
Arg Ser Ala Ser Thr Ala Ser Thr Ser Val Ser Cys Ile Trp Gly Cys
          50           55           60
Lys Asp Cys Gly Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr
65           70           75           80
Ala Ser Ala Val Thr Val Arg Ser Thr Ile Arg Arg Leu Arg Glu Gln
          85           90           95
Ile Glu Gly
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
Met Ala Lys Arg Thr Lys Lys Val Gly Ile Val Gly Lys Tyr Gly Thr
1           5           10           15
Arg Tyr Gly Ala Ser Ile Arg Lys Gln Ile Lys Lys Met Glu Val Ser
          20           25           30
Gln His Ser Lys Tyr Phe Cys Glu Leu Tyr Leu Gly Leu Gln Gly Leu
          35           40           45
Trp Gln Gly Gln Gly Arg Trp Cys Leu His Asn Glu His Arg Gln Cys
          50           55           60
Gly His Cys
65
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1498039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Val	Arg	Val	Ser	Gly	Ser	Arg	Leu	Arg	Arg	Trp	Arg	Ser	Ala	Ser
1				5					10					15	
Thr	Ala	Ser	Thr	Ser	Val	Ser	Cys	Ile	Trp	Gly	Cys	Lys	Asp	Cys	Gly
			20					25					30		
Lys	Val	Lys	Ala	Gly	Gly	Ala	Tyr	Thr	Met	Asn	Thr	Ala	Ser	Ala	Val
		35					40					45			
Thr	Val	Arg	Ser	Thr	Ile	Arg	Arg	Leu	Arg	Glu	Gln	Ile	Glu	Gly	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2253 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2253

(D) OTHER INFORMATION: / Ceres Seq. ID 1498043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

aaaaccacac	acacagcttc	ttcactgaga	gcttttttct	agggtttctc	tctttgtttc	60
ttacaatgcg	actcttcttc	acaccgtcaa	tgtccaatct	ctccatattc	ttctcgattc	120
ttctcctttc	tcttcctctt	ccgtcaatcg	gagatctcgc	cgccgacaaa	tccgctcttc	180
tctctttttc	ttccgccgtc	ggtggtcgta	cattactctg	ggacgtcaag	caaacctcac	240
catgcaactg	gaccggcgtc	ttatgcgacg	gtggctcgtg	tactgctctt	cgtcttcccg	300
gtgaaacgct	ctccgggtcat	ataccggagg	gtatttttgg	taatttaact	cagctccgga	360
cgcttagtct	ccgtctcaat	ggtcttactg	gttctcttcc	tttgatctc	ggaagatgct	420
ccgatcttcg	gcgtttgtac	ctgcagggtta	acagattctc	cggtgagatt	ccggagggtt	480
tgtttagtct	tagtaacctt	gttaggttga	atctagctga	gaatgaattt	agtggagaga	540
tctcgtcagg	gtttaaaaac	cttactaggc	ttaagactct	gtacctggag	aataacaagc	600
tctctggctc	tcttttagac	ttggatttgc	ctttggatca	gttcaacgtt	tctaataact	660
tgttgaacgg	atctatacct	aagagtttgc	agaagtttga	ttctgattcg	tttgtgggaa	720
cttctctctg	cggcaaaccg	cttggtgtct	gctctaata	gggaactgtg	ccaagccagc	780
caattttctg	tggcaatatt	cccggaaact	ttgaaggacg	tgaggagaag	aagaaaagga	840
agaagctttc	tgggtggagct	atagctggaa	tagtgattgg	atgtgtggtt	ggtttgtccc	900
tgattgttat	gattttgatg	gttctcttta	ggaaaaaggg	gaacgagaga	acaagggccca	960
ttgaccttgc	aaccatcaag	caccatgaag	ttgaaattcc	tggcgagaaa	gcggccgtgg	1020
aagcaccgga	gaataggagc	tatgtaaatg	agtactctcc	gtctgcagtg	aaagctgtgg	1080
aagtgaacag	ttcaggggat	aagaagttag	tgttttttgg	gaatgcgaca	aaggtcttcg	1140
atcttgagga	tctgttgaga	gcttcagcgg	aggttctggg	gaaaggaacg	ttcgggacag	1200
cttataaagc	ggtgcttgac	gcggtgacat	tgggtgctgt	gaagagactg	aaggatgtaa	1260
cgatggcgga	cagagagttt	aaggagaaga	ttgaggttgt	tggggcgatg	gatcatgaga	1320
acttggtgcc	cttgagagcg	tactattaca	gtggagacga	gaagctgctt	gtctatgact	1380
tcatgcctat	gggaagctta	tcagctctct	tacacggaaa	caaaggtgca	ggccggcctc	1440
cattgaactg	ggaagtcaga	tcaggcatcg	cccttgagac	tgctcgtggc	ttagactatc	1500
ttcactcaca	agacccactg	agctctcacg	gaaacgtcaa	gtcctccaat	atcctcttaa	1560
caaactccca	tgacgcacga	gtgtctgatt	toggcctggc	tcagcttgta	agcgcctcat	1620
ccacaacccc	aaaccggggc	actgggtacc	gtgcgccaga	agtaactgac	ccgaggcgtg	1680
tctcacagaa	agcggacgtg	tacagctttg	gtgtggtgtt	gctagagttg	ctcaccggaa	1740
aagctccgtc	taactcggtg	atgaacgagg	aaggaatgga	tttgccgagg	tgggtgcatt	1800
cagtggcgag	agaggagtgg	aggaatgagg	tttttgactc	ggagctgatg	agtatcgaga	1860
cagttgtctc	ggtggaagaa	gagatggcgg	aaatgctgca	gctgggcatt	gactgtacag	1920
agcagcacc	agacaagcgg	ccagttatgg	tggaggtggg	gagaaggatc	caggagttgc	1980
gccaatcggg	tgcagatcgg	gtggggtaag	accatcagat	gaaaggagac	ttgagacatg	2040
agtctgttcg	atgatctgaa	gcggcgacgt	tttcagtgtt	tagttttaag	aatatggcgg	2100

gaattagagt tggggtcggt aattagatgt ttttaatttt ttttttttgt ttttttggtt 2160  
tctttcatgt gtgggcactg atgatgagga gtttcgtggt gggtgtaatt attagtgcct 2220  
ttaacttttaa ctttattttc aatattgttt ttc

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Asn	His	Thr	His	Ser	Phe	Phe	Thr	Glu	Ser	Phe	Phe	Leu	Gly	Phe	Leu		
1				5				10						15			
Ser	Leu	Phe	Leu	Thr	Met	Arg	Leu	Phe	Thr	Pro	Ser	Met	Ser	Asn			
			20					25					30				
Leu	Ser	Ile	Phe	Phe	Ser	Ile	Leu	Leu	Ser	Leu	Pro	Leu	Pro	Ser			
			35				40					45					
Ile	Gly	Asp	Leu	Ala	Ala	Asp	Lys	Ser	Ala	Leu	Leu	Ser	Phe	Arg	Ser		
			50				55					60					
Ala	Val	Gly	Gly	Arg	Thr	Leu	Leu	Trp	Asp	Val	Lys	Gln	Thr	Ser	Pro		
65					70					75					80		
Cys	Asn	Trp	Thr	Gly	Val	Leu	Cys	Asp	Gly	Gly	Arg	Val	Thr	Ala	Leu		
					85				90						95		
Arg	Leu	Pro	Gly	Glu	Thr	Leu	Ser	Gly	His	Ile	Pro	Glu	Gly	Ile	Phe		
			100					105					110				
Gly	Asn	Leu	Thr	Gln	Leu	Arg	Thr	Leu	Ser	Leu	Arg	Leu	Asn	Gly	Leu		
			115				120					125					
Thr	Gly	Ser	Leu	Pro	Leu	Asp	Leu	Gly	Arg	Cys	Ser	Asp	Leu	Arg	Arg		
			130				135					140					
Leu	Tyr	Leu	Gln	Gly	Asn	Arg	Phe	Ser	Gly	Glu	Ile	Pro	Glu	Val	Leu		
145					150					155					160		
Phe	Ser	Leu	Ser	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ala	Glu	Asn	Glu	Phe		
					165				170						175		
Ser	Gly	Glu	Ile	Ser	Ser	Gly	Phe	Lys	Asn	Leu	Thr	Arg	Leu	Lys	Thr		
			180					185					190				
Leu	Tyr	Leu	Glu	Asn	Asn	Lys	Leu	Ser	Gly	Ser	Leu	Leu	Asp	Leu	Asp		
			195			200						205					
Leu	Ser	Leu	Asp	Gln	Phe	Asn	Val	Ser	Asn	Asn	Leu	Leu	Asn	Gly	Ser		
			210			215					220						
Ile	Pro	Lys	Ser	Leu	Gln	Lys	Phe	Asp	Ser	Asp	Ser	Phe	Val	Gly	Thr		
225					230					235					240		
Ser	Leu	Cys	Gly	Lys	Pro	Leu	Val	Val	Cys	Ser	Asn	Glu	Gly	Thr	Val		
					245				250					255			
Pro	Ser	Gln	Pro	Ile	Ser	Val	Gly	Asn	Ile	Pro	Gly	Thr	Val	Glu	Gly		
			260					265					270				
Arg	Glu	Glu	Lys	Lys	Lys	Arg	Lys	Lys	Leu	Ser	Gly	Gly	Ala	Ile	Ala		
			275				280					285					
Gly	Ile	Val	Ile	Gly	Cys	Val	Val	Gly	Leu	Ser	Leu	Ile	Val	Met	Ile		
			290			295					300						
Leu	Met	Val	Leu	Phe	Arg	Lys	Lys	Gly	Asn	Glu	Arg	Thr	Arg	Ala	Ile		
305					310				315					320			
Asp	Leu	Ala	Thr	Ile	Lys	His	His	Glu	Val	Glu	Ile	Pro	Gly	Glu	Lys		
					325				330					335			
Ala	Ala	Val	Glu	Ala	Pro	Glu	Asn	Arg	Ser	Tyr	Val	Asn	Glu	Tyr	Ser		
			340				345						350				
Pro	Ser	Ala	Val	Lys	Ala	Val	Glu	Val	Asn	Ser	Ser	Gly	Met	Lys	Lys		
			355				360						365				

```

Leu Val Phe Phe Gly Asn Ala Thr Lys Val Phe Asp Leu Glu Asp Leu
 370                      375                      380
Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly Thr Phe Gly Thr Ala
385                      390                      395                      400
Tyr Lys Ala Val Leu Asp Ala Val Thr Leu Val Ala Val Lys Arg Leu
                      405                      410                      415
Lys Asp Val Thr Met Ala Asp Arg Glu Phe Lys Glu Lys Ile Glu Val
                      420                      425                      430
Val Gly Ala Met Asp His Glu Asn Leu Val Pro Leu Arg Ala Tyr Tyr
                      435                      440                      445
Tyr Ser Gly Asp Glu Lys Leu Leu Val Tyr Asp Phe Met Pro Met Gly
450                      455                      460
Ser Leu Ser Ala Leu Leu His Gly Asn Lys Gly Ala Gly Arg Pro Pro
465                      470                      475                      480
Leu Asn Trp Glu Val Arg Ser Gly Ile Ala Leu Gly Ala Ala Arg Gly
                      485                      490                      495
Leu Asp Tyr Leu His Ser Gln Asp Pro Leu Ser Ser His Gly Asn Val
                      500                      505                      510
Lys Ser Ser Asn Ile Leu Leu Thr Asn Ser His Asp Ala Arg Val Ser
                      515                      520                      525
Asp Phe Gly Leu Ala Gln Leu Val Ser Ala Ser Ser Thr Thr Pro Asn
530                      535                      540
Arg Ala Thr Gly Tyr Arg Ala Pro Glu Val Thr Asp Pro Arg Arg Val
545                      550                      555                      560
Ser Gln Lys Ala Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu
                      565                      570                      575
Leu Thr Gly Lys Ala Pro Ser Asn Ser Val Met Asn Glu Glu Gly Met
                      580                      585                      590
Asp Leu Ala Arg Trp Val His Ser Val Ala Arg Glu Glu Trp Arg Asn
595                      600                      605
Glu Val Phe Asp Ser Glu Leu Met Ser Ile Glu Thr Val Val Ser Val
610                      615                      620
Glu Glu Glu Met Ala Glu Met Leu Gln Leu Gly Ile Asp Cys Thr Glu
625                      630                      635                      640
Gln His Pro Asp Lys Arg Pro Val Met Val Glu Val Val Arg Arg Ile
                      645                      650                      655
Gln Glu Leu Arg Gln Ser Gly Ala Asp Arg Val Gly
                      660                      665

```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..647
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

Met Arg Leu Phe Phe Thr Pro Ser Met Ser Asn Leu Ser Ile Phe Phe
 1                      5                      10                      15
Ser Ile Leu Leu Leu Ser Leu Pro Leu Pro Ser Ile Gly Asp Leu Ala
                      20                      25                      30
Ala Asp Lys Ser Ala Leu Leu Ser Phe Arg Ser Ala Val Gly Gly Arg
35                      40                      45
Thr Leu Leu Trp Asp Val Lys Gln Thr Ser Pro Cys Asn Trp Thr Gly
50                      55                      60
Val Leu Cys Asp Gly Gly Arg Val Thr Ala Leu Arg Leu Pro Gly Glu
65                      70                      75                      80
Thr Leu Ser Gly His Ile Pro Glu Gly Ile Phe Gly Asn Leu Thr Gln

```

85										90					95				
Leu	Arg	Thr	Leu	Ser	Leu	Arg	Leu	Asn	Gly	Leu	Thr	Gly	Ser	Leu	Pro				
			100					105					110						
Leu	Asp	Leu	Gly	Arg	Cys	Ser	Asp	Leu	Arg	Arg	Leu	Tyr	Leu	Gln	Gly				
		115					120					125							
Asn	Arg	Phe	Ser	Gly	Glu	Ile	Pro	Glu	Val	Leu	Phe	Ser	Leu	Ser	Asn				
		130				135					140								
Leu	Val	Arg	Leu	Asn	Leu	Ala	Glu	Asn	Glu	Phe	Ser	Gly	Glu	Ile	Ser				
	145				150					155					160				
Ser	Gly	Phe	Lys	Asn	Leu	Thr	Arg	Leu	Lys	Thr	Leu	Tyr	Leu	Glu	Asn				
				165					170					175					
Asn	Lys	Leu	Ser	Gly	Ser	Leu	Leu	Asp	Leu	Asp	Leu	Ser	Leu	Asp	Gln				
			180					185					190						
Phe	Asn	Val	Ser	Asn	Asn	Leu	Leu	Asn	Gly	Ser	Ile	Pro	Lys	Ser	Leu				
		195					200					205							
Gln	Lys	Phe	Asp	Ser	Asp	Ser	Phe	Val	Gly	Thr	Ser	Leu	Cys	Gly	Lys				
		210				215					220								
Pro	Leu	Val	Val	Cys	Ser	Asn	Glu	Gly	Thr	Val	Pro	Ser	Gln	Pro	Ile				
	225				230						235				240				
Ser	Val	Gly	Asn	Ile	Pro	Gly	Thr	Val	Glu	Gly	Arg	Glu	Glu	Lys	Lys				
				245					250					255					
Lys	Arg	Lys	Lys	Leu	Ser	Gly	Gly	Ala	Ile	Ala	Gly	Ile	Val	Ile	Gly				
			260					265					270						
Cys	Val	Val	Gly	Leu	Ser	Leu	Ile	Val	Met	Ile	Leu	Met	Val	Leu	Phe				
			275				280					285							
Arg	Lys	Lys	Gly	Asn	Glu	Arg	Thr	Arg	Ala	Ile	Asp	Leu	Ala	Thr	Ile				
		290				295					300								
Lys	His	His	Glu	Val	Glu	Ile	Pro	Gly	Glu	Lys	Ala	Ala	Val	Glu	Ala				
					310						315				320				
Pro	Glu	Asn	Arg	Ser	Tyr	Val	Asn	Glu	Tyr	Ser	Pro	Ser	Ala	Val	Lys				
				325					330					335					
Ala	Val	Glu	Val	Asn	Ser	Ser	Gly	Met	Lys	Lys	Leu	Val	Phe	Phe	Gly				
			340					345					350						
Asn	Ala	Thr	Lys	Val	Phe	Asp	Leu	Glu	Asp	Leu	Leu	Arg	Ala	Ser	Ala				
		355					360					365							
Glu	Val	Leu	Gly	Lys	Gly	Thr	Phe	Gly	Thr	Ala	Tyr	Lys	Ala	Val	Leu				
		370				375					380								
Asp	Ala	Val	Thr	Leu	Val	Ala	Val	Lys	Arg	Leu	Lys	Asp	Val	Thr	Met				
					390				395					400					
Ala	Asp	Arg	Glu	Phe	Lys	Glu	Lys	Ile	Glu	Val	Val	Gly	Ala	Met	Asp				
				405					410					415					
His	Glu	Asn	Leu	Val	Pro	Leu	Arg	Ala	Tyr	Tyr	Tyr	Tyr	Ser	Gly	Asp	Glu			
			420				425						430						
Lys	Leu	Leu	Val	Tyr	Asp	Phe	Met	Pro	Met	Gly	Ser	Leu	Ser	Ala	Leu				
			435				440					445							
Leu	His	Gly	Asn	Lys	Gly	Ala	Gly	Arg	Pro	Pro	Leu	Asn	Trp	Glu	Val				
					455						460								
Arg	Ser	Gly	Ile	Ala	Leu	Gly	Ala	Ala	Arg	Gly	Leu	Asp	Tyr	Leu	His				
					470						475				480				
Ser	Gln	Asp	Pro	Leu	Ser	Ser	His	Gly	Asn	Val	Lys	Ser	Ser	Asn	Ile				
				485					490					495					
Leu	Leu	Thr	Asn	Ser	His	Asp	Ala	Arg	Val	Ser	Asp	Phe	Gly	Leu	Ala				
			500					505					510						
Gln	Leu	Val	Ser	Ala	Ser	Ser	Thr	Thr	Pro	Asn	Arg	Ala	Thr	Gly	Tyr				
			515				520					525							
Arg	Ala	Pro	Glu	Val	Thr	Asp	Pro	Arg	Arg	Val	Ser	Gln	Lys	Ala	Asp				
		530				535					540								
Val	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu	Leu	Leu	Thr	Gly	Lys	Ala				
					550				555					560					
Pro	Ser	Asn	Ser	Val	Met	Asn	Glu	Glu	Gly	Met	Asp	Leu	Ala	Arg	Trp				
				565					570					575					

Val His Ser Val Ala Arg Glu Glu Trp Arg Asn Glu Val Phe Asp Ser  
580 585 590  
Glu Leu Met Ser Ile Glu Thr Val Val Ser Val Glu Glu Glu Met Ala  
595 600 605  
Glu Met Leu Gln Leu Gly Ile Asp Cys Thr Glu Gln His Pro Asp Lys  
610 615 620  
Arg Pro Val Met Val Glu Val Val Arg Arg Ile Gln Glu Leu Arg Gln  
625 630 635 640  
Ser Gly Ala Asp Arg Val Gly  
645

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..639

(D) OTHER INFORMATION: / Ceres Seq. ID 1498046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ser Asn Leu Ser Ile Phe Phe Ser Ile Leu Leu Leu Ser Leu Pro  
1 5 10 15  
Leu Pro Ser Ile Gly Asp Leu Ala Ala Asp Lys Ser Ala Leu Leu Ser  
20 25 30  
Phe Arg Ser Ala Val Gly Gly Arg Thr Leu Leu Trp Asp Val Lys Gln  
35 40 45  
Thr Ser Pro Cys Asn Trp Thr Gly Val Leu Cys Asp Gly Gly Arg Val  
50 55 60  
Thr Ala Leu Arg Leu Pro Gly Glu Thr Leu Ser Gly His Ile Pro Glu  
65 70 75 80  
Gly Ile Phe Gly Asn Leu Thr Gln Leu Arg Thr Leu Ser Leu Arg Leu  
85 90 95  
Asn Gly Leu Thr Gly Ser Leu Pro Leu Asp Leu Gly Arg Cys Ser Asp  
100 105 110  
Leu Arg Arg Leu Tyr Leu Gln Gly Asn Arg Phe Ser Gly Glu Ile Pro  
115 120 125  
Glu Val Leu Phe Ser Leu Ser Asn Leu Val Arg Leu Asn Leu Ala Glu  
130 135 140  
Asn Glu Phe Ser Gly Glu Ile Ser Ser Gly Phe Lys Asn Leu Thr Arg  
145 150 155 160  
Leu Lys Thr Leu Tyr Leu Glu Asn Asn Lys Leu Ser Gly Ser Leu Leu  
165 170 175  
Asp Leu Asp Leu Ser Leu Asp Gln Phe Asn Val Ser Asn Asn Leu Leu  
180 185 190  
Asn Gly Ser Ile Pro Lys Ser Leu Gln Lys Phe Asp Ser Asp Ser Phe  
195 200 205  
Val Gly Thr Ser Leu Cys Gly Lys Pro Leu Val Val Cys Ser Asn Glu  
210 215 220  
Gly Thr Val Pro Ser Gln Pro Ile Ser Val Gly Asn Ile Pro Gly Thr  
225 230 235 240  
Val Glu Gly Arg Glu Glu Lys Lys Lys Arg Lys Lys Leu Ser Gly Gly  
245 250 255  
Ala Ile Ala Gly Ile Val Ile Gly Cys Val Val Gly Leu Ser Leu Ile  
260 265 270  
Val Met Ile Leu Met Val Leu Phe Arg Lys Lys Gly Asn Glu Arg Thr  
275 280 285  
Arg Ala Ile Asp Leu Ala Thr Ile Lys His His Glu Val Glu Ile Pro  
290 295 300  
Gly Glu Lys Ala Ala Val Glu Ala Pro Glu Asn Arg Ser Tyr Val Asn

305		310		315		320
Glu Tyr Ser Pro Ser	Ala Val Lys Ala Val	Glu Val Asn Ser Ser	Gly			
	325		330		335	
Met Lys Lys Leu Val	Phe Phe Gly Asn Ala Thr	Lys Val Phe Asp Leu				
	340		345		350	
Glu Asp Leu Leu Arg	Ala Ser Ala Glu Val	Leu Gly Lys Gly Thr	Phe			
	355		360		365	
Gly Thr Ala Tyr Lys	Ala Val Leu Asp Ala Val	Thr Leu Val Ala Val				
	370		375		380	
Lys Arg Leu Lys Asp	Val Thr Met Ala Asp	Arg Glu Phe Lys Glu	Lys			
	385		390		395	400
Ile Glu Val Val Gly	Ala Met Asp His Glu	Asn Leu Val Pro Leu	Arg			
	405		410		415	
Ala Tyr Tyr Tyr Ser	Gly Asp Glu Lys Leu	Leu Val Tyr Asp Phe	Met			
	420		425		430	
Pro Met Gly Ser Leu	Ser Ala Leu Leu His	Gly Asn Lys Gly Ala	Gly			
	435		440		445	
Arg Pro Pro Leu Asn	Trp Glu Val Arg Ser	Gly Ile Ala Leu Gly	Ala			
	450		455		460	
Ala Arg Gly Leu Asp	Tyr Leu His Ser Gln	Asp Pro Leu Ser Ser	His			
	465		470		475	480
Gly Asn Val Lys Ser	Ser Asn Ile Leu Leu	Thr Asn Ser His Asp	Ala			
	485		490		495	
Arg Val Ser Asp Phe	Gly Leu Ala Gln Leu	Val Ser Ala Ser Ser	Thr			
	500		505		510	
Thr Pro Asn Arg Ala	Thr Gly Tyr Arg Ala	Pro Glu Val Thr Asp	Pro			
	515		520		525	
Arg Arg Val Ser Gln	Lys Ala Asp Val Tyr	Ser Phe Gly Val Val	Leu			
	530		535		540	
Leu Glu Leu Leu Thr	Gly Lys Ala Pro Ser	Asn Ser Val Met Asn	Glu			
	545		550		555	560
Glu Gly Met Asp Leu	Ala Arg Trp Val His	Ser Val Ala Arg Glu	Glu			
	565		570		575	
Trp Arg Asn Glu Val	Phe Asp Ser Glu Leu	Met Ser Ile Glu Thr	Val			
	580		585		590	
Val Ser Val Glu Glu	Glu Met Ala Glu Met	Leu Gln Leu Gly Ile	Asp			
	595		600		605	
Cys Thr Glu Gln His	Pro Asp Lys Arg Pro	Val Met Val Glu Val	Val			
	610		615		620	
Arg Arg Ile Gln Glu	Leu Arg Gln Ser Gly	Ala Asp Arg Val Gly				
	625		630		635	

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..852
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

acaccatcca ctctactcaa catggactcc tccaaactct catctctctc tctttgcctc	60
tctctcattt gcattatcta tctcccccaa cattctctcg catgcggctc ttgcaacca	120
cggaagggcg gaaagcactc ccctaaagcc cctaagctac cagttcctcc ggtgaccgtc	180
cctaagctac cagttcctcc ggtgaccgtc cctaagctac cagttcctcc ggtgaccgtc	240
cctaagctac ccgttcctcc tgtgamcatc cctaagctac ccgttcctcc agtgactgta	300
cctaagctac ccgttcctcc tgtgaccgtc cccaagctac ccgttcctcc agtgaccgtc	360
cccaaggagg aacgggtagc ttaggtacag tcaactggtg aacgggtagc ttaggggtg	420
tcacggagkg ggaggaggcc acggacatgg aggcacacac ggaggagggg gccacggact	480

```
tgacggatac ggaggaggtg gaggacacta tggaggaggt ggaggacact acggaggagg 540
tggaggacac tacgaaggag gtgaggacac tacggaggag gtggtggagg acacggaggt 600
ggaggacact acggaggtgg tggaggagga tacggaggtg gaggaggaca ccacggagga 660
ggaggccacg ggctaaacga acctgttcag actaagccgg gtgtttaaaa ctatataata 720
ycttcactac catgcatgat tgcataata tatatacgct tatgtattat ctatatgcct 780
ataaataaac catggtgagt ttgtaacgca gtgccttcag aaatgttcgg aataaatttc 840
cataatatta gt
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1498048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
Thr Pro Ser Thr Leu Asn Met Asp Ser Ser Lys Leu Ser Ser Leu
1          5          10          15
Ser Leu Cys Leu Phe Leu Ile Cys Ile Ile Tyr Leu Pro Gln His Ser
20          25          30
Leu Ala Cys Gly Ser Cys Asn Pro Arg Lys Gly Gly Lys His Ser Pro
35          40          45
Lys Ala Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro
50          55          60
Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val
65          70          75          80
Pro Lys Leu Pro Val Pro Pro Val Xaa Ile Pro Lys Leu Pro Val Pro
85          90          95
Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys
100          105          110
Leu Pro Val Pro Pro Val Thr Val Pro Lys Glu Glu Arg Val Ala
115          120          125
```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
Met Asp Ser Ser Lys Leu Ser Ser Leu Ser Leu Cys Leu Phe Leu Ile
1          5          10          15
Cys Ile Ile Tyr Leu Pro Gln His Ser Leu Ala Cys Gly Ser Cys Asn
20          25          30
Pro Arg Lys Gly Gly Lys His Ser Pro Lys Ala Pro Lys Leu Pro Val
35          40          45
Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro
50          55          60
Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro
65          70          75          80
Val Xaa Ile Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu
85          90          95
Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr
100          105          110
```



Val Pro Lys Glu Glu Arg Val Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
1      5      10      15
Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu Val
20     25     30
Glu Asp Thr Thr Lys Glu Val Arg Thr Leu Arg Arg Arg Trp Trp Arg
35     40     45
Thr Arg Arg Trp Arg Thr Leu Arg Arg Trp Trp Arg Arg Ile Arg Arg
50     55     60
Trp Arg Arg Thr Pro Arg Arg Arg Arg Pro Arg Ala Lys Arg Thr Cys
65     70     75     80
Ser Asp
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1095
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
gtagatcttt ttctgctctt tctctctctc tctctctctc tctctctctc tctctcttgt 60
attattttcta tctccccgc cgtcgaaaga gaaacgtcga tcggagaacc tttgaaatgt 120
cgactggatt agatatgtct ctgcacgaca tgatcgccaa gaaccgtaag tctcgtgggtg 180
gagccggccc cgctcgtgga accggatccg gatccggacc gggtcgact cgccgcaaca 240
accctaatacg gaaatcaacc cgatctgctc cataccaatc agccaaggcg ccggagtcca 300
cctgggggtca cgacatgttc tccgatagat ctgaagatca ccgatcggga cgttcctccg 360
ccggaatcga aactggaacc aagctctaca ttccaattt ggattacggg gtcatgaacg 420
aagacatcaa ggaactgttt gctgaagttg gagaacttaa acgctacaca gttcattttg 480
atagaagtgg aagatcaaag ggaactgctg aagtagtgta ttctcggcgt ggcgatgcac 540
tcgcagctgt gaagaagtat aatgatgttc agctggatgg aaaacccatg aagatagaga 600
ttgtgggcac taatcttcaa actgctgcag cccgctctgg tagacctgcg aatggaaact 660
ccaatgggtgc tccatggaga ggaggacaag ggagaggagg tcaacgaggt ggtggacgag 720
gaggcgggtg ccgaggtggt ggtggtcgtg gtaggcgtcc tggtaaagggc cctgcagaga 780
agatttctgc ggaagatctt gatgcggatc ttgataagta ccattctgga gatattgaga 840
caaactaagg aacgtgactg atcttctcaa accggtaggg gttttaggag gaagagaatc 900
gagaaaatgt ttgccagag ctttaccact tagcgccttt ttggctgtgt tgttcatttg 960
tttcattaga atgactttac agaattgaga atatgtgtta tttaaagttg ttgtctatct 1020
taataccctc aagtgaaggg cagaggaagg aataccaatt tcgtttacag atcatatgca 1080
ggcaaaagag ttttc
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..281  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Arg	Ser	Phe	Ser	Ala	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser	Leu
1			5					10					15		
Ser	Leu	Leu	Tyr	Phe	Tyr	Leu	Pro	Arg	Arg	Arg	Lys	Arg	Asn	Val	
			20				25					30			
Asp	Arg	Arg	Thr	Phe	Glu	Met	Ser	Thr	Gly	Leu	Asp	Met	Ser	Leu	Asp
		35					40					45			
Asp	Met	Ile	Ala	Lys	Asn	Arg	Lys	Ser	Arg	Gly	Gly	Ala	Gly	Pro	Ala
	50					55					60				
Arg	Gly	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Gly	Pro	Thr	Arg	Arg	Asn	Asn
65				70					75					80	
Pro	Asn	Arg	Lys	Ser	Thr	Arg	Ser	Ala	Pro	Tyr	Gln	Ser	Ala	Lys	Ala
			85					90						95	
Pro	Glu	Ser	Thr	Trp	Gly	His	Asp	Met	Phe	Ser	Asp	Arg	Ser	Glu	Asp
			100					105					110		
His	Arg	Ser	Gly	Arg	Ser	Ser	Ala	Gly	Ile	Glu	Thr	Gly	Thr	Lys	Leu
			115				120					125			
Tyr	Ile	Ser	Asn	Leu	Asp	Tyr	Gly	Val	Met	Asn	Glu	Asp	Ile	Lys	Glu
	130					135					140				
Leu	Phe	Ala	Glu	Val	Gly	Glu	Leu	Lys	Arg	Tyr	Thr	Val	His	Phe	Asp
145				150					155					160	
Arg	Ser	Gly	Arg	Ser	Lys	Gly	Thr	Ala	Glu	Val	Val	Tyr	Ser	Arg	Arg
			165					170						175	
Gly	Asp	Ala	Leu	Ala	Ala	Val	Lys	Lys	Tyr	Asn	Asp	Val	Gln	Leu	Asp
		180					185					190			
Gly	Lys	Pro	Met	Lys	Ile	Glu	Ile	Val	Gly	Thr	Asn	Leu	Gln	Thr	Ala
		195				200						205			
Ala	Ala	Pro	Ser	Gly	Arg	Pro	Ala	Asn	Gly	Asn	Ser	Asn	Gly	Ala	Pro
	210					215					220				
Trp	Arg	Gly	Gly	Gln	Gly	Arg	Gly	Gly	Gln	Arg	Gly	Gly	Gly	Arg	Gly
225				230					235					240	
Gly	Gly	Gly	Arg	Gly	Gly	Gly	Gly	Arg	Gly	Arg	Arg	Pro	Gly	Lys	Gly
			245					250					255		
Pro	Ala	Glu	Lys	Ile	Ser	Ala	Glu	Asp	Leu	Asp	Ala	Asp	Leu	Asp	Lys
		260					265						270		
Tyr	His	Ser	Gly	Asp	Met	Glu	Thr	Asn							
		275					280								

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..243  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met	Ser	Thr	Gly	Leu	Asp	Met	Ser	Leu	Asp	Asp	Met	Ile	Ala	Lys	Asn
1				5					10					15	
Arg	Lys	Ser	Arg	Gly	Gly	Ala	Gly	Pro	Ala	Arg	Gly	Thr	Gly	Ser	Gly
			20					25					30		
Ser	Gly	Pro	Gly	Pro	Thr	Arg	Arg	Asn	Asn	Pro	Asn	Arg	Lys	Ser	Thr

Met	Ser	Leu	Asp	Asp	Met	Ile	Ala	Lys	Asn	Arg	Lys	Ser	Arg	Gly	Gly
1				5					10					15	
Ala	Gly	Pro	Ala	Arg	Gly	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Gly	Pro	Thr
			20					25					30		
Arg	Arg	Asn	Asn	Pro	Asn	Arg	Lys	Ser	Thr	Arg	Ser	Ala	Pro	Tyr	Gln
		35					40					45			
Ser	Ala	Lys	Ala	Pro	Glu	Ser	Thr	Trp	Gly	His	Asp	Met	Phe	Ser	Asp
	50					55					60				
Arg	Ser	Glu	Asp	His	Arg	Ser	Gly	Arg	Ser	Ser	Ala	Gly	Ile	Glu	Thr
65				70						75				80	
Gly	Thr	Lys	Leu	Tyr	Ile	Ser	Asn	Leu	Asp	Tyr	Gly	Val	Met	Asn	Glu
			85						90					95	
Asp	Ile	Lys	Glu	Leu	Phe	Ala	Glu	Val	Gly	Glu	Leu	Lys	Arg	Tyr	Thr
			100					105					110		
Val	His	Phe	Asp	Arg	Ser	Gly	Arg	Ser	Lys	Gly	Thr	Ala	Glu	Val	Val
		115				120						125			
Tyr	Ser	Arg	Arg	Gly	Asp	Ala	Leu	Ala	Ala	Val	Lys	Lys	Tyr	Asn	Asp
	130				135					140					
Val	Gln	Leu	Asp	Gly	Lys	Pro	Met	Lys	Ile	Glu	Ile	Val	Gly	Thr	Asn
145				150						155				160	
Leu	Gln	Thr	Ala	Ala	Ala	Pro	Ser	Gly	Arg	Pro	Ala	Asn	Gly	Asn	Ser
			165						170					175	

Asn Gly Ala Pro Trp Arg Gly Gly Gln Gly Arg Gly Gly Gln Arg Gly  
180 185 190  
Gly Gly Arg Gly Gly Gly Gly Arg Gly Gly Gly Gly Arg Gly Arg Arg  
195 200 205  
Pro Gly Lys Gly Pro Ala Glu Lys Ile Ser Ala Glu Asp Leu Asp Ala  
210 215 220  
Asp Leu Asp Lys Tyr His Ser Gly Asp Met Glu Thr Asn  
225 230 235

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

scagcgggttc cyggtcaagc acctcctttt aacaacaagc tttgcgacat aagacacgtg	60
tcaagcaggg acgagaacgt taagagacgg agccgtgggtg catgcaagga agagagaaac	120
gtgaggtcctt tgagtcatga gtcgtcactg agtcacgagt caccggtgtc ttctgaggag	180
acgacgacgg aggaaccaa gacttggatc gggcttgagc tgactttggg gttggagcct	240
ttagcacgtg gaaatcacgt ggtggtaccg atgaagaaaa gaaagttaga gaggtgtggc	300
acgtctgagg atgaggacac gtgtaagatt gagcttggac tgggtgtgcag tgagtgaatg	360
gttctttttt tgtggctggg ctttaattaca agttttgggt ttgagtttta ggtgtacaaa	420
tagagattaa cgaatctctc ttttttctct ttttgagttt tatgttttgk tttgktttct	480
tttgcatggt cgggtgttctt cataaatatg tatgatgaat gataaagagg tcttaactt	

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Xaa Ala Val Xaa Gly Gln Ala Pro Pro Phe Asn Asn Lys Leu Cys Asp	
1 5 10 15	
Ile Arg His Val Ser Ser Arg Asp Glu Asn Val Lys Arg Arg Ser Arg	
20 25 30	
Gly Ala Cys Lys Glu Glu Arg Asn Val Arg Ser Leu Ser His Glu Ser	
35 40 45	
Ser Leu Ser His Glu Ser Pro Val Ser Ser Glu Glu Thr Thr Thr Glu	
50 55 60	
Glu Pro Lys Thr Trp Ile Gly Leu Glu Leu Thr Leu Gly Leu Glu Pro	
65 70 75 80	
Leu Ala Arg Gly Asn His Val Val Val Pro Met Lys Lys Arg Lys Leu	
85 90 95	
Glu Arg Cys Gly Thr Ser Glu Asp Glu Asp Thr Cys Lys Ile Glu Leu	
100 105 110	
Gly Leu Val Cys Ser Glu	
115	

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..676  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498063  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

aaaaaaaaaca	aaaagatctg	aaacaaaaaat	ggtgaatcaa	agaaagctac	aagaagaaga	60
agagcgaaaa	ggagaattat	cctctcatta	caaccaaaagt	agttgagtat	ttgcagccag	120
taatgtgtcg	agagcttctc	tgcaaatttc	cagataactc	tgcttttgga	ttcgactact	180
cacagagctc	tcttttgtct	cctctcttgc	ctcgaaatta	cgccagtcct	tcagatctag	240
actccgacag	ttgcgtttgt	cggaatctta	agctagggga	gtttcaagta	ggcaagaaga	300
agaagatgaa	gatgatgtca	atgaagaaga	acaagaagaa	gagtaaatta	ctgaaactag	360
acataccttc	aatgaagaat	gatgattctt	ctcctaaaaat	tggctgtttt	cctcttccta	420
ccaagggatg	gaatggtgtg	ttaaaggcag	cttcaaaaca	tttcaagaaa	tcgaaaaaga	480
agagagattc	attcgtgat	gccaaagcttc	tcgacttcaa	atactaagat	tatagcaact	540
tcaattgctt	ttcattgtat	tcaataatta	ctagaccttt	gatgaattgt	gaagttgagc	600
tgtttctatt	atggtcatca	tgtaatcatt	tggagtgttt	gatcatagat	atatccatga	660
ctgcttttga	tttctg					

(2) INFORMATION FOR SEQ ID NO:158:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 134 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..134  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498064  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met	Cys	Arg	Glu	Leu	Leu	Cys	Lys	Phe	Pro	Asp	Asn	Ser	Ala	Phe	Gly
1			5						10					15	
Phe	Asp	Tyr	Ser	Gln	Ser	Ser	Leu	Trp	Ser	Pro	Leu	Leu	Pro	Arg	Asn
			20					25					30		
Tyr	Ala	Ser	Pro	Ser	Asp	Leu	Asp	Ser	Asp	Ser	Cys	Val	Cys	Arg	Asn
			35				40					45			
Leu	Lys	Leu	Gly	Glu	Phe	Gln	Val	Gly	Lys	Lys	Lys	Lys	Met	Lys	Met
			50				55					60			
Met	Ser	Met	Lys	Lys	Asn	Lys	Lys	Lys	Ser	Lys	Leu	Leu	Lys	Leu	Asp
					70				75					80	
Ile	Pro	Ser	Met	Lys	Asn	Asp	Asp	Ser	Ser	Pro	Lys	Ile	Gly	Cys	Phe
				85					90					95	
Pro	Leu	Pro	Thr	Lys	Gly	Trp	Asn	Gly	Val	Leu	Lys	Ala	Ala	Ser	Lys
				100				105					110		
His	Phe	Lys	Lys	Ser	Lys	Lys	Lys	Arg	Asp	Ser	Phe	Ala	Asp	Ala	Lys
			115				120					125			
Leu	Leu	Asp	Phe	Lys	Tyr										

(2) INFORMATION FOR SEQ ID NO:159:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 73 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..73  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met Lys Met Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu  
1 5 10 15  
Lys Leu Asp Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile  
20 25 30  
Gly Cys Phe Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala  
35 40 45  
Ala Ser Lys His Phe Lys Lys Ser Lys Lys Arg Asp Ser Phe Ala  
50 55 60  
Asp Ala Lys Leu Leu Asp Phe Lys Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu Lys Leu  
1 5 10 15  
Asp Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile Gly Cys  
20 25 30  
Phe Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala Ala Ser  
35 40 45  
Lys His Phe Lys Lys Ser Lys Lys Lys Arg Asp Ser Phe Ala Asp Ala  
50 55 60  
Lys Leu Leu Asp Phe Lys Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

aacatttctca	gagaagccgt	cttcttcctc	cttcaatctc	tctcgttcgt	atcatctgct	60
ctgcgatttc	aatggcgagc	cgttggttga	gacctgaggt	gtatcctttg	ttcgctgcta	120
ccggagttgc	cgttgggata	tgtgcgtttt	ccttgatcag	aaacatcacc	ggaaaccctg	180
aagtcagatg	caccaaggag	aacagggctg	ctggaatttt	ggataacccat	gcagagggag	240
agaagtataa	ggaaaatttc	ctgaggaaga	ggaattaggt	ttatccgata	tgattctcag	300
gttttcttgt	ttcttaactc	aaaatgtaag	aggtacttcc	ataacaagtt	gaagccatcc	360
aagcttgcat	ggactgccat	gtacagaaag	caacacaaga	aggatgcagc	acaagaggct	420
gtgaagagaa	ggagacgtgc	caccaagaag	ccatactcaa	gggccattgt	tggtgctacc	480
ttggaagtaa	ttcagaagaa	gagagctgag	aagcctgaag	ttcgtgatgc	agccagggaa	540
gctgctctgc	gtgagatcaa	ggaaagaatc	aaaaagacca	aagatgaaaa	gaaggctaag	600
aaggtggaat	ttgcttctaa	gcaacagaag	gtcaaggcta	atttcccca	agctgctgct	660
gcattccaag	gtcctaaggt	gggaggtggt	ggtggcaaac	gctgaagagc	ttaaagccat	720
cttttctcac	tctgcgtctt	ttctgctagt	agctactttt	agtagttgat	gttcatttct	780
gaatatttgc	aaaacataaa	ccttggtatt	ttcgtttttg	tctctcactt	ttgctactct	840
tataatatca	gacttgagaa	ttttgctgc				

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 91 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..91  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498068  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:  
His Ser Gln Arg Ser Arg Leu Leu Pro Pro Ser Ile Ser Leu Val Arg  
1                    5                    10                    15  
Ile Ile Cys Ser Ala Ile Ser Met Ala Ser Arg Trp Leu Arg Pro Glu  
                    20                    25                    30  
Val Tyr Pro Leu Phe Ala Ala Thr Gly Val Ala Val Gly Ile Cys Ala  
                    35                    40                    45  
Phe Ser Leu Ile Arg Asn Ile Thr Gly Asn Pro Glu Val Arg Cys Thr  
50                    55                    60  
Lys Glu Asn Arg Ala Ala Gly Ile Leu Asp Asn His Ala Glu Gly Glu  
65                    70                    75                    80  
Lys Tyr Lys Glu Asn Phe Leu Arg Lys Arg Asn  
                    85                    90  
(2) INFORMATION FOR SEQ ID NO:163:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 108 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..108  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498069  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:  
Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys  
1                    5                    10                    15  
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly  
                    20                    25                    30  
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val  
35                    40                    45  
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile  
50                    55                    60  
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Phe Ala Ser  
65                    70                    75                    80  
Lys Gln Gln Lys Val Lys Ala Asn Phe Pro Lys Ala Ala Ala Ala Ser  
                    85                    90                    95  
Lys Gly Pro Lys Val Gly Gly Gly Gly Gly Lys Arg  
100                    105  
(2) INFORMATION FOR SEQ ID NO:164:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 80 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..80  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498070  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Gln	Pro	Gly	Lys	Leu	Leu	Cys	Val	Arg	Ser	Arg	Lys	Glu	Ser	Lys
1				5					10					15	
Arg	Pro	Lys	Met	Lys	Arg	Arg	Leu	Arg	Arg	Trp	Asn	Leu	Leu	Leu	Ser
			20					25					30		
Asn	Arg	Arg	Ser	Arg	Leu	Ile	Ser	Pro	Lys	Leu	Leu	Leu	His	Pro	Arg
			35				40					45			
Val	Leu	Arg	Trp	Glu	Val	Val	Val	Ala	Asn	Ala	Glu	Glu	Leu	Lys	Ala
	50					55					60				
Ile	Phe	Ser	His	Ser	Ala	Ser	Phe	Leu	Leu	Val	Ala	Thr	Phe	Ser	Ser
65					70				75					80	

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

accaccgaaa	cccactaaga	atacagcaaa	tcgtctcttc	gccattaaaa	caccttcctt	60
tgcaaacaaa	gcttcaaact	ttctcttaaa	acacccccaa	atcagcaaag	ataggggtaa	120
tcgaagaacc	tcaccgtaag	tccactgagg	attcaagttc	ttgctttggt	ttaagggaaga	180
agaacagcaa	aaacctcaag	gagaagaaga	agtcaaagat	gactcagagt	caaaccaacg	240
acggagctgg	agctggagct	gttacgacgg	tagaatctgt	tcctcctcag	cctcaatctc	300
agcctcagcc	tcagccgcag	cagcagagca	acgagatggg	tctgcatacg	ggaagcttga	360
gttttagtag	tcatatgtcg	agagaagacg	aagagatgac	tcgttctgct	ctttcggcgt	420
ttagagctaa	agaagatgag	attgagaaga	ggaggatgga	agttcgtgaa	cggatccaag	480
ctcaattggg	tcgggtcgaa	caagaaacca	aacgtctctc	tactattcgt	gaggagcttg	540
agtctatggc	agatcctatg	aggaaggaag	tttctgtggg	tcgtaagaag	attgatagtg	600
ttaacaaaaga	actcaaacct	ctagggttcca	ctgttcaaaa	gaaggaaagg	gaatacaaaag	660
aagcacttga	tgayattcaa	cgagaagaac	agggagaaaag	tacagctgat	cacaaaactc	720
atggagctgg	aacagttggg	tggagaaagc	gagaagttga	ggatgattaa	gctggaggag	780
ctgagcaaga	gcatagaaac	cgtgtgaaaa	agggtgttca	agaagaacta	attgggttct	840
tttgtgtgat	gtacctacct	agtttaaaat	tttcatcatg	taagatgtgt	gggttgcttt	900
tttttttatt	gbtatagttt	ttttaagtc	tttgggggtt	tgatttgtaa	aatttgkggg	960
ttctctcttw	tttttgatta	accaaattta	gggatatggg	aaaatgggag	attcttagga	1020
tactgaaact	catcacagtg	attattcttt	ctttctctgt	attatgtttt	gtatctgtct	1080
tttgaagaat	ttattatttt	tttt				

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	Thr	Gln	Ser	Gln	Thr	Asn	Asp	Gly	Ala	Gly	Ala	Gly	Ala	Val	Thr
1				5					10					15	
Thr	Val	Glu	Ser	Val	Pro	Pro	Gln	Pro	Gln	Ser	Gln	Pro	Gln	Pro	Gln
				20				25					30		
Pro	Gln	Gln	Gln	Ser	Asn	Glu	Met	Val	Leu	His	Thr	Gly	Ser	Leu	Ser
			35				40					45			



Phe Ser Ser His Met Ser Arg Glu Asp Glu Glu Met Thr Arg Ser Ala  
50 55 60  
Leu Ser Ala Phe Arg Ala Lys Glu Asp Glu Ile Glu Lys Arg Arg Met  
65 70 75 80  
Glu Val Arg Glu Arg Ile Gln Ala Gln Leu Gly Arg Val Glu Gln Glu  
85 90 95  
Thr Lys Arg Leu Ser Thr Ile Arg Glu Leu Glu Ser Met Ala Asp  
100 105 110  
Pro Met Arg Lys Glu Val Ser Val Arg Lys Lys Ile Asp Ser Val  
115 120 125  
Asn Lys Glu Leu Lys Pro Leu Gly Ser Thr Val Gln Lys Lys Glu Arg  
130 135 140  
Glu Tyr Lys Glu Ala Leu Asp Xaa Ile Gln Arg Glu Glu Gln Gly Glu  
145 150 155 160  
Ser Thr Ala Asp His Lys Thr His Gly Asp Gly Thr Val Gly Trp Arg  
165 170 175  
Lys Arg Glu Val Glu Asp Asp  
180

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Met Val Leu His Thr Gly Ser Leu Ser Phe Ser Ser His Met Ser Arg  
1 5 10 15  
Glu Asp Glu Glu Met Thr Arg Ser Ala Leu Ser Ala Phe Arg Ala Lys  
20 25 30  
Glu Asp Glu Ile Glu Lys Arg Arg Met Glu Val Arg Glu Arg Ile Gln  
35 40 45  
Ala Gln Leu Gly Arg Val Glu Gln Glu Thr Lys Arg Leu Ser Thr Ile  
50 55 60  
Arg Glu Glu Leu Glu Ser Met Ala Asp Pro Met Arg Lys Glu Val Ser  
65 70 75 80  
Val Val Arg Lys Lys Ile Asp Ser Val Asn Lys Glu Leu Lys Pro Leu  
85 90 95  
Gly Ser Thr Val Gln Lys Lys Glu Arg Glu Tyr Lys Glu Ala Leu Asp  
100 105 110  
Xaa Ile Gln Arg Glu Glu Gln Gly Glu Ser Thr Ala Asp His Lys Thr  
115 120 125  
His Gly Asp Gly Thr Val Gly Trp Arg Lys Arg Glu Val Glu Asp Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Arg Glu Asp Glu Glu Met Thr Arg Ser Ala Leu Ser Ala Phe  
1 5 10 15  
Arg Ala Lys Glu Asp Glu Ile Glu Lys Arg Arg Met Glu Val Arg Glu  
20 25 30  
Arg Ile Gln Ala Gln Leu Gly Arg Val Glu Gln Glu Thr Lys Arg Leu  
35 40 45  
Ser Thr Ile Arg Glu Glu Leu Glu Ser Met Ala Asp Pro Met Arg Lys  
50 55 60  
Glu Val Ser Val Val Arg Lys Lys Ile Asp Ser Val Asn Lys Glu Leu  
65 70 75 80  
Lys Pro Leu Gly Ser Thr Val Gln Lys Lys Glu Arg Glu Tyr Lys Glu  
85 90 95  
Ala Leu Asp Xaa Ile Gln Arg Glu Glu Gln Gly Glu Ser Thr Ala Asp  
100 105 110  
His Lys Thr His Gly Asp Gly Thr Val Gly Trp Arg Lys Arg Glu Val  
115 120 125  
Glu Asp Asp  
130

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..757
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

aacccaaaaca aaacataaaaa aaacaagtgg aagctttaaa acgagagggga gagagcaaaa 60  
atggcgacgt cgggaacgta cgtgacggaa gttccgctaa aaggatcggc cgagaaatac 120  
tacaagaggt ggaagaacga gaaccatgtc ttccctgatg ctatcggcca ccacatccaa 180  
aatgttaccg ttcacgaagg cgaacatgac tctcacgggt ctatcaggag ttggaactac 240  
acatgggatg gaaaggagga ggtgttcaag gagagaagag agatagacga tgagaccaa 300  
acgttgacgt taagaggact tgagggtcac gtgatggagc agctcaaagt gtacgacgtc 360  
gtctaccaat tcattcccaa atctgaggat acctgcacgc gcaaaatcac tttaatatgg 420  
gagaagcgca acgatgattc cccagaacca agcggctaca tgaaattcgt caagagcttg 480  
gttgctgaca tgggaaacca cgttagcaaa acttaatcat cattcccaca gtcgtcgtcg 540  
tcgtcatcat catcatcatc atcatcatca tcatcatcat catcatcatc atcatcrtca 600  
tcactatctc gatttataag ttaagatggt ttcagtataa taaatgggggt cttgtgggatc 660  
gttcattttct atgtgtaaac cgtttggttc tgtatgatgc ttcgatatat tgttatgttc 720  
atgatcatat gtcgggttcg atataatgat tcttaag

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser  
1 5 10 15  
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro  
20 25 30  
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu

35	40	45
His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly		
50	55	60
Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys		
65	70	75
Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys		
85	90	95
Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys		
100	105	110
Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro		
115	120	125
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met		
130	135	140
Gly Asn His Val Ser Lys Thr		
145	150	

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1944
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

atccccaaaag	gagaaaaaca	aacmaaaaaa	caagaacaaa	acaaaaacca	aaaaaacaaa	60
aaaataaaatg	gcaagaattt	cactagggat	atgtctgatg	ttagtagtag	catcaagtgt	120
gatctatgaa	gcgcaaggaa	cgttcttact	aaaccattac	ttgaagaaga	attttccaaa	180
aaaatgcaac	gagttttacg	cttacgctaa	caagggtatg	ataacgttgg	tgaccgatct	240
cgaaggtagc	agtccggcca	ctacagagtt	caagactttc	tttacacagt	tcaagtctta	300
catgtctttc	atcgagacaa	catcggcctc	aacaaaaaat	gttgatgccg	agatgacagc	360
taaatgtgac	ggtcttttca	aggccatgtc	tgcattgagt	gctagtaaag	gcgtcaaadc	420
agcggatgct	gggagtatga	agatgaccat	gttgtcgatg	ggaaagactt	tggttgagca	480
gaagaagaat	acaaagataa	tgacattgaa	ggaaaagaaa	gagttgggtc	tagatatggg	540
gaaatggact	aaaatggctg	ctacatttgt	gaagtcggcc	tccgagcaga	aaggaaagtc	600
tatcaatata	gcatcttatg	gtcttgatgt	cgatgttaac	gatagttcta	ttgtcgggtg	660
agctgcaagt	agtgaatcat	cctccactaa	atctggatct	gtttccagta	gcggaagtgt	720
ttctaccaag	tcgaaagaat	cgagtagtag	tggaaagttc	gccagtgga	gtgttgctac	780
caaattccaaa	gaatccagcg	gtggaagtgc	tgctacccaa	tccaaagaat	ctagcgggtg	840
aagtgtgtgt	accaaaatcca	aagaatctag	tgggtggaag	gtactacag	gtaaaacttc	900
gggcagtcgg	agcggaaagtc	ctaaggccag	cccactctgt	tcagttagt	gcaaatcatc	960
ttcaaaaagga	agcgcaagt	ctcaaggga	cgcaagtgt	caagggaagt	caagtgtcta	1020
aggaagcgca	agtgtcaag	gaagtgcga	tgctcaaa	agagaaagt	gggcaatggc	1080
tatgtccaag	agcagagaaa	caaagacatc	gagccaaaga	caatccaaat	catcgagtga	1140
aagttcatct	tctagcacia	ccaccacaac	agtgaacaa	gtcgagagt	agacttccaa	1200
agaagtaatg	tcattcataa	tgcaactcga	gaagaagtat	gcagcaaagg	cggaactcaa	1260
ggtcttcttc	gagtctctaa	agtcttccat	gcaagcttcc	gcaagcggtg	gttccaaaac	1320
cgcgaaagac	tatgtttctg	cctcaaaaag	agccactgg	aaactctccg	aagccatggc	1380
ttcagtgagt	tccaaaaatg	tcaataaagc	aaagatgaag	agcaacttgg	acactagcaa	1440
agatgaaatg	ctgaggtgtg	tcaaacaaat	tcaagatc	aacgataaaa	tggtgagtg	1500
caagaccgtg	tcattcaaac	aacagtcaga	gtcgaagc	acaatcacca	agtggaagaa	1560
ggtcaccacc	caatttggtg	agaccgctgc	ttcttcaagt	tcacgtcat	cctcatctc	1620
atcctcatcc	tcattctctg	ctgcttctca	gcagcagggc	aatgcagcaa	tggtcaagac	1680
taattgagtt	taaaggtgaa	gttactttat	tgcgcaaaag	atcaccaaga	aagacacaac	1740
cagtaatgcc	aaatattata	ataagtagtt	aactattaga	tcatttctct	tgtaataaaa	1800
actaagatcg	gtataggtaa	gcattgcatg	cttataaacc	gatgtatgca	agtaataact	1860
ctgtaaaaaa	acgttacaga	tagattgtaa	ccgctttgta	tggttaacata	caaaagtga	1920
tgatacctat	gaaagggatt	tttg				

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 446 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..446  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498078  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Ala	Arg	Ile	Ser	Leu	Gly	Ile	Cys	Leu	Met	Leu	Val	Val	Ala	Ser
1				5					10					15	
Ser	Val	Ile	Tyr	Glu	Ala	Gln	Gly	Thr	Phe	Leu	Leu	Asn	His	Tyr	Leu
			20					25					30		
Lys	Lys	Asn	Phe	Pro	Lys	Lys	Cys	Asn	Glu	Phe	Thr	Pro	Tyr	Ala	Asn
		35					40					45			
Lys	Gly	Met	Ile	Thr	Leu	Val	Thr	Asp	Leu	Glu	Gly	Ser	Ser	Pro	Ala
	50					55					60				
Thr	Thr	Glu	Phe	Lys	Thr	Phe	Phe	Thr	Gln	Phe	Lys	Ser	Tyr	Met	Ser
65					70					75				80	
Phe	Ile	Glu	Thr	Thr	Ser	Ala	Ser	Thr	Lys	Asn	Val	Asp	Ala	Glu	Met
				85					90					95	
Thr	Ala	Lys	Cys	Asp	Gly	Leu	Phe	Lys	Ala	Met	Ser	Ala	Leu	Ser	Ala
			100					105					110		
Ser	Lys	Gly	Val	Lys	Ser	Ala	Asp	Ala	Gly	Ser	Met	Lys	Met	Thr	Met
		115					120					125			
Leu	Ser	Met	Gly	Lys	Thr	Leu	Val	Glu	Gln	Lys	Lys	Asn	Thr	Lys	Ile
	130					135						140			
Met	Thr	Leu	Lys	Glu	Lys	Lys	Glu	Leu	Val	Ile	Asp	Met	Val	Lys	Trp
145					150					155				160	
Thr	Lys	Met	Val	Ala	Thr	Phe	Val	Lys	Ser	Ala	Ser	Glu	Gln	Lys	Gly
				165					170					175	
Lys	Ser	Ile	Asn	Ile	Ala	Ser	Tyr	Gly	Leu	Asp	Val	Asp	Val	Asn	Asp
			180					185					190		
Ser	Ser	Ile	Val	Gly	Gly	Ala	Ala	Ser	Ser	Glu	Ser	Ser	Ser	Thr	Lys
		195					200					205			
Ser	Gly	Ser	Val	Ser	Ser	Ser	Gly	Ser	Val	Ser	Thr	Lys	Ser	Lys	Glu
	210					215					220				
Ser	Ser	Ser	Ser	Gly	Ser	Ser	Ala	Ser	Gly	Ser	Val	Ala	Thr	Lys	Ser
225					230					235				240	
Lys	Glu	Ser	Ser	Gly	Gly	Ser	Ala	Ala	Thr	Lys	Ser	Lys	Glu	Ser	Ser
				245					250					255	
Gly	Gly	Ser	Ala	Ala	Thr	Lys	Ser	Lys	Glu	Ser	Ser	Gly	Gly	Ser	Ala
		260						265					270		
Thr	Thr	Gly	Lys	Thr	Ser	Gly	Ser	Pro	Ser	Gly	Ser	Pro	Lys	Ala	Ser
		275				280						285			
Pro	Ser	Gly	Ser	Val	Ser	Gly	Lys	Ser	Ser	Ser	Lys	Gly	Ser	Ala	Ser
	290					295					300				
Ala	Gln	Gly	Ser	Ala	Ser	Ala	Gln	Gly	Ser	Ala	Ser	Ala	Gln	Gly	Ser
305					310					315				320	
Ala	Ser	Ala	Gln	Gly	Ser	Ala	Ser	Ala	Glu	Arg	Arg	Glu	Ser	Gly	Ala
			325						330					335	
Met	Ala	Met	Ser	Lys	Ser	Arg	Glu	Thr	Lys	Thr	Ser	Ser	Gln	Arg	Gln
		340						345					350		
Ser	Lys	Ser	Ser	Ser	Glu	Ser	Ser	Ser	Ser	Ser	Thr	Thr	Thr	Thr	Thr
		355					360					365			
Val	Lys	Gln	Val	Glu	Ser	Glu	Thr	Ser	Lys	Glu	Val	Met	Ser	Phe	Ile
	370					375					380				
Met	Gln	Leu	Glu	Lys	Lys	Tyr	Ala	Ala	Lys	Ala	Glu	Leu	Lys	Val	Phe
385					390					395					400

Phe Glu Ser Leu Lys Ser Ser Met Gln Ala Ser Ala Ser Val Gly Ser  
405 410 415  
Lys Thr Ala Lys Asp Tyr Val Ser Ala Ser Lys Ala Ala Thr Gly Lys  
420 425 430  
Leu Ser Glu Ala Met Ala Ser Val Ser Ser Lys Asn Val Lys  
435 440 445

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..436

(D) OTHER INFORMATION: / Ceres Seq. ID 1498079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Met Leu Val Val Ala Ser Ser Val Ile Tyr Glu Ala Gln Gly Thr Phe  
1 5 10 15  
Leu Leu Asn His Tyr Leu Lys Lys Asn Phe Pro Lys Lys Cys Asn Glu  
20 25 30  
Phe Thr Pro Tyr Ala Asn Lys Gly Met Ile Thr Leu Val Thr Asp Leu  
35 40 45  
Glu Gly Ser Ser Pro Ala Thr Thr Glu Phe Lys Thr Phe Phe Thr Gln  
50 55 60  
Phe Lys Ser Tyr Met Ser Phe Ile Glu Thr Thr Ser Ala Ser Thr Lys  
65 70 75 80  
Asn Val Asp Ala Glu Met Thr Ala Lys Cys Asp Gly Leu Phe Lys Ala  
85 90 95  
Met Ser Ala Leu Ser Ala Ser Lys Gly Val Lys Ser Ala Asp Ala Gly  
100 105 110  
Ser Met Lys Met Thr Met Leu Ser Met Gly Lys Thr Leu Val Glu Gln  
115 120 125  
Lys Lys Asn Thr Lys Ile Met Thr Leu Lys Glu Lys Lys Glu Leu Val  
130 135 140  
Ile Asp Met Val Lys Trp Thr Lys Met Val Ala Thr Phe Val Lys Ser  
145 150 155 160  
Ala Ser Glu Gln Lys Gly Lys Ser Ile Asn Ile Ala Ser Tyr Gly Leu  
165 170 175  
Asp Val Asp Val Asn Asp Ser Ser Ile Val Gly Gly Ala Ala Ser Ser  
180 185 190  
Glu Ser Ser Ser Thr Lys Ser Gly Ser Val Ser Ser Ser Gly Ser Val  
195 200 205  
Ser Thr Lys Ser Lys Glu Ser Ser Ser Ser Gly Ser Ser Ala Ser Gly  
210 215 220  
Ser Val Ala Thr Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr  
225 230 235 240  
Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr Lys Ser Lys Glu  
245 250 255  
Ser Ser Gly Gly Ser Ala Thr Thr Gly Lys Thr Ser Gly Ser Pro Ser  
260 265 270  
Gly Ser Pro Lys Ala Ser Pro Ser Gly Ser Val Ser Gly Lys Ser Ser  
275 280 285  
Ser Lys Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser  
290 295 300  
Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln  
305 310 315 320  
Arg Arg Glu Ser Gly Ala Met Ala Met Ser Lys Ser Arg Glu Thr Lys  
325 330 335  
Thr Ser Ser Gln Arg Gln Ser Lys Ser Ser Ser Glu Ser Ser Ser Ser

Met	Ile	Thr	Leu	Val	Thr	Asp	Leu	Glu	Gly	Ser	Ser	Pro	Ala	Thr	Thr
1				5					10					15	
Glu	Phe	Lys	Thr	Phe	Phe	Thr	Gln	Phe	Lys	Ser	Tyr	Met	Ser	Phe	Ile
			20					25					30		
Glu	Thr	Thr	Ser	Ala	Ser	Thr	Lys	Asn	Val	Asp	Ala	Glu	Met	Thr	Ala
			35				40					45			
Lys	Cys	Asp	Gly	Leu	Phe	Lys	Ala	Met	Ser	Ala	Leu	Ser	Ala	Ser	Lys
	50					55					60				
Gly	Val	Lys	Ser	Ala	Asp	Ala	Gly	Ser	Met	Lys	Met	Thr	Met	Leu	Ser
65					70					75					80
Met	Gly	Lys	Thr	Leu	Val	Glu	Gln	Lys	Lys	Asn	Thr	Lys	Ile	Met	Thr
				85					90					95	
Leu	Lys	Glu	Lys	Lys	Glu	Leu	Val	Ile	Asp	Met	Val	Lys	Trp	Thr	Lys
			100					105					110		
Met	Val	Ala	Thr	Phe	Val	Lys	Ser	Ala	Ser	Glu	Gln	Lys	Gly	Lys	Ser
			115				120					125			
Ile	Asn	Ile	Ala	Ser	Tyr	Gly	Leu	Asp	Val	Asp	Val	Asn	Asp	Ser	Ser
	130					135				140					
Ile	Val	Gly	Gly	Ala	Ala	Ser	Ser	Glu	Ser	Ser	Ser	Thr	Lys	Ser	Gly
145					150					155					160
Ser	Val	Ser	Ser	Ser	Gly	Ser	Val	Ser	Thr	Lys	Ser	Lys	Glu	Ser	Ser
				165					170					175	
Ser	Ser	Gly	Ser	Ser	Ala	Ser	Gly	Ser	Val	Ala	Thr	Lys	Ser	Lys	Glu
			180				185					190			
Ser	Ser	Gly	Gly	Ser	Ala	Ala	Thr	Lys	Ser	Lys	Glu	Ser	Ser	Gly	Gly
		195					200					205			
Ser	Ala	Ala	Thr	Lys	Ser	Lys	Glu	Ser	Ser	Gly	Gly	Ser	Ala	Thr	Thr
						215					220				
Gly	Lys	Thr	Ser	Gly	Ser	Pro	Ser	Gly	Ser	Pro	Lys	Ala	Ser	Pro	Ser
225					230					235					240
Gly	Ser	Val	Ser	Gly	Lys	Ser	Ser	Ser	Lys	Gly	Ser	Ala	Ser	Ala	Gln
				245					250					255	
Gly	Ser	Ala	Ser	Ala	Gln	Gly	Ser	Ala	Ser	Ala	Gln	Gly	Ser	Ala	Ser
				260				265				270			
Ala	Gln	Gly	Ser	Ala	Ser	Ala	Gln	Arg	Arg	Glu	Ser	Gly	Ala	Met	Ala
		275					280					285			

Met Ser Lys Ser Arg Glu Thr Lys Thr Ser Ser Gln Arg Gln Ser Lys  
290 295 300  
Ser Ser Ser Glu Ser Ser Ser Ser Ser Thr Thr Thr Thr Val Lys  
305 310 315 320  
Gln Val Glu Ser Glu Thr Ser Lys Glu Val Met Ser Phe Ile Met Gln  
325 330 335  
Leu Glu Lys Lys Tyr Ala Ala Lys Ala Glu Leu Lys Val Phe Phe Glu  
340 345 350  
Ser Leu Lys Ser Ser Met Gln Ala Ser Ala Ser Val Gly Ser Lys Thr  
355 360 365  
Ala Lys Asp Tyr Val Ser Ala Ser Lys Ala Ala Thr Gly Lys Leu Ser  
370 375 380  
Glu Ala Met Ala Ser Val Ser Ser Lys Asn Val Lys  
385 390 395

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

attaacaaat	ttgtttctgat	ctatttttatt	ttattttttgg	tatcaggaag	agaagaaacc	60
agaagcagca	gaggaaaaga	aaatggaaga	gaagaaacca	gaagagaaaa	aagaaggaga	120
agacaagaaa	gtggatgctg	agaaaaaagg	agaagattct	gacaagaagc	ctcaagaagg	180
agaaactaac	aaagattcca	aagaagattc	tgctccggcg	gcgcctgagg	ctccagcacc	240
gcctcctccg	ccgcaagagg	ttgtttcttaa	ggtttacatg	cactgtgaag	gatgtgctag	300
aaaagtccgc	cgttgtctca	aaggcttcga	aggagtggaa	gatgtgatga	ctgattgtaa	360
aacggggaaa	gtgggtggtga	aagggtgagaa	agctgatcca	ttgaaaagtat	tagctagagt	420
tcagaggaag	acccaccgtc	aagttcaggc	tagtgtttgt	ggactttgaa	gatggacgta	480
agaggtatct	gaagaaatca	gctaagtggt	ttaggagatt	gttgaaggga	gcratgggtg	540
ggacgaatga	gcaggtggct	gttattttaat	aaaccacgag	tcattgggtca	atttagtcta	600
ctgtttcttt	tgctctatgt	acagaaagaa	aataaacttt	ccaaaataag	aggtggcctt	660
gtttggactt	tggatggttac	tatatatatt	ggtaattctt	ggcgtttggt	agtttccaaa	720
ccaaacatta	ataaataaat	aaataaaaaga	gtttgaggtt			

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met Glu Glu Lys Lys Pro Glu Glu Lys Lys Glu Gly Glu Asp Lys Lys  
1 5 10 15  
Val Asp Ala Glu Lys Lys Gly Glu Asp Ser Asp Lys Lys Pro Gln Glu  
20 25 30  
Gly Glu Thr Asn Lys Asp Ser Lys Glu Asp Ser Ala Pro Ala Ala Pro  
35 40 45  
Glu Ala Pro Ala Pro Pro Pro Pro Gln Glu Val Val Leu Lys Val  
50 55 60  
Tyr Met His Cys Glu Gly Cys Ala Arg Lys Val Arg Arg Cys Leu Lys  
65 70 75 80

Gly	Phe	Glu	Gly	Val	Glu	Asp	Val	Met	Thr	Asp	Cys	Lys	Thr	Gly	Lys
				85					90					95	
Val	Val	Val	Lys	Gly	Glu	Lys	Ala	Asp	Pro	Leu	Lys	Val	Leu	Ala	Arg
			100					105					110		
Val	Gln	Arg	Lys	Thr	His	Arg	Gln	Val	Gln	Ala	Ser	Val	Cys	Gly	Leu
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1498085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Met	Leu	Arg	Lys	Lys	Glu	Lys	Ile	Leu	Thr	Arg	Ser	Leu	Lys	Lys	Glu
1			5						10					15	
Lys	Leu	Thr	Lys	Ile	Pro	Lys	Lys	Ile	Leu	Leu	Arg	Arg	Arg	Leu	Arg
			20					25					30		
Leu	Gln	His	Arg	Leu	Leu	Arg	Arg	Lys	Arg	Leu	Phe	Leu	Arg	Phe	Thr
			35				40					45			
Cys	Thr	Val	Lys	Asp	Val	Leu	Glu	Lys	Ser	Ala	Val	Val	Ser	Lys	Ala
			50			55					60				
Ser	Lys	Glu	Trp	Lys	Met										
65					70										

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1498086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Val	Gly	Arg	Met	Ser	Arg	Trp	Leu	Leu	Phe	Asn	Lys	Pro	Arg	Val
1				5				10						15	
Ile	Gly	Gln	Phe	Ser	Leu	Leu	Phe	Leu	Leu	Tyr	Val	Gln	Lys	Glu	
			20					25				30			
Asn	Lys	Leu	Ser	Lys	Ile	Arg	Gly	Gly	Phe	Val	Trp	Thr	Leu	Asp	Val
			35				40					45			
Thr	Ile	Tyr	Ile	Gly	Asn	Ser	Trp	Arg	Leu	Leu	Val	Ser	Lys	Pro	Asn
			50			55					60				
Ile	Asn	Lys													
65															

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -



(B) LOCATION: 1..748

(D) OTHER INFORMATION: / Ceres Seq. ID 1498090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

aaatcactta	cttaacatac	taagagagtt	attagaactt	gcaaaaaatg	gcttccaagg	60
ctttgattct	gttaggtctc	ttctcagttc	ttctcgtcgt	ctccgaagtg	tctgccgcaa	120
ggaatcgggc	atggtgaagc	cagagagtga	ggaaactgtg	caacctgaag	gttatrgcgg	180
tggccacgga	ggacatggtg	gtcacggagg	gggaggaggc	cacggacatg	gaggacacaa	240
cggaggaggg	ggccacggac	ttgacggata	cggaggaggt	ggaggacact	atggaggarg	300
tggaggacac	tacggaggag	gtggaggaca	ctacggagga	ggtggaggac	actacggagg	360
aggtggtgga	gaggattaaa	gctactgttt	cttgtgatgt	tggaggagga	gcgtagtttt	420
ttttcagaag	aagtaagaat	aagagaaaaa	gaaggattaa	gagcggttat	ggtttctcat	480
tttgtgtttt	ttgaaatcca	aaggaagtca	agaacgcacc	ttttgcgttt	aatttctatc	540
caagctgatg	aaaaaaggta	aagtggttcg	ggtattgact	tctgctggaa	accacggttt	600
taaattgtct	attttgcgtt	tcgttgacag	ttttttgaac	accttttggg	tttccccttt	660
ttgcgttctc	cgacccaagt	tgctcarwttc	tttgttgttt	tgtattgtaa	gcccttttgt	720
tgcacttgac	agatatggag	ttaaaatc				

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1498091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Asn	His	Leu	Leu	Asn	Ile	Leu	Arg	Glu	Leu	Glu	Leu	Ala	Lys	Asn	
1				5				10					15		
Gly	Phe	Gln	Gly	Phe	Asp	Ser	Val	Arg	Ser	Leu	Leu	Ser	Ser	Ser	Arg
				20				25					30		
Arg	Leu	Arg	Ser	Val	Cys	Arg	Lys	Glu	Ser	Gly	Met	Val	Lys	Pro	Glu
				35				40					45		
Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Xaa	Gly	Gly	His	Gly	Gly
				50				55				60			
His	Gly	Gly	His	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	Gly	His	Asn
65				70				75						80	
Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	His
				85				90						95	
Tyr	Gly	Gly	Xaa	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly	Gly	His	Tyr	Gly
				100				105					110		
Gly	Gly	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly	Glu	Asp				
				115				120			125				

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1498092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Xaa
1				5				10					15		
Gly	Gly	His	Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly
				20				25					30		
His	Gly	Gly	His	Asn	Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly

35 40 45  
Gly Gly Gly Gly His Tyr Gly Gly Xaa Gly Gly His Tyr Gly Gly Gly  
50 55 60  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly  
65 70 75 80  
Glu Asp

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Val Val Thr Glu Gly Glu Glu Ala Thr Asp Met Glu Asp Thr Thr  
1 5 10 15  
Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Val Glu Asp Thr  
20 25 30  
Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu  
35 40 45  
Glu Val Glu Asp Thr Thr Glu Glu Val Val Glu Arg Ile Lys Ala Thr  
50 55 60  
Val Ser Cys Asp Val Gly Gly Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

aaaaattaaa agtgttcttg ttgctgtaga acacaaacag aacaaacaaa aaatcaattg 60  
aagagtctct cagtcgttag gggaagcaaa tagagaaatg gctagcttta ctgcctccgc 120  
ttccaccgtc tccgccgctc gtccggctct ccttctcaag cctaccgtcg ccattctctgc 180  
tcctgttctt ggtttgcctc caatgggtaa gaagaaggga ggagtgaatg gttcaatgga 240  
gacaaagcag gaaacgtctc agtcatgggg gctggagttt cagctgcagc aacagctgct 300  
ttgacggcgg tgatgagcaa tcccgcgatg gcttttggtt atgagaggat gtcaacagaa 360  
ggaacaggat tacccttttg tctaagcaac aacctcttgg gttggattct gtttgagtc 420  
tttggtttga wctggacttt cttcttcgtc tacacttcat ctctcgagga ggatgaagaa 480  
tctggtcttt cactctgaag gaagaatcaa tctttcgtct tctcatttcc attttcatgt 540  
gagaacatga atcaaaagt ttcacccttc tagtttcttg taattgttaa gtaaagacta 600  
aaaactagaa gggatgaacac tattcattca ttctcatcat gtcacggaa tctgaaatcc 660  
cgccgtttgc gtcacaaacc gccgcagcgg aggaatctcg agagaagacc agcaagaaag 720  
cggctaagaa ggaagctgcc aagctagaga agttaagacc tcgtcaagaa caagaggaag 780  
caacgcgtcg aacagcttcg atctctctgg aagagaatga cgagttttcc aataactacg 840  
gcgacgtgac tcttaccgag ttgcaatcgt cgccggatcc gaaagccggg aagtggatag 900  
aggctgttga gggaaaggag tggaccgatg tgagcgattt ggtggaagag atgttggat 960  
cagaggttct gatcagaggc cgagtgcaca cgaatcgtcc aacgtctaac aaattgggg 1020  
ttgtggtctt gagggagagc ggatcaactg ttcagtgcgt ggtagccaa tcagagaaga 1080  
ccaaactagg tgccaacatg gttaaataatc tcaagcagct gagtcgcgaa tcctttgtcg 1140  
atgttatcgg tgcgtcact ctccccaagg agccgctgac ggaactacg cagcaggttg 1200

aaattcaagt gagaaaagtg tactgcatca acaaatcctt ggccaaatta ccacttagtg 1260  
tggaggatgc tgctcggagt gaagcagata tcgaagcatc tcttcagact ccactctccag 1320  
ctgctcgtgt caatcaggat acacgtttga actatagggt gctcgacctc agaacaccgg 1380  
ctaatacaagc catcttccag cttcagtagc aagtcgaata tgccttcaga gaaaaattac 1440  
gatttaagaa ttttgttgga atccacacac caaaactgat ggctggtagt agtgaaggag 1500  
gttctgctgt atttaggttg gaatac

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1498098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Ser Ser Glu Ser Glu Ile Pro Pro Leu Ser Ser Ser Thr Ala Ala  
1 5 10 15  
Ala Glu Glu Ser Gly Glu Lys Thr Ser Lys Lys Ala Ala Lys Lys Glu  
20 25 30  
Ala Ala Lys Leu Glu Lys Leu Arg Arg Arg Gln Glu Gln Glu Glu Ala  
35 40 45  
Thr Arg Arg Thr Ala Ser Ile Ser Leu Glu Glu Asn Asp Glu Phe Ser  
50 55 60  
Asn Asn Tyr Gly Asp Val Thr Leu Thr Glu Leu Gln Ser Ser Ala Asp  
65 70 75 80  
Pro Lys Ala Gly Lys Trp Ile Glu Ala Val Glu Gly Lys Glu Trp Thr  
85 90 95  
Asp Val Ser Asp Leu Val Glu Glu Met Leu Glu Ser Glu Val Leu Ile  
100 105 110  
Arg Gly Arg Val His Thr Asn Arg Pro Thr Ser Asn Lys Leu Gly Phe  
115 120 125  
Val Val Leu Arg Glu Ser Gly Ser Thr Val Gln Cys Val Val Ser Gln  
130 135 140  
Ser Glu Lys Thr Lys Leu Gly Ala Asn Met Val Lys Tyr Leu Lys Gln  
145 150 155 160  
Leu Ser Arg Glu Ser Phe Val Asp Val Ile Gly Val Val Thr Leu Pro  
165 170 175  
Lys Glu Pro Leu Thr Gly Thr Thr Gln Gln Val Glu Ile Gln Val Arg  
180 185 190  
Lys Val Tyr Cys Ile Asn Lys Ser Leu Ala Lys Leu Pro Leu Ser Val  
195 200 205  
Glu Asp Ala Ala Arg Ser Glu Ala Asp Ile Glu Ala Ser Leu Gln Thr  
210 215 220  
Pro Ser Pro Ala Ala Arg Val Asn Gln Asp Thr Arg Leu Asn Tyr Arg  
225 230 235 240  
Val Leu Asp Leu Arg Thr Pro Ala Asn Gln Ala Ile Phe Gln Leu Gln  
245 250 255  
Tyr Glu Val Glu Tyr Ala Phe Arg Glu Lys Leu Arg Phe Lys Asn Phe  
260 265 270  
Val Gly Ile His Thr Pro Lys Leu Met Ala Gly Ser Ser Glu Gly Gly  
275 280 285  
Ser Ala Val Phe Arg Leu Glu Tyr  
290 295

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..192  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498099  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```
Met Leu Glu Ser Glu Val Leu Ile Arg Gly Arg Val His Thr Asn Arg
1          5          10          15
Pro Thr Ser Asn Lys Leu Gly Phe Val Val Leu Arg Glu Ser Gly Ser
          20          25          30
Thr Val Gln Cys Val Val Ser Gln Ser Glu Lys Thr Lys Leu Gly Ala
          35          40          45
Asn Met Val Lys Tyr Leu Lys Gln Leu Ser Arg Glu Ser Phe Val Asp
          50          55          60
Val Ile Gly Val Val Thr Leu Pro Lys Glu Pro Leu Thr Gly Thr Thr
          65          70          75          80
Gln Gln Val Glu Ile Gln Val Arg Lys Val Tyr Cys Ile Asn Lys Ser
          85          90          95
Leu Ala Lys Leu Pro Leu Ser Val Glu Asp Ala Ala Arg Ser Glu Ala
          100         105         110
Asp Ile Glu Ala Ser Leu Gln Thr Pro Ser Pro Ala Ala Arg Val Asn
          115         120         125
Gln Asp Thr Arg Leu Asn Tyr Arg Val Leu Asp Leu Arg Thr Pro Ala
          130         135         140
Asn Gln Ala Ile Phe Gln Leu Gln Tyr Glu Val Glu Tyr Ala Phe Arg
          145         150         155         160
Glu Lys Leu Arg Phe Lys Asn Phe Val Gly Ile His Thr Pro Lys Leu
          165         170         175
Met Ala Gly Ser Ser Glu Gly Gly Ser Ala Val Phe Arg Leu Glu Tyr
          180         185         190
```

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 697 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..697  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498100  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
aacaccttct ttaatccaga acaacaaaaa aaccaaacag aagaagaaaa aagaaaaaaa      60
actacaaaaa aaaaaaatct ctgcccgctt ctccgttctc ggggttgctg cgaaattgga      120
ccaaattgat caaaccttac ccagaaatca tttttggtca caggggatag gcgggcagat      180
ttaaaaaatt tcttcttttt ttcttctggt tgaatttgta ttgattcgtg aaattgtgtg      240
tgtttgatgg gttttttggt ggatacgcaa aaggaaggag gtggacattc atggggttac      300
gttagaagtt tggttagaag gaaacaagtc gactctgcta atggccaatc tcatggtcac      360
caacttgcta gagccctcac tgttcctcat ctcgttgcaa ttggtgttgg agcaacaata      420
ggagctggag tttatattct tgtaggaaca gttgcgagag agcattcagg accttctctt      480
gctttgtctt ttcttattgc tggaattgct gctgggtctt ctgcgttttg ttatgctgaa      540
ctctctagtc gttgtcnttc agctgggagt gcgtatcact attcttacat ttgtgttggt      600
gaaggtgttg cgtggataat cggttgggag ttgattctca agtgtaagat tgtacttgta      660
aacaaaaaat gtattatata aaagtgttat ttgttcc
```

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 144 amino acids  
    (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498101  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met	Gly	Phe	Leu	Val	Asp	Thr	Gln	Lys	Glu	Gly	Gly	Gly	His	Ser	Trp
1				5					10					15	
Gly	Tyr	Val	Arg	Ser	Leu	Val	Arg	Arg	Lys	Gln	Val	Asp	Ser	Ala	Asn
			20					25					30		
Gly	Gln	Ser	His	Gly	His	Gln	Leu	Ala	Arg	Ala	Leu	Thr	Val	Pro	His
		35					40					45			
Leu	Val	Ala	Ile	Gly	Val	Gly	Ala	Thr	Ile	Gly	Ala	Gly	Val	Tyr	Ile
	50					55					60				
Leu	Val	Gly	Thr	Val	Ala	Arg	Glu	His	Ser	Gly	Pro	Ser	Leu	Ala	Leu
65					70					75				80	
Ser	Phe	Leu	Ile	Ala	Gly	Ile	Ala	Ala	Gly	Leu	Ser	Ala	Phe	Cys	Tyr
			85					90						95	
Ala	Glu	Leu	Ser	Ser	Arg	Cys	Xaa	Ser	Ala	Gly	Ser	Ala	Tyr	His	Tyr
		100						105					110		
Ser	Tyr	Ile	Cys	Val	Gly	Glu	Gly	Val	Ala	Trp	Ile	Ile	Gly	Trp	Ala
		115					120					125			
Leu	Ile	Leu	Lys	Cys	Lys	Ile	Val	Leu	Val	Asn	Lys	Lys	Cys	Ile	Ile
	130						135					140			

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..771  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

acaatccaat	caaaacacac	agagagaaga	aaaactcaga	agaaaagcca	aagagtga	60
caaaaatggc	gtcgacgact	ctctcaatcg	caacaacaat	ccgttcctca	tcttatccta	120
ctctcgttcc	catcaatcac	ttcccttccc	gaaccamcac	catcgaattc	ccctctcgtc	180
tcggtgggtg	ttcatcatcc	acattgaccc	accgtgcaac	ccatctccgt	ccaatcgccg	240
ccgtcgaagc	tccggagaaa	atcgagaaga	tcggatccga	aatctcatcc	ctaaccctcg	300
aagaagctcg	tatcctcgtc	gactatctcc	aagacaaatt	cggtgtctcc	ccactctctt	360
tagccccgcg	agcagcgggc	gttgetgtct	cagccgacgg	tggcgcgggc	gctgtagtgg	420
aagagcaaac	agagttcgat	gtggttatca	atgaagttcc	cagcagttcc	cgtattgcag	480
tgattaaagc	tgttagggtc	ttaactagct	tggcgttgaa	ggaagctaag	gagctaatac	540
aaggattacc	aaagaagttt	aaagaaggta	tcactaaaga	tgaagctgaa	gaagctaaga	600
agactcttga	agaagctggg	gctaaagtct	ccattgctta	aggtttttat	taaaaaaaaa	660
aaagaagttg	ttatcttttc	tggaatttga	ttggtctttt	gtgttggtta	gtatagtttg	720
cgctctggaat	tggttgagaaa	ttgttgtaat	ttgaatcaca	tttggtttcc	c	

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1498103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Asn	Pro	Ile	Lys	Thr	His	Arg	Glu	Lys	Lys	Asn	Ser	Glu	Glu	Lys	Pro
1				5					10					15	
Lys	Ser	Glu	Thr	Lys	Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr
			20					25					30		
Ile	Arg	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro
		35					40					45			
Ser	Arg	Thr	Xaa	Thr	Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Gly	Ser
		50				55					60				
Ser	Ser	Thr	Leu	Thr	His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala
65					70					75				80	
Val	Glu	Ala	Pro	Glu	Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser
				85					90					95	
Leu	Thr	Leu	Glu	Glu	Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys
			100					105					110		
Phe	Gly	Val	Ser	Pro	Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Val	Ala	
		115					120					125			
Ala	Pro	Ala	Asp	Gly	Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu
		130				135					140				
Phe	Asp	Val	Val	Ile	Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val
145					150					155				160	
Ile	Lys	Ala	Val	Arg	Ala	Leu	Thr	Ser	Leu	Ala	Leu	Lys	Glu	Ala	Lys
				165					170					175	
Glu	Leu	Ile	Glu	Gly	Leu	Pro	Lys	Lys	Phe	Lys	Glu	Gly	Ile	Thr	Lys
			180					185					190		
Asp	Glu	Ala	Glu	Glu	Ala	Lys	Lys	Thr	Leu	Glu	Glu	Ala	Gly	Ala	Lys
		195					200					205			
Val	Ser	Ile	Ala												
															210

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1498104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr	Ile	Arg	Ser	Ser	Ser
1					5					10				15	
Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro	Ser	Arg	Thr	Xaa	Thr
			20					25					30		
Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Gly	Ser	Ser	Ser	Thr	Leu	Thr
		35					40					45			
His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala	Val	Glu	Ala	Pro	Glu
		50				55					60				
Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser	Leu	Thr	Leu	Glu	Glu
65					70					75				80	
Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys	Phe	Gly	Val	Ser	Pro
			85					90					95		
Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Ala	Val	Ala	Ala	Pro	Ala	Asp	Gly
			100					105					110		
Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu	Phe	Asp	Val	Val	Ile
		115						120				125			
Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val	Ile	Lys	Ala	Val	Arg

130	135	140
Ala Leu Thr Ser Leu	Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly	
145	150	155
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu		160
	165	170
Ala Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala		175
	180	185
		190

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

aattgctctc	tcaattttctc	tctcctccc	cttctgcttc	tctcccttaa	caagaacccat	60
gagctcctcc	gatggcggct	cctctaggg	ttcgattcct	taccatctcc	gcaaaaacct	120
tcagaaaatc	agagagtata	ccgaaagca	gcactcggat	gaggatatct	ttgccgtcta	180
taaggattcc	ttcaatgatc	ctcatgagac	cgctcagaag	ctcctcttct	tagatacatt	240
tcatgaggtg	agaagtaaaa	gggagaaaa	gaaggagcct	atagtgccag	ttacacaacc	300
aagtggcaga	ggtggctcga	ggaactttgc	ttcaagtaac	tcttatcaag	gtagtggaa	360
aaatgcttct	tttaaaagg	aaaatggagc	taatcatgta	acaagagggt	ctagaactgc	420
tcagcctgcc	actaacaaag	camgcaacat	cacagtacct	aatgaaacaa	aggtttctgg	480
tctctgtagt	attctgagtg	aggctagcaa	tcataaagct	caagatgatc	cttctttgat	540
ttctgcttca	cgttgccagta	ccagtcaga	tcaagccatt	gaaattgaga	ctgcgtccaa	600
acaaggcaaa	aatcaatcgc	ttcctaagcc	agatgttagc	gaacagtcac	acgtaacatt	660
ccctttccac	cttcagggtg	ccaaaggact	gcaaaatggg	ctgacgtttg	gcagttttga	720
ttccaatttt	gtgaaagagg	tatcttctag	caatggtgct	agtggcggat	atgactcaaa	780
ttttgagttc	tctcacggga	caggggatga	tgagagggaa	tcttctccca	ctaccaatgg	840
tattactggg	gttgcttcgg	ctagagaaga	aacatcaaca	gtttctgaag	ataaggatta	900
tgggatatac	aattotgcaa	ctggagctga	gcctgtgggt	cactcggatc	acattgtccc	960
acctgtagaa	gaagtaccga	aggaggaagc	tttatcaaac	acagaaactc	atcaaattgc	1020
ttatggtcaa	gaagctccac	tcagtggtgt	tggctctgtc	ccctcgttgt	cagcaatagg	1080
ccaaccgggt	aacacagaag	cagcggagac	tcagcccggg	aattccaact	ctccagctat	1140
ttcattagta	tcatactctc	cagatcagag	ctccatagca	gcagccactc	aacagacaaa	1200
ttttcttagg	cagcaatacc	ctcccaattt	cttcccttac	ggctatttct	caccgtatta	1260
tatgccaccg	ccgtacattc	accagttctt	gagcccaaac	gggatccctc	agcagtctta	1320
ttttccacaa	ggagctgctc	taacagcacc	ttctcatgca	aaaccagttg	acaacactga	1380
aaaccctccc	accacaaaac	cttacctaca	cacttctccc	atggttgcta	gcagcatccc	1440
atctacaacc	accttaaat	ctatccatag	tgaagaaaag	gcattctcacc	tgactgaaag	1500
tgcagctgca	tggattgggc	agggatttgg	caacctgcag	gtgaatccaa	tgtataacct	1560
agcataccaa	ggtcagccac	ttggttttcc	agtcgtgcag	gctgggtcatg	gtggcctcat	1620
gggaatgcac	gaaccaaac	agcccatggc	agctgcttta	actacatatc	agaccttacc	1680
accaccgcca	cacacaacaa	cggctatggg	tccgagcgtg	gtgggtggata	cggttctcaa	1740
cgtagtggtg	gtgggttacg	agggctctca	cgttccagtt	atgggttcggg	gtcagggtcc	1800
gggtcgggct	caggttcagg	aaaccgtctc	tacgtgggca	acctttcttg	gggtgttgat	1860
gacatggcac	ttgagaactt	gtttaacgag	caaggaaagg	tagttgragc	taggggtwgc	1920
gatctacgac	agggacagcg	gtagatccaa	gggttttgga	tttgtgacac	ttagctcttc	1980
ccaagaggtt	cagaaggcga	tcaattcctt	gaatggagca	gatttggatg	gaagacaaat	2040
aagagtctca	gaggtcgagg	ctaggccacc	aagaggccaa	ttttgagcgg	tcacacctct	2100
ttcatattct	caaaaaatgc	aaattctgga	gggttctttg	aagcatatag	ggttagtggg	2160
aaatggcggt	ttcagacagt	aactaaaact	cactgctggg	gcacgctagg	ctttatccgc	2220
ctttgatgca	tgaaggctcg	taaggaatgg	tctttttttg	agaaagataa	caattagatt	2280
aaagcagaga	acccatgttt	cttgtctgtt	cgaatcctgc	gagattgggt	gtagttgaag	2340
ttgcattttc	ttcttgctct	ttttgttggt	attttgacac	aatttggctt	tttggcatat	2400
gagagtgact	gtagcagttc	gttttatttg	atgttcttga	tcc		

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: peptide  
 (B) LOCATION: 1..633  
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498110  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ile	Ala	Leu	Ser	Ile	Ser	Leu	Ser	Ser	Arg	Phe	Cys	Phe	Ser	Pro	Leu
1				5					10					15	
Thr	Arg	Thr	Met	Ser	Ser	Ser	Asp	Gly	Gly	Ser	Ser	Arg	Val	Ser	Ile
			20					25					30		
Pro	Tyr	His	Leu	Arg	Lys	Thr	Leu	Gln	Lys	Ile	Arg	Glu	Tyr	Thr	Gly
		35				40						45			
Lys	Gln	His	Ser	Asp	Glu	Asp	Ile	Phe	Ala	Val	Tyr	Lys	Asp	Ser	Phe
	50					55					60				
Asn	Asp	Pro	His	Glu	Thr	Ala	Gln	Lys	Leu	Leu	Phe	Leu	Asp	Thr	Phe
65				70						75					80
His	Glu	Val	Arg	Ser	Lys	Arg	Glu	Lys	Lys	Lys	Glu	Pro	Ile	Val	Pro
			85						90					95	
Val	Thr	Gln	Pro	Ser	Gly	Arg	Gly	Gly	Arg	Arg	Asn	Phe	Ala	Ser	Ser
			100					105					110		
Asn	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Asn	Ala	Ser	Phe	Lys	Arg	Glu	Asn
	115					120					125				
Gly	Ala	Asn	His	Val	Thr	Arg	Gly	Ser	Arg	Thr	Ala	Gln	Pro	Ala	Thr
	130					135					140				
Asn	Lys	Ala	Xaa	Asn	Ile	Thr	Val	Pro	Asn	Glu	Thr	Lys	Val	Ser	Gly
145					150					155					160
Pro	Ala	Ser	Ile	Leu	Ser	Glu	Val	Ser	Asn	His	Lys	Ala	Gln	Asp	Asp
			165						170					175	
Pro	Ser	Leu	Ile	Ser	Ala	Ser	Arg	Cys	Ser	Ser	Gln	Ser	Asp	Gln	Ala
		180						185					190		
Ile	Glu	Ile	Glu	Thr	Ala	Ser	Lys	Gln	Gly	Lys	Asn	Gln	Ser	Leu	Pro
	195						200					205			
Lys	Pro	Asp	Val	Ser	Glu	Gln	Ser	His	Val	Thr	Phe	Pro	Phe	His	Leu
	210					215					220				
Gln	Val	Ala	Lys	Gly	Leu	Gln	Asn	Gly	Leu	Thr	Phe	Gly	Ser	Phe	Asp
225					230					235					240
Ser	Asn	Phe	Val	Lys	Glu	Val	Ser	Ser	Ser	Asn	Gly	Ala	Ser	Gly	Gly
			245						250					255	
Tyr	Asp	Ser	Asn	Phe	Glu	Ser	Ser	His	Gly	Thr	Gly	Asp	Asp	Glu	Arg
		260						265					270		
Glu	Ser	Ser	Pro	Thr	Thr	Asn	Gly	Ile	Thr	Gly	Val	Ala	Ser	Ala	Arg
		275				280						285			
Glu	Glu	Thr	Ser	Thr	Val	Ser	Glu	Asp	Lys	Asp	Tyr	Gly	Ile	Ser	Asn
	290					295					300				
Ser	Ala	Thr	Gly	Ala	Glu	Pro	Val	Val	His	Ser	Asp	His	Ile	Val	Pro
305					310					315					320
Pro	Val	Glu	Glu	Val	Pro	Lys	Glu	Glu	Ala	Leu	Ser	Asn	Thr	Glu	Thr
			325						330					335	
His	Gln	Ile	Ala	Tyr	Gly	Gln	Glu	Ala	Pro	Leu	Ser	Val	Phe	Gly	Leu
		340						345					350		
Val	Pro	Ser	Leu	Ser	Ala	Ile	Gly	Gln	Pro	Val	Asn	Thr	Glu	Ala	Ala
		355				360						365			
Glu	Thr	Gln	Pro	Gly	Asn	Ser	Asn	Ser	Pro	Ala	Ile	Ser	Leu	Val	Ser
	370					375					380				
Tyr	Pro	Pro	Asp	Gln	Ser	Ser	Ile	Ala	Ala	Ala	Thr	Gln	Gln	Thr	Asn
385				390						395					400



```

Phe Leu Arg Gln Gln Tyr Pro Pro Asn Phe Phe Pro Tyr Gly Tyr Xaa
      405                      410                      415
Ser Pro Tyr Tyr Met Pro Pro Pro Tyr Ile His Gln Phe Leu Ser Pro
      420                      425                      430
Asn Gly Ile Pro Gln Gln Ser Tyr Phe Pro Gln Gly Ala Ala Leu Thr
      435                      440                      445
Ala Pro Ser His Ala Lys Pro Val Asp Asn Thr Glu Asn Pro Pro Thr
      450                      455                      460
Thr Asn Pro Tyr Leu His Thr Ser Pro Met Val Ala Ser Ser Ile Pro
      465                      470                      475                      480
Ser Thr Thr Thr Leu Asn Ser Ile His Ser Glu Glu Lys Ala Ser His
      485                      490                      495
Leu Thr Glu Ser Ala Ala Ala Trp Ile Gly Gln Gly Phe Gly Asn Leu
      500                      505                      510
Gln Val Asn Pro Met Tyr Asn Leu Ala Tyr Gln Gly Gln Pro Leu Gly
      515                      520                      525
Phe Pro Val Val Gln Ala Gly His Gly Gly Leu Met Gly Met His Gln
      530                      535                      540
Pro Thr Gln Pro Met Ala Ala Ala Leu Thr Thr Tyr Gln Thr Leu Pro
      545                      550                      555                      560
Pro Pro Pro His Thr Thr Thr Ala Met Val Pro Ser Val Val Val Asp
      565                      570                      575
Thr Val Leu Asn Val Val Val Val Val Thr Glu Gly Leu Asn Val Pro
      580                      585                      590
Val Met Val Arg Gly Gln Gly Pro Val Arg Ala Gln Val Gln Glu Thr
      595                      600                      605
Val Ser Thr Trp Ala Thr Phe Leu Gly Val Leu Met Thr Trp His Leu
      610                      615                      620
Arg Thr Cys Leu Thr Ser Lys Glu Arg
      625                      630

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(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..614
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

Met Ser Ser Ser Asp Gly Gly Ser Ser Arg Val Ser Ile Pro Tyr His
1      5      10      15
Leu Arg Lys Thr Leu Gln Lys Ile Arg Glu Tyr Thr Gly Lys Gln His
      20      25      30
Ser Asp Glu Asp Ile Phe Ala Val Tyr Lys Asp Ser Phe Asn Asp Pro
      35      40      45
His Glu Thr Ala Gln Lys Leu Leu Phe Leu Asp Thr Phe His Glu Val
      50      55      60
Arg Ser Lys Arg Glu Lys Lys Lys Glu Pro Ile Val Pro Val Thr Gln
      65      70      75      80
Pro Ser Gly Arg Gly Gly Arg Arg Asn Phe Ala Ser Ser Asn Ser Tyr
      85      90      95
Gln Gly Ser Gly Arg Asn Ala Ser Phe Lys Arg Glu Asn Gly Ala Asn
      100     105     110
His Val Thr Arg Gly Ser Arg Thr Ala Gln Pro Ala Thr Asn Lys Ala
      115     120     125
Xaa Asn Ile Thr Val Pro Asn Glu Thr Lys Val Ser Gly Pro Ala Ser
      130     135     140
Ile Leu Ser Glu Val Ser Asn His Lys Ala Gln Asp Asp Pro Ser Leu

```

145		150		155		160
Ile Ser Ala Ser Arg	Cys Ser Ser Gln Ser Asp Gln Ala Ile Glu Ile					
	165		170			175
Glu Thr Ala Ser Lys	Gln Gly Lys Asn Gln Ser Leu Pro Lys Pro Asp					
	180		185			190
Val Ser Glu Gln Ser His	Val Thr Phe Pro Phe His Leu Gln Val Ala					
	195		200			205
Lys Gly Leu Gln Asn Gly	Leu Thr Phe Gly Ser Phe Asp Ser Asn Phe					
	210		215			220
Val Lys Glu Val Ser Ser	Asn Gly Ala Ser Gly Gly Tyr Asp Ser					
	225		230			235
Asn Phe Glu Ser Ser His	Gly Thr Gly Asp Asp Glu Arg Glu Ser Ser					
	245		250			255
Pro Thr Thr Asn Gly Ile	Thr Gly Val Ala Ser Ala Arg Glu Glu Thr					
	260		265			270
Ser Thr Val Ser Glu Asp	Lys Asp Tyr Gly Ile Ser Asn Ser Ala Thr					
	275		280			285
Gly Ala Glu Pro Val Val	His Ser Asp His Ile Val Pro Pro Val Glu					
	290		295			300
Glu Val Pro Lys Glu Glu	Ala Leu Ser Asn Thr Glu Thr His Gln Ile					
	305		310			315
Ala Tyr Gly Gln Glu Ala	Pro Leu Ser Val Phe Gly Leu Val Pro Ser					
	325		330			335
Leu Ser Ala Ile Gly Gln	Pro Val Asn Thr Glu Ala Ala Glu Thr Gln					
	340		345			350
Pro Gly Asn Ser Asn Ser	Pro Ala Ile Ser Leu Val Ser Tyr Pro Pro					
	355		360			365
Asp Gln Ser Ser Ile Ala	Ala Ala Thr Gln Gln Thr Asn Phe Leu Arg					
	370		375			380
Gln Gln Tyr Pro Pro Asn	Phe Phe Pro Tyr Gly Tyr Xaa Ser Pro Tyr					
	385		390			395
Tyr Met Pro Pro Pro Tyr	Ile His Gln Phe Leu Ser Pro Asn Gly Ile					
	405		410			415
Pro Gln Gln Ser Tyr Phe	Pro Gln Gly Ala Ala Leu Thr Ala Pro Ser					
	420		425			430
His Ala Lys Pro Val Asp	Asn Thr Glu Asn Pro Pro Thr Thr Asn Pro					
	435		440			445
Tyr Leu His Thr Ser Pro	Met Val Ala Ser Ser Ile Pro Ser Thr Thr					
	450		455			460
Thr Leu Asn Ser Ile His	Ser Glu Glu Lys Ala Ser His Leu Thr Glu					
	465		470			475
Ser Ala Ala Ala Trp Ile	Gly Gln Gly Phe Gly Asn Leu Gln Val Asn					
	485		490			495
Pro Met Tyr Asn Leu Ala	Tyr Gln Gly Gln Pro Leu Gly Phe Pro Val					
	500		505			510
Val Gln Ala Gly His Gly	Gly Leu Met Gly Met His Gln Pro Thr Gln					
	515		520			525
Pro Met Ala Ala Ala Leu	Thr Thr Tyr Gln Thr Leu Pro Pro Pro Pro					
	530		535			540
His Thr Thr Thr Ala Met	Val Pro Ser Val Val Val Asp Thr Val Leu					
	545		550			555
Asn Val Val Val Val Val	Thr Glu Gly Leu Asn Val Pro Val Met Val					
	565		570			575
Arg Gly Gln Gly Pro Val	Arg Ala Gln Val Gln Glu Thr Val Ser Thr					
	580		585			590
Trp Ala Thr Phe Leu Gly	Val Leu Met Thr Trp His Leu Arg Thr Cys					
	595		600			605
Leu Thr Ser Lys Glu Arg						
	610					

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..657  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498112  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:  
actcaactta aactctttta gtaacaatgg tttcttcttc ttttaaccaag cttgtgttct 60  
ttggttgtct cctcctgctc acattcacgg acaaccttgt ggctggaaaa tctggcaaa 120  
tgaagctcaa tctttactac gaatcacttt gtcccgttg tcaggaattc atcgctgatg 180  
acctaggtaa aatctttgac tacgatctct acacaatcac tgatctcaag ctgtttccat 240  
ttggtaatgc cgaactctcc gataatctga ctgtcacttg ccagcatggt gaagaggaat 300  
gcaactaaa cgcccttgaa gcttgagatc agtgattgtg tagagatcgt agtcaaagat 360  
tttacagaag tcattctcca gtcccaagag gaagaccttg atcaatgcag aaaacagaag 420  
cttcgaagaa tgagtttttc gaaagggtaa atttatctat gttgtgtttt gagttagaag 480  
atgctttttg atgttttgaa atccttgtaa actttgggat cttagacttt tatcttaaaa 540  
tcagtagaaa cttcataatg gcgctttgtc acgatctgtt acttggttca tatactcttt 600  
tcattcgtca ttaattattc taartcccat ataaattaac aatgacacaa gtttgcc  
(2) INFORMATION FOR SEQ ID NO:195:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498113  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:  
Leu Asn Leu Asn Ser Phe Ser Asn Asn Gly Phe Phe Phe Phe Asn Gln  
1 5 10 15  
Ala Cys Val Leu Trp Leu Ser Pro Pro Ala His Ile His Gly Gln Pro  
20 25 30  
Cys Gly Trp Lys Ile Trp Gln Ser Glu Ala Gln Ser Leu Leu Arg Ile  
35 40 45  
Thr Leu Ser Arg Leu Ser Gly Ile His Arg Arg  
50 55  
(2) INFORMATION FOR SEQ ID NO:196:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..99  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498114  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:  
Met Val Ser Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu  
1 5 10 15  
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val  
20 25 30  
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Gln Glu Phe  
35 40 45  
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile  
50 55 60

Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn  
65 70 75 80  
Leu Thr Val Thr Cys Gln His Gly Glu Glu Glu Cys Lys Leu Asn Ala  
85 90 95  
Leu Glu Ala

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

tcctttcttt	gagtcgcttc	acttctcttg	catccttcaa	actcatccac	agcaaggaat	60
ggctacagca	gcagcaccag	cagtgatttc	atggacaaga	tcaggcattg	tgtccaaatc	120
cggacaaacc	cagaagaaat	ctgagatgaa	agtttcttac	ataactggac	ttaactcata	180
tggtggtctc	aaggcacaga	acaacaaggt	tgtctcaatg	ggatcaccac	tctgcacaga	240
acagtgtttt	gctaacgttg	tgatgtctct	caaaggaaga	agaggtaatg	gaggagcctt	300
atccaccacg	tgtaacgctg	tcggagagat	tttcaagatt	gcagcaaaac	actgttctgt	360
gaagagtggg	ataagtatct	agcaatgttc	tggcaacttg	tacctccgag	tgaagaagac	420
acacctgagg	ctaactcaga	ccacatcctg	aaaacaacca	caggagatga	agaacagggt	480
tcaagcacat	tagcagagaa	gtaaaaccta	cacatttgat	cgtggtttcc	tctttgtaca	540
gtcaaagtcg	tggtggagga	gataagtaag	tctctcagtt	gctgagaaca	taacaattta	600
caaattcacc	acttgatttt	gatgtggttt	taattcgttc	tggactcgca	tatcttttgg	660
tttacttcgt	cccagtcacg	ttagtaataa	aacgaaatcc	agcatgcttg	tactttgtat	720
ggaaacatca	ttagtcttcc	gattcccgat	tattaagaaa	gggttttcga	tt	

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Pro	Phe	Phe	Glu	Ser	Leu	His	Phe	Ser	Cys	Ile	Leu	Gln	Thr	His	Pro
1			5						10					15	
Gln	Gln	Gly	Met	Ala	Thr	Ala	Ala	Ala	Pro	Ala	Val	Ile	Ser	Trp	Thr
			20					25				30			
Arg	Ser	Gly	Ile	Val	Ser	Lys	Ser	Gly	Gln	Thr	Gln	Lys	Lys	Ser	Glu
		35				40					45				
Met	Lys	Val	Ser	Tyr	Ile	Thr	Gly	Leu	Asn	Ser	Tyr	Gly	Gly	Leu	Lys
	50					55					60				
Ala	Gln	Asn	Asn	Lys	Val	Val	Ser	Met	Gly	Ser	Pro	Leu	Cys	Thr	Glu
65				70					75					80	
Gln	Cys	Phe	Ala	Asn	Val	Val	Met	Ser	Leu	Lys	Gly	Arg	Arg	Gly	Asn
			85					90						95	
Gly	Gly	Ala	Leu	Ser	Thr	Thr	Cys	Asn	Ala	Val	Gly	Glu	Ile	Phe	Lys
		100					105						110		
Ile	Ala	Ala	Lys	His	Cys	Ser	Val	Lys	Ser	Gly	Ile	Ser	Ile		
		115				120						125			

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498121  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:  
Met Ala Thr Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly  
1 5 10 15  
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val  
20 25 30  
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn  
35 40 45  
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe  
50 55 60  
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn Gly Gly Ala  
65 70 75 80  
Leu Ser Thr Thr Cys Asn Ala Val Gly Glu Ile Phe Lys Ile Ala Ala  
85 90 95  
Lys His Cys Ser Val Lys Ser Gly Ile Ser Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..78  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys  
1 5 10 15  
Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu  
20 25 30  
Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn  
35 40 45  
Gly Gly Ala Leu Ser Thr Thr Cys Asn Ala Val Gly Glu Ile Phe Lys  
50 55 60  
Ile Ala Ala Lys His Cys Ser Val Lys Ser Gly Ile Ser Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..671  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

cacctakaac atcctaatacg aaaaccggcg ccaccattaa aatctctcga tctctatctg	60
cgaaatttca cggtaggtat ttgaaatggc gacagttcca ggacaattga tctgggagat	120
cgtgaagaac aacaactgtt tcttggtgaa gcagttcggg agaggaaact ctaaggttca	180

```
attcagcaag gagactaaca acctcaccaa cgttcactct tacaagcact ctgggtcttg 240
aaacaaaaag actgtgacca tccaggccgc tgacaaggac caagctgttg tgctcgccac 300
caccaagacc aagaagcaga acaagcctaa gctctctgtc aacaagtcta tcctcaagaa 360
ggaattcccc aggatgtcaa aggctgttgc taaccagggtg gtggacaact actacaggcc 420
ggacttgaag aaagctgcac ttgctagact cagcgccatc agcaaaggtc tcaggggttg 480
caagtccggt gccaagcaaa gaaacagaca agcttaagct tcttctttca caatctgttt 540
tttttgaagt aaaagatttt gtytgaacag gttttattta agttgttgct ttgaagtttg 600
aaccataatg ctattctcct ttttcattat ccttattata aaggagttag aagtttatct 660
tgttatgctt g
```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
Met Ala Thr Val Pro Gly Gln Leu Ile Trp Glu Ile Val Lys Asn Asn
1      5      10      15
Asn Cys Phe Leu Val Lys Gln Phe Gly Arg Gly Asn Ser Lys Val Gln
20     25     30
Phe Ser Lys Glu Thr Asn Asn Leu Thr Asn Val His Ser Tyr Lys His
35     40     45
Ser Gly Leu Ala Asn Lys Lys Thr Val Thr Ile Gln Ala Ala Asp Lys
50     55     60
Asp Gln Ala Val Val Leu Ala Thr Thr Lys Thr Lys Lys Gln Asn Lys
65     70     75     80
Pro Lys Leu Ser Val Asn Lys Ser Ile Leu Lys Lys Glu Phe Pro Arg
85     90     95
Met Ser Lys Ala Val Ala Asn Gln Val Val Asp Asn Tyr Tyr Arg Pro
100    105    110
Asp Leu Lys Lys Ala Ala Leu Ala Arg Leu Ser Ala Ile Ser Lys Gly
115    120    125
Leu Arg Val Ala Lys Ser Gly Ala Lys Gln Arg Asn Arg Gln Ala
130    135    140
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1065
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```
taatttcgac tttttagat ctttttctgc tctttctctc tctctctctc tctctctctc 60
tctctctctc ttgtattatt tctatctccc ccgccgtcga aagagaaacg tcgatcgagg 120
aacctttgaa atgtcgactg gattagatat gtctctcgac gacatgatcg ccaagaaccg 180
taagtctcgt ggtggagccg gccccgctcg tggaaccgga tccggatccg gaccgggtcc 240
gactcgccgc aacaacccta atcggaatc aaccgatct gctccatacc aatcagccaa 300
ggcgccggag tccacctggg gtcacgacat gttctccgat agatctgaag atcaccgatc 360
gggacgttcc tccgccgga tcgaaactgg aaccaagctc tacatttcca atttgatta 420
cggtgtcatg aacgaagaca tcaaggaact gtttggtga aggttgaga acttaaagc 480
tacacagttc attttgatag aagtggaaaga tcaaagggaa ctgctgaagt agtgattct 540
cggcgtggcg atgcactcgc agctgtgaag aagtataatg atgttcasct ggatggaaaa 600
```

```
cccatgaaga tagagattgt gggcactaat cttcaaaactg ctgcagcccc gtctggtaga      660
cctgcgaatg gaaactccaa tgggtgctcca tggagaggag gacaagggag aggaggtcaa      720
caacgaggtg gtggacgagg aggcggtggc cgaggtggtg gtggtcgtgg taggcgtcct      780
ggtaagggcc ctgcagagaa gatttctgcg gaagatcttg atgcggatct tgataagtac      840
cattctggag atatggagac aaactaagga acgtgactga tcttctcaaa ccggtagggg      900
ttttaggagg aagagaatcg agaaaatggt tgccagaggc tttaccactt agcgcccttt      960
tggctgtggt gttcatttgt ttcattagaa tgactttaca gaattgagaa tatgtgttat     1020
ttaaagttgt tgtctatctt aataccctca agtgaaaggc agagg
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
Asn Phe Asp Phe Cys Arg Ser Phe Ser Ala Leu Ser Leu Ser Leu Ser
1      5      10      15
Leu Ser Leu Ser Leu Ser Leu Leu Tyr Tyr Phe Tyr Leu Pro Arg Arg
20      25      30
Arg Lys Arg Asn Val Asp Arg Arg Thr Phe Glu Met Ser Thr Gly Leu
35      40      45
Asp Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly
50      55      60
Gly Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro
65      70      75      80
Thr Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr
85      90      95
Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser
100      105      110
Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu
115      120      125
Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Tyr Gly Val Met Asn
130      135      140
Glu Asp Ile Lys Glu Leu Phe Gly
145      150
```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```
Met Ser Thr Gly Leu Asp Met Ser Leu Asp Met Ile Ala Lys Asn
1      5      10      15
Arg Lys Ser Arg Gly Gly Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly
20      25      30
Ser Gly Pro Gly Pro Thr Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr
35      40      45
Arg Ser Ala Pro Tyr Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly
50      55      60
His Asp Met Phe Ser Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser
```

(2) INFORMATION FOR SEQ ID NO:206:

(A) LENGTH: 103 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME

(B) LOCATION: 1..103

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ser Leu Asp Asp Met Ile Ala Lys Asn Arg L

(2) INFORMATION FOR SEQ ID NO:207:

(A) LENGTH: 1247 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1247

(D) OTHER INFORMATION: / Ceres Seq. ID 1498133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ctcttgcttc	tcttcactca	caatctcaca	gcaaagcctc	tcgttgctag	aggaatcaaa	60
caatggtggt	tgtgaagtcc	accaagtcga	atgcttactt	caagaggtac	caagtgaagt	120
tcaggagaag	aagagatgga	aagactgact	acagggcaag	gatccgtctt	atcaaccaag	180
acaagaacaa	gtacaatata	cctaagtatc	gttttggtgt	ccggtttacc	aacaaagaca	240
tagtggcaca	gattgtatct	gcaagcattg	ctggtgacat	tgtaaagct	tctgcttacg	300
cacatgaact	gcctcagtat	ggtctcactg	ttggtcttca	aaactatgct	gcagcttact	360
gtactggcct	tcttttggtc	cgccgtgttt	taaagatggt	ggaaatggat	gacgagtatg	420
agggaaacgt	tgaggccact	ggagaggact	tttccgttga	gccaactgat	tcagggagac	480
ctttccgtgc	tcttcttgat	gttggaactta	tcaggaccac	aacaggaaac	cgtgtgttcg	540
gtgctcttaa	gggtgctttg	gatggtggtc	ttgatatccc	tcacagtgac	aagagattttg	600
ctgggttcca	caaggagaac	aagcaacttg	atgctgaaat	ccacaggaac	tacatctatg	660
gtggccatgt	ctcaaaactac	atgaagctgt	tgggagaaga	tgagccagag	aagttacaaa	720
ctcacttcag	tgcttacatc	aagaaaggag	ttgaagctga	gagcattgag	gagttgtaca	780
agaaggttca	cgcagctatt	cgtgctgrcc	ccaaccsaag	gaaaaccgtg	aaacctgctc	840
ccaagcaaca	caagaggtac	aacttgaaga	aacttactta	cgaggagagg	aagaacaagt	900
tgatcgagag	agtcaggcat	tgaatggagc	aggtggtgat	gatgatgatg	aggacgatga	960
asagtaaatc	agtcaaagcct	tctttatctc	atgctctctg	tagtttttta	tcttttgagc	1020
ttaatgcctc	aaattttctg	ttttcagact	aaaacactca	gcttttggtg	tcacatttta	1080



attgtgttcg aggattttga tattgaggat acatttttctt tgaagtatca ttatcttatt 1140  
attacctcca tcataatttt caagaattttg tatgacaata gtttgatgac ttgattttat 1200  
ctgtagtttg ctattgttaa atgtaagaac tgtttagactt catctat

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1498134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met	Val	Phe	Val	Lys	Ser	Thr	Lys	Ser	Asn	Ala	Tyr	Phe	Lys	Arg	Tyr
1			5						10					15	
Gln	Val	Lys	Phe	Arg	Arg	Arg	Arg	Asp	Gly	Lys	Thr	Asp	Tyr	Arg	Ala
			20					25					30		
Arg	Ile	Arg	Leu	Ile	Asn	Gln	Asp	Lys	Asn	Lys	Tyr	Asn	Thr	Pro	Lys
			35				40					45			
Tyr	Arg	Phe	Val	Val	Arg	Phe	Thr	Asn	Lys	Asp	Ile	Val	Ala	Gln	Ile
			50				55				60				
Val	Ser	Ala	Ser	Ile	Ala	Gly	Asp	Ile	Val	Lys	Ala	Ser	Ala	Tyr	Ala
65					70					75				80	
His	Glu	Leu	Pro	Gln	Tyr	Gly	Leu	Thr	Val	Gly	Leu	Thr	Asn	Tyr	Ala
				85					90					95	
Ala	Ala	Tyr	Cys	Thr	Gly	Leu	Leu	Leu	Ala	Arg	Arg	Val	Leu	Lys	Met
			100					105					110		
Leu	Glu	Met	Asp	Asp	Glu	Tyr	Glu	Gly	Asn	Val	Glu	Ala	Thr	Gly	Glu
			115				120					125			
Asp	Phe	Ser	Val	Glu	Pro	Thr	Asp	Ser	Arg	Arg	Pro	Phe	Arg	Ala	Leu
			130				135				140				
Leu	Asp	Val	Gly	Leu	Ile	Arg	Thr	Thr	Thr	Gly	Asn	Arg	Val	Phe	Gly
145					150					155				160	
Ala	Leu	Lys	Gly	Ala	Leu	Asp	Gly	Gly	Leu	Asp	Ile	Pro	His	Ser	Asp
			165					170						175	
Lys	Arg	Phe	Ala	Gly	Phe	His	Lys	Glu	Asn	Lys	Gln	Leu	Asp	Ala	Glu
			180					185					190		
Ile	His	Arg	Asn	Tyr	Ile	Tyr	Gly	Gly	His	Val	Ser	Asn	Tyr	Met	Lys
			195				200					205			
Leu	Leu	Gly	Glu	Asp	Glu	Pro	Glu	Lys	Leu	Gln	Thr	His	Phe	Ser	Ala
			210				215				220				
Tyr	Ile	Lys	Lys	Gly	Val	Glu	Ala	Glu	Ser	Ile	Glu	Glu	Leu	Tyr	Lys
225					230					235				240	
Lys	Val	His	Ala	Ala	Ile	Arg	Ala	Xaa	Pro	Asn	Xaa	Arg	Lys	Thr	Val
			245						250					255	
Lys	Pro	Ala	Pro	Lys	Gln	His	Lys	Arg	Tyr	Asn	Leu	Lys	Lys	Leu	Thr
			260					265					270		
Tyr	Glu	Glu	Arg	Lys	Asn	Lys	Leu	Ile	Glu	Arg	Val	Arg	His		
			275				280					285			

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Met	Leu	Glu	Met	Asp	Asp	Glu	Tyr	Glu	Gly	Asn	Val	Glu	Ala	Thr	Gly	
1				5					10					15		
Glu	Asp	Phe	Ser	Val	Glu	Pro	Thr	Asp	Ser	Arg	Arg	Pro	Phe	Arg	Ala	
			20					25					30			
Leu	Leu	Asp	Val	Gly	Leu	Ile	Arg	Thr	Thr	Thr	Gly	Asn	Arg	Val	Phe	
		35					40					45				
Gly	Ala	Leu	Lys	Gly	Ala	Leu	Asp	Gly	Gly	Leu	Asp	Ile	Pro	His	Ser	
	50					55					60					
Asp	Lys	Arg	Phe	Ala	Gly	Phe	His	Lys	Glu	Asn	Lys	Gln	Leu	Asp	Ala	
65					70					75					80	
Glu	Ile	His	Arg	Asn	Tyr	Ile	Tyr	Gly	Gly	His	Val	Ser	Asn	Tyr	Met	
				85					90					95		
Lys	Leu	Leu	Gly	Glu	Asp	Glu	Pro	Glu	Lys	Leu	Gln	Thr	His	Phe	Ser	
			100					105					110			
Ala	Tyr	Ile	Lys	Lys	Gly	Val	Glu	Ala	Glu	Ser	Ile	Glu	Glu	Leu	Tyr	
	115						120						125			
Lys	Lys	Val	His	Ala	Ala	Ile	Arg	Ala	Xaa	Pro	Asn	Xaa	Arg	Lys	Thr	
	130					135					140					
Val	Lys	Pro	Ala	Pro	Lys	Gln	His	Lys	Arg	Tyr	Asn	Leu	Lys	Lys	Leu	
145					150					155					160	
Thr	Tyr	Glu	Glu	Arg	Lys	Asn	Lys	Leu	Ile	Glu	Arg	Val	Arg	His		
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1498136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met	Asp	Asp	Glu	Tyr	Glu	Gly	Asn	Val	Glu	Ala	Thr	Gly	Glu	Asp	Phe	
1				5					10					15		
Ser	Val	Glu	Pro	Thr	Asp	Ser	Arg	Arg	Pro	Phe	Arg	Ala	Leu	Leu	Asp	
			20					25					30			
Val	Gly	Leu	Ile	Arg	Thr	Thr	Thr	Gly	Asn	Arg	Val	Phe	Gly	Ala	Leu	
		35					40					45				
Lys	Gly	Ala	Leu	Asp	Gly	Gly	Leu	Asp	Ile	Pro	His	Ser	Asp	Lys	Arg	
	50					55					60					
Phe	Ala	Gly	Phe	His	Lys	Glu	Asn	Lys	Gln	Leu	Asp	Ala	Glu	Ile	His	
65					70					75					80	
Arg	Asn	Tyr	Ile	Tyr	Gly	Gly	His	Val	Ser	Asn	Tyr	Met	Lys	Leu	Leu	
			85					90					95			
Gly	Glu	Asp	Glu	Pro	Glu	Lys	Leu	Gln	Thr	His	Phe	Ser	Ala	Tyr	Ile	
			100					105					110			
Lys	Lys	Gly	Val	Glu	Ala	Glu	Ser	Ile	Glu	Glu	Leu	Tyr	Lys	Lys	Val	
	115						120						125			
His	Ala	Ala	Ile	Arg	Ala	Xaa	Pro	Asn	Xaa	Arg	Lys	Thr	Val	Lys	Pro	
	130					135					140					
Ala	Pro	Lys	Gln	His	Lys	Arg	Tyr	Asn	Leu	Lys	Lys	Leu	Thr	Tyr	Glu	
145					150					155					160	
Glu	Arg	Lys	Asn	Lys	Leu	Ile	Glu	Arg	Val	Arg	His					
				165					170							

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1186 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

aaaaaattcg	ctattcaatt	cctttagtaa	gcttcacttt	tcacacttct	ctcactttct	60
ggtcagaaac	tttgtggatc	tagaagaaca	cacaaatcac	aagagtgaac	aaagatgaac	120
gacttgatga	cgaaatcggt	tatgagttac	gttgacttga	aaaaagcagc	gatgaaggat	180
atggaagcag	gacctgactt	tgatcttgag	atggcttcga	cgaaagcaga	caagatggat	240
gagaatctgt	catctttctt	acaagaagca	gagtatgtga	aagcagagat	gggttttatt	300
agtagacact	ggctcggatt	gaavcragta	ccatgaagag	agtaaagggtg	ttcacaaggc	360
agagtctgtg	aagtctcttc	gtaacaagat	ctctaakgag	atttgtgtctg	gtttgaggaa	420
ggcgaaatcg	attaagtcga	agctggaaga	gatggataaa	gcaaacaagg	agattaaaag	480
gctctctggg	actccggttt	acaggagcag	aaccgctgtg	actaacgggc	tgaggaagaa	540
acttaaggga	gtgmtgatgg	agtttcaggg	gctgaggcaa	aagatgatga	gtgagtacaa	600
ggagactggt	gagagaaggt	acttcactgt	cactggagaa	catgctaata	atgagatgat	660
tgagaagatc	attactgata	acgctggagg	tgaagagttt	ctcacgcgag	caattcagga	720
acatggtaaa	ggaaaggtct	tggaaactgt	ggttgagatt	caagataggt	acgatgcagc	780
aaaggagatt	gagaagagtc	tggtggagct	tcaccaagtg	tttcttgata	tggtctgtgat	840
ggttgaatcg	caaggtgaac	agatggacga	gatcgagcat	catgtgatta	atgagagcca	900
ttacgtggct	gatggagcta	atgagctgaa	gactgcaaag	agtcatcaga	gaaacagcag	960
aaaatggatg	tgcattggta	tcatttgtct	gcttttgatc	attctcattg	ttgttatccc	1020
catcattacc	agtttcagct	cttcttgaga	tactggctat	gttcactcct	tttgttttgt	1080
ttcgctcttc	tttgtaccaa	tggatgtctt	aatccttttg	tgttcttaaa	ggatgtctta	1140
atcctttcgt	gtcttgtatc	caatttcaat	gaaatgggtga	atgttt		

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met	Asp	Lys	Ala	Asn	Lys	Glu	Ile	Lys	Arg	Leu	Ser	Gly	Thr	Pro	Val
1			5					10						15	
Tyr	Arg	Ser	Arg	Thr	Ala	Val	Thr	Asn	Gly	Leu	Arg	Lys	Lys	Leu	Lys
			20					25					30		
Xaa	Val	Xaa	Met	Glu	Phe	Gln	Gly	Leu	Arg	Gln	Lys	Met	Met	Ser	Glu
			35				40					45			
Tyr	Lys	Glu	Thr	Val	Glu	Arg	Arg	Tyr	Phe	Thr	Val	Thr	Gly	Glu	His
			50				55				60				
Ala	Asn	Asp	Glu	Met	Ile	Glu	Lys	Ile	Ile	Thr	Asp	Asn	Ala	Gly	Gly
65					70				75					80	
Glu	Glu	Phe	Leu	Thr	Arg	Ala	Ile	Gln	Glu	His	Gly	Lys	Gly	Lys	Val
			85					90						95	
Leu	Glu	Thr	Val	Val	Glu	Ile	Gln	Asp	Arg	Tyr	Asp	Ala	Ala	Lys	Glu
			100					105					110		
Ile	Glu	Lys	Ser	Leu	Leu	Glu	Leu	His	Gln	Val	Phe	Leu	Asp	Met	Ala
			115					120					125		
Val	Met	Val	Glu	Ser	Gln	Gly	Glu	Gln	Met	Asp	Glu	Ile	Glu	His	His
			130				135				140				
Val	Ile	Asn	Ala	Ser	His	Tyr	Val	Ala	Asp	Gly	Ala	Asn	Glu	Leu	Lys
145					150					155					160

Thr Ala Lys Ser His Gln Arg Asn Ser Arg Lys Trp Met Cys Ile Gly  
                  165                  170                  175  
Ile Ile Val Leu Leu Leu Ile Ile Leu Ile Val Val Ile Pro Ile Ile  
                  180                  185                  190  
Thr Ser Phe Ser Ser Ser  
                  195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met Glu Phe Gln Gly Leu Arg Gln Lys Met Met Ser Glu Tyr Lys Glu  
1                  5                  10                  15  
Thr Val Glu Arg Arg Tyr Phe Thr Val Thr Gly Glu His Ala Asn Asp  
                  20                  25                  30  
Glu Met Ile Glu Lys Ile Ile Thr Asp Asn Ala Gly Gly Glu Glu Phe  
                  35                  40                  45  
Leu Thr Arg Ala Ile Gln Glu His Gly Lys Gly Lys Val Leu Glu Thr  
50                  55                  60  
Val Val Glu Ile Gln Asp Arg Tyr Asp Ala Ala Lys Glu Ile Glu Lys  
65                  70                  75                  80  
Ser Leu Leu Glu Leu His Gln Val Phe Leu Asp Met Ala Val Met Val  
                  85                  90                  95  
Glu Ser Gln Gly Glu Gln Met Asp Glu Ile Glu His His Val Ile Asn  
                  100                  105                  110  
Ala Ser His Tyr Val Ala Asp Gly Ala Asn Glu Leu Lys Thr Ala Lys  
                  115                  120                  125  
Ser His Gln Arg Asn Ser Arg Lys Trp Met Cys Ile Gly Ile Ile Val  
130                  135                  140  
Leu Leu Leu Ile Ile Leu Ile Val Val Ile Pro Ile Ile Thr Ser Phe  
145                  150                  155                  160  
Ser Ser Ser

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Met Ser Glu Tyr Lys Glu Thr Val Glu Arg Arg Tyr Phe Thr Val  
1                  5                  10                  15  
Thr Gly Glu His Ala Asn Asp Glu Met Ile Glu Lys Ile Ile Thr Asp  
                  20                  25                  30  
Asn Ala Gly Gly Glu Glu Phe Leu Thr Arg Ala Ile Gln Glu His Gly  
                  35                  40                  45  
Lys Gly Lys Val Leu Glu Thr Val Val Glu Ile Gln Asp Arg Tyr Asp  
50                  55                  60  
Ala Ala Lys Glu Ile Glu Lys Ser Leu Leu Glu Leu His Gln Val Phe

```
65          70          75          80
Leu Asp Met Ala Val Met Val Glu Ser Gln Gly Glu Gln Met Asp Glu
      85          90          95
Ile Glu His His Val Ile Asn Ala Ser His Tyr Val Ala Asp Gly Ala
      100         105         110
Asn Glu Leu Lys Thr Ala Lys Ser His Gln Arg Asn Ser Arg Lys Trp
      115         120         125
Met Cys Ile Gly Ile Ile Val Leu Leu Ile Ile Leu Ile Val Val
      130         135         140
Ile Pro Ile Ile Thr Ser Phe Ser Ser Ser
145          150
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..768
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
accaaaatct cttctctctc ttccattgtc ttcctctaata ggaaccaacc gagaaatcta      60
tgttactaga aactactagt accacgaaga tggagaccaa atacgaagat atgttaccag      120
ttatggcgga gaagatggat gttgaagagt ttgtatcaga gttatgcaaa ggtttcagtt      180
tgcttgcgga tccagagaga catctcatca cagctgagtc tctaagacga aactcagggg      240
tacttggaat tgaaggtagt agcaaggaag atgctcaagg aatgggttaga gaaggagacs      300
tcgatggaga tggkgctctt aaccaaaccg aattctgcgt tctcatgggt cggttaagcc      360
ctgagatgat ggaagacgcc graacttggk tggaatgggg ttgggtcatg ggatcctttc      420
aagaaaacct atattcatca gagatcttga gcttaacaaa ggacgaagct aaatcgattg      480
gttcacaaaa cagaggaagt ataatgcacg ttttcttcaa actccgatct cagatccgta      540
atttcatggg accttcttca gaagattctc ttcctctttc ttgcaaatac aagcgtcaac      600
gataaaatga ttcatataag gttgagattt tgtgatttgt ctgttctttt tttacttttg      660
tgcaatggag tataatgaat gtataattcg tctttttttt ttaaacttga tggtgtattt      720
tgctataatt aatttgccta gattattatt aatcaattta tttatttt
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```
Gln Asn Leu Phe Ser Leu Phe His Cys Leu Pro Leu Met Glu Pro Thr
1          5          10          15
Glu Lys Ser Met Leu Leu Glu Thr Thr Ser Thr Thr Lys Met Glu Thr
      20          25          30
Lys Tyr Glu Asp Met Leu Pro Val Met Ala Glu Lys Met Asp Val Glu
      35          40          45
Glu Phe Val Ser Glu Leu Cys Lys Gly Phe Ser Leu Leu Ala Asp Pro
      50          55          60
Glu Arg His Leu Ile Thr Ala Glu Ser Leu Arg Arg Asn Ser Gly Ile
      65          70          75          80
Leu Gly Ile Glu Gly Met Ser Lys Glu Asp Ala Gln Gly Met Val Arg
      85          90          95
Glu Gly Asp Xaa Asp Gly Asp Xaa Ala Leu Asn Gln Thr Glu Phe Cys
```

	100		105		110										
Val	Leu	Met	Val	Arg	Leu	Ser	Pro	Glu	Met	Met	Glu	Asp	Ala	Xaa	Thr
	115						120					125			
Trp	Xaa	Glu	Trp	Gly	Trp	Val	Met	Gly	Ser	Phe	Gln	Glu	Asn	Leu	Tyr
	130						135					140			
Ser	Ser	Glu	Ile	Leu	Ser	Leu	Thr	Lys	Asp	Glu	Ala	Lys	Ser	Ile	Gly
145					150					155					160
Ser	Gln	Asn	Arg	Gly	Ser	Ile	Met	His	Val	Phe	Phe	Lys	Leu	Arg	Ser
			165						170					175	
Gln	Ile	Arg	Asn	Phe	Met	Gly	Pro	Ser	Ser	Glu	Asp	Ser	Leu	Pro	Leu
			180					185					190		
Ser	Cys	Lys	Tyr	Lys	Arg	Gln	Arg								
	195						200								

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met	Glu	Pro	Thr	Glu	Lys	Ser	Met	Leu	Leu	Glu	Thr	Thr	Ser	Thr	Thr
1			5					10						15	
Lys	Met	Glu	Thr	Lys	Tyr	Glu	Asp	Met	Leu	Pro	Val	Met	Ala	Glu	Lys
			20					25					30		
Met	Asp	Val	Glu	Glu	Phe	Val	Ser	Glu	Leu	Cys	Lys	Gly	Phe	Ser	Leu
		35					40					45			
Leu	Ala	Asp	Pro	Glu	Arg	His	Leu	Ile	Thr	Ala	Glu	Ser	Leu	Arg	Arg
		50				55					60				
Asn	Ser	Gly	Ile	Leu	Gly	Ile	Glu	Gly	Met	Ser	Lys	Glu	Asp	Ala	Gln
65				70						75					80
Gly	Met	Val	Arg	Glu	Gly	Asp	Xaa	Asp	Gly	Asp	Xaa	Ala	Leu	Asn	Gln
			85					90						95	
Thr	Glu	Phe	Cys	Val	Leu	Met	Val	Arg	Leu	Ser	Pro	Glu	Met	Met	Glu
			100					105					110		
Asp	Ala	Xaa	Thr	Trp	Xaa	Glu	Trp	Gly	Trp	Val	Met	Gly	Ser	Phe	Gln
		115					120					125			
Glu	Asn	Leu	Tyr	Ser	Ser	Glu	Ile	Leu	Ser	Leu	Thr	Lys	Asp	Glu	Ala
		130				135					140				
Lys	Ser	Ile	Gly	Ser	Gln	Asn	Arg	Gly	Ser	Ile	Met	His	Val	Phe	Phe
145					150					155					160
Lys	Leu	Arg	Ser	Gln	Ile	Arg	Asn	Phe	Met	Gly	Pro	Ser	Ser	Glu	Asp
			165					170						175	
Ser	Leu	Pro	Leu	Ser	Cys	Lys	Tyr	Lys	Arg	Gln	Arg				
			180					185							

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1498144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Leu Leu Glu Thr Thr Ser Thr Thr Lys Met Glu Thr Lys Tyr Glu  
1 5 10 15  
Asp Met Leu Pro Val Met Ala Glu Lys Met Asp Val Glu Glu Phe Val  
20 25 30  
Ser Glu Leu Cys Lys Gly Phe Ser Leu Leu Ala Asp Pro Glu Arg His  
35 40 45  
Leu Ile Thr Ala Glu Ser Leu Arg Arg Asn Ser Gly Ile Leu Gly Ile  
50 55 60  
Glu Gly Met Ser Lys Glu Asp Ala Gln Gly Met Val Arg Glu Gly Asp  
65 70 75 80  
Xaa Asp Gly Asp Xaa Ala Leu Asn Gln Thr Glu Phe Cys Val Leu Met  
85 90 95  
Val Arg Leu Ser Pro Glu Met Met Glu Asp Ala Xaa Thr Trp Xaa Glu  
100 105 110  
Trp Gly Trp Val Met Gly Ser Phe Gln Glu Asn Leu Tyr Ser Ser Glu  
115 120 125  
Ile Leu Ser Leu Thr Lys Asp Glu Ala Lys Ser Ile Gly Ser Gln Asn  
130 135 140  
Arg Gly Ser Ile Met His Val Phe Phe Lys Leu Arg Ser Gln Ile Arg  
145 150 155 160  
Asn Phe Met Gly Pro Ser Ser Glu Asp Ser Leu Pro Leu Ser Cys Lys  
165 170 175  
Tyr Lys Arg Gln Arg  
180

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

atttcgagat cctctcggtt tggttggttt tctgtaacga tcccatctat tgtttctcgc	60
tggtctcaga ttcgactaac ttggatatct ccgatactga agaagcctcc ttcttctttt	120
tccgctcttc ccgatgccga tcgataagat cttcaaagat gatgctagtg aagagaaggg	180
agaacgtgcg aggatggcat catttggttg tgcaatggct atcagtgatc tggttaagtc	240
tacttttaggg ccaaagggca tggataaaat cttacaatct actggtagag gtcattgcgt	300
caactgttact aacgatgggt ctactattct caagtcactt cacatagaca accctgcagc	360
taaagttctt gttgacatct cgaaagttca agatgatgag gttggtgatg gaactacctc	420
tgttggtgtc ttggccggcg agcttctgag ggaagcagaa aagcttggtg cttctaagat	480
tcacctatg accatcatag caggttacag aatggcttcg gaatgtgctc gtaatgcttt	540
actgaaaaga gtcattgata acaaggacaa tgcagagaag tttaggtcag acttggtgaa	600
gattgcatg actactttat gttccaaaat tctctcacag gacaaggaac attttgcaga	660
aatggccgtg gatgctgttt tcaggctaaa gggaagcaca aacttggaag ctattcagat	720
catcaaaaaa cctggagggg ctctgaagga ttcgtttttg gatgaagggt ttattcttga	780
caagaaaata ggaattgggc agcctaagcg catagagaat gcaaatatct tagtagctaa	840
tactgctatg gataccgata aagtgaagat ttacggtgca cgtgtccgtg tggattccat	900
gaccaaggtt gctgagattg aaggtcaaca gtttgaccct aacgcctcta agcttgctt	960
cgagcgtgtc tttaaaggca tgttcggcat gaccactgac cctgccgctg tccaagagct	1020
cgaaggtaag ctccagaaag tcttggtatg ctacgaggct aggtctcgcca aatctgagtt	1080
cttggtggtt gattccttca ctcttgctga tcttcaccac ctcccagcca tccattactt	1140
gttggttact gactccaagg tgctctttga ctctcgccct aagggttagcg agtgaattaa	1200
gaagatctct gccaggcctg cttgggctaa gggtattgac ctccagaagc agtagtgacc	1260
ctctctcttt cttoacttct tttcttttcc ttttgcccaa ataaacgagt ccagtgattt	1320
tcttttcttg gottatgtac ttgtgttttc agtattattt atgtcatcat catcctcctc	1380
ttttgtgtta ttgttggtt cattcacatt tgtgcaatta aaaaccagag tttaaacgcc	1440

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met	Pro	Ile	Asp	Lys	Ile	Phe	Lys	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Gly
1				5				10						15	
Glu	Arg	Ala	Arg	Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser	Asp
			20					25					30		
Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu	Gln
		35					40					45			
Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala	Thr
	50					55					60				
Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu	Val
65					70					75				80	
Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser
			85					90					95		
Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Leu	Val
			100					105					110		
Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met	Ala
		115					120					125			
Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn	Lys
	130					135					140				
Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met	Thr
145					150					155				160	
Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala	Glu
			165						170					175	
Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu	Glu
		180						185					190		
Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser	Phe
		195					200					205			
Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln	Pro
	210					215					220				
Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met	Asp
225				230						235				240	
Thr	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Ala	Arg	Val	Arg	Val	Asp	Ser	Met
			245						250					255	
Thr	Lys	Val	Ala	Glu	Ile	Glu	Gly	Gln	Gln	Phe	Asp	Pro	Asn	Ala	Ser
		260					265						270		
Lys	Leu	Ala	Phe	Glu	Arg	Val	Phe	Lys	Gly	Met	Phe	Gly	Met	Thr	Thr
		275					280					285			
Asp	Pro	Ala	Ala	Val	Gln	Glu	Leu	Glu	Gly	Lys	Leu	Gln	Lys	Val	Leu
	290					295					300				
Asp	Val	Tyr	Glu	Ala	Arg	Leu	Ala	Lys	Ser	Glu	Phe	Leu	Ala	Gly	Asp
305				310						315				320	
Ser	Phe	Thr	Leu	Ala	Asp	Leu	His	His	Leu	Pro	Ala	Ile	His	Tyr	Leu
			325						330					335	
Leu	Gly	Thr	Asp	Ser	Lys	Val	Leu	Phe	Asp	Ser	Arg	Pro	Lys	Val	Ser
			340					345					350		
Glu															

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..333
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser	Asp	Leu	Val	Lys	Ser
1				5					10					15	
Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu	Gln	Ser	Thr	Gly	Arg
			20					25					30		
Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala	Thr	Ile	Leu	Lys	Ser
		35					40					45			
Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu	Val	Asp	Ile	Ser	Lys
	50					55				60					
Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser	Val	Val	Val	Leu
65				70					75						80
Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Leu	Val	Ala	Ser	Lys	Ile
			85						90					95	
His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met	Ala	Ser	Glu	Cys	Ala
		100						105					110		
Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn	Lys	Asp	Asn	Ala	Glu
	115						120					125			
Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met	Thr	Thr	Leu	Cys	Ser
	130				135						140				
Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala	Glu	Met	Ala	Val	Asp
145				150					155					160	
Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu	Glu	Ala	Ile	Gln	Ile
			165					170						175	
Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser	Phe	Leu	Asp	Glu	Gly
		180						185					190		
Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln	Pro	Lys	Arg	Ile	Glu
	195					200					205				
Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met	Asp	Thr	Asp	Lys	Val
	210					215					220				
Lys	Ile	Tyr	Gly	Ala	Arg	Val	Arg	Val	Asp	Ser	Met	Thr	Lys	Val	Ala
225				230					235					240	
Glu	Ile	Glu	Gly	Gln	Gln	Phe	Asp	Pro	Asn	Ala	Ser	Lys	Leu	Ala	Phe
			245						250					255	
Glu	Arg	Val	Phe	Lys	Gly	Met	Phe	Gly	Met	Thr	Thr	Asp	Pro	Ala	Ala
		260				265						270			
Val	Gln	Glu	Leu	Glu	Gly	Lys	Leu	Gln	Lys	Val	Leu	Asp	Val	Tyr	Glu
	275					280						285			
Ala	Arg	Leu	Ala	Lys	Ser	Glu	Phe	Leu	Ala	Gly	Asp	Ser	Phe	Thr	Leu
	290					295					300				
Ala	Asp	Leu	His	His	Leu	Pro	Ala	Ile	His	Tyr	Leu	Leu	Gly	Thr	Asp
305				310					315					320	
Ser	Lys	Val	Leu	Phe	Asp	Ser	Arg	Pro	Lys	Val	Ser	Glu			
			325					330							

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 326 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1498148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```
Met Ala Ile Ser Asp Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met
1      5      10      15
Asp Lys Ile Leu Gln Ser Thr Gly Arg Gly His Ala Val Thr Val Thr
20     25     30
Asn Asp Gly Ala Thr Ile Leu Lys Ser Leu His Ile Asp Asn Pro Ala
35     40     45
Ala Lys Val Leu Val Asp Ile Ser Lys Val Gln Asp Asp Glu Val Gly
50     55     60
Asp Gly Thr Thr Ser Val Val Val Leu Ala Gly Glu Leu Leu Arg Glu
65     70     75     80
Ala Glu Lys Leu Val Ala Ser Lys Ile His Pro Met Thr Ile Ile Ala
85     90     95
Gly Tyr Arg Met Ala Ser Glu Cys Ala Arg Asn Ala Leu Leu Lys Arg
100    105    110
Val Ile Asp Asn Lys Asp Asn Ala Glu Lys Phe Arg Ser Asp Leu Leu
115    120    125
Lys Ile Ala Met Thr Thr Leu Cys Ser Lys Ile Leu Ser Gln Asp Lys
130    135    140
Glu His Phe Ala Glu Met Ala Val Asp Ala Val Phe Arg Leu Lys Gly
145    150    155    160
Ser Thr Asn Leu Glu Ala Ile Gln Ile Ile Lys Lys Pro Gly Gly Ser
165    170    175
Leu Lys Asp Ser Phe Leu Asp Glu Gly Phe Ile Leu Asp Lys Lys Ile
180    185    190
Gly Ile Gly Gln Pro Lys Arg Ile Glu Asn Ala Asn Ile Leu Val Ala
195    200    205
Asn Thr Ala Met Asp Thr Asp Lys Val Lys Ile Tyr Gly Ala Arg Val
210    215    220
Arg Val Asp Ser Met Thr Lys Val Ala Glu Ile Glu Gly Gln Gln Phe
225    230    235    240
Asp Pro Asn Ala Ser Lys Leu Ala Phe Glu Arg Val Phe Lys Gly Met
245    250    255
Phe Gly Met Thr Thr Asp Pro Ala Ala Val Gln Glu Leu Glu Gly Lys
260    265    270
Leu Gln Lys Val Leu Asp Val Tyr Glu Ala Arg Leu Ala Lys Ser Glu
275    280    285
Phe Leu Ala Gly Asp Ser Phe Thr Leu Ala Asp Leu His His Leu Pro
290    295    300
Ala Ile His Tyr Leu Leu Gly Thr Asp Ser Lys Val Leu Phe Asp Ser
305    310    315    320
Arg Pro Lys Val Ser Glu
325
```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..964

(D) OTHER INFORMATION: / Ceres Seq. ID 1498149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```
aatccattcc tttccaatcc acgtccaaaa aacaaaacca aaaaaaaaaa aaaaaaaaaag      60
acaaaaaaaa atgaacactc caataaaact cgcctttctc attctctgca ttgccctaac      120
cgcaaccgca tttatagtcc cagcaaaacg tgacgccgtt tcaccacacc accaaaaagc      180
cgtcgatgga atctgcagcg ttgtgcaaga caaacgtcta tgcagcatta ccttaagaaa      240
cgtcccaagc gatgatcccg ccgttttggg tcgttactta gccacggcag cagaagcgtc      300
```

```
cggttaaaaag ggtttgaagt tcctctccgg aatcaaacca aaatacaaaag gaaacgcctt 360
cgccacaaca tgcatacccg gctgckwgaa acagctacac aacgccttgg acgactttgc 420
agattttctgg aaagccgcag gaaaaaatct aacgagcatg gctgagaatt mcttcacatg 480
taagaagaag atgacttcca tcttcactta ccattccact tgtctcgatg acatttacga 540
caagacgttg cacaaagtgg tcgaaggagg gattggcctt gggaaaagaa tgagtgggtga 600
gtctgtggat gtgttcgctg gaatgggcaa agtctttaac actttcaaca ttaagaccaa 660
acttaaccag aaagataccg acacgttgct cccaccacct ttgtcctttt actactattg 720
atatttattta tcaatatata ttatatatca taaaacacaa caaaatgtac tgcttcggtc 780
gatggtgatg aataattttc atcgattggg ttttcagata ttttggggat cttgtaacca 840
aaggttcctt ttgatgtatg tttgtattta atatgttatg gattataatc atgtatggac 900
ctcgtgattg gaaaggatat ggaataatgt gattatctaa taataaaaac gtaattaata 960
tcgc
```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```
Ile His Ser Phe Pro Ile His Val Gln Lys Thr Lys Pro Lys Lys Lys
1          5          10          15
Lys Lys Lys Arg Gln Lys Lys Met Asn Thr Pro Ile Lys Leu Ala Phe
20          25          30
Leu Ile Leu Cys Ile Ala Leu Thr Ala Thr Ala Phe Ile Val Pro Ala
35          40          45
Lys Arg Asp Ala Val Ser Pro His His Gln Lys Ala Val Asp Gly Ile
50          55          60
Cys Ser Val Val Gln Asp Lys Arg Leu Cys Ser Ile Thr Leu Arg Asn
65          70          75          80
Val Pro Ser Asp Asp Pro Ala Val Leu Val Arg Tyr Leu Ala Thr Ala
85          90          95
Ala Glu Ala Ser Val Lys Lys Gly Leu Lys Phe Leu Ser Gly Ile Lys
100          105          110
Pro Lys Tyr Lys Gly Asn Ala Phe Ala Thr Thr Cys Ile Thr Gly Cys
115          120          125
Xaa Lys Gln Leu His Asn Ala Leu Asp Asp Phe Ala Asp Phe Trp Lys
130          135          140
Ala Ala Gly Lys Asn Leu Thr Ser Met Ala Glu Asn Xaa Phe Thr Cys
145          150          155          160
Lys Lys Lys Met Thr Ser Ile Phe Thr Tyr His Ser Thr Cys Leu Asp
165          170          175
Asp Ile Tyr Asp Lys Thr Leu His Lys Val Val Glu Gly Gly Ile Gly
180          185          190
Leu Gly Lys Arg Met Ser Gly Glu Ser Val Asp Val Phe Ala Gly Met
195          200          205
Gly Lys Val Phe Asn Thr Phe Asn Ile Lys Thr Lys Leu Asn Gln Lys
210          215          220
Asp Thr Asp Thr Leu Leu Pro Pro Leu Ser Phe Tyr Tyr Tyr
225          230          235
```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1498151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```
Met Asn Thr Pro Ile Lys Leu Ala Phe Leu Ile Leu Cys Ile Ala Leu
1          5          10          15
Thr Ala Thr Ala Phe Ile Val Pro Ala Lys Arg Asp Ala Val Ser Pro
20          25          30
His His Gln Lys Ala Val Asp Gly Ile Cys Ser Val Val Gln Asp Lys
35          40          45
Arg Leu Cys Ser Ile Thr Leu Arg Asn Val Pro Ser Asp Asp Pro Ala
50          55          60
Val Leu Val Arg Tyr Leu Ala Thr Ala Ala Glu Ala Ser Val Lys Lys
65          70          75          80
Gly Leu Lys Phe Leu Ser Gly Ile Lys Pro Lys Tyr Lys Gly Asn Ala
85          90          95
Phe Ala Thr Thr Cys Ile Thr Gly Cys Xaa Lys Gln Leu His Asn Ala
100         105         110
Leu Asp Asp Phe Ala Asp Phe Trp Lys Ala Ala Gly Lys Asn Leu Thr
115         120         125
Ser Met Ala Glu Asn Xaa Phe Thr Cys Lys Lys Lys Met Thr Ser Ile
130         135         140
Phe Thr Tyr His Ser Thr Cys Leu Asp Asp Ile Tyr Asp Lys Thr Leu
145         150         155         160
His Lys Val Val Glu Gly Gly Ile Gly Leu Gly Lys Arg Met Ser Gly
165         170         175
Glu Ser Val Asp Val Phe Ala Gly Met Gly Lys Val Phe Asn Thr Phe
180         185         190
Asn Ile Lys Thr Lys Leu Asn Gln Lys Asp Thr Asp Thr Leu Leu Pro
195         200         205
Pro Pro Leu Ser Phe Tyr Tyr Tyr
210         215
```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1498152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```
aaaaacatta ctcattcaca aaaccatctt aaagcaacta cacaaatctt gaaattttct      60
catattttct atttactata taaactttta atcaaataca gattaactat ggctgaggag      120
tacaagaaca acgttcccga gcacgagaca ccaacggctg caacagagga atcaccagcg      180
acgacaacag aggttacgga tcgtggattg tttgatttct tggggaagaa ggaagaggaa      240
gtgaaacctc aagagacaac gacgctcgag tctgagttcg atcataaggc tcagatctct      300
gaaccggagt tagctgcgga sacgaggaag tgaaggagaa caagattact ctgctcaacr      360
agtcctcagt ggctctcctg aatacwtgca tcccatgaat cttagcacca tcttcaccgt      420
tgrttc
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1498153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Lys	Asn	Ile	Thr	His	Ser	Gln	Asn	His	Leu	Lys	Ala	Thr	Thr	Gln	Ile
1				5					10					15	
Leu	Lys	Phe	Ser	His	Ile	Phe	Tyr	Leu	Leu	Tyr	Lys	Leu	Leu	Ile	Lys
			20					25					30		
Ser	Arg	Leu	Thr	Met	Ala	Glu	Glu	Tyr	Lys	Asn	Asn	Val	Pro	Glu	His
		35					40					45			
Glu	Thr	Pro	Thr	Val	Ala	Thr	Glu	Glu	Ser	Pro	Ala	Thr	Thr	Thr	Glu
	50					55					60				
Val	Thr	Asp	Arg	Gly	Leu	Phe	Asp	Phe	Leu	Gly	Lys	Lys	Glu	Glu	Glu
65				70					75					80	
Val	Lys	Pro	Gln	Glu	Thr	Thr	Thr	Leu	Glu	Ser	Glu	Phe	Asp	His	Lys
			85					90						95	
Ala	Gln	Ile	Ser	Glu	Pro	Glu	Leu	Ala	Xaa	Thr	Arg	Lys			
			100				105								

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1498154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met	Ala	Glu	Glu	Tyr	Lys	Asn	Asn	Val	Pro	Glu	His	Glu	Thr	Pro	Thr
1				5					10					15	
Val	Ala	Thr	Glu	Glu	Ser	Pro	Ala	Thr	Thr	Thr	Glu	Val	Thr	Asp	Arg
			20					25					30		
Gly	Leu	Phe	Asp	Phe	Leu	Gly	Lys	Glu	Glu	Glu	Val	Lys	Pro	Gln	
		35				40					45				
Glu	Thr	Thr	Thr	Leu	Glu	Ser	Glu	Phe	Asp	His	Lys	Ala	Gln	Ile	Ser
	50				55						60				
Glu	Pro	Glu	Leu	Ala	Ala	Xaa	Thr	Arg	Lys						
65				70											

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1011 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1011

(D) OTHER INFORMATION: / Ceres Seq. ID 1498155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

tcttcatata	ttattatatt	cgattttgca	tcctgctctg	aagacgatat	tagcaatcat	60
ggagcgtcta	acatctcttc	ctcgtttgat	gattgtctct	gatcttgatc	atactatggg	120
tgatcatcat	gatactgaga	atctatctct	gctgagattc	aattcgttgt	gggaacacgc	180
ttatcgccat	gactctcttc	ttgtgttttc	tacgggaaga	tcaccgacat	tgtataaaga	240
actgagaaa	gagaaacctt	tggtgacccc	tgatattacc	attatgtctg	taggaactga	300
gattacttat	ggtaaactta	tggttcctga	tcattggttg	gttgaggctc	tgaacaataa	360
atggggattg	ggtattgtca	aacaagaagc	tagcaacttc	cctgagttaa	agcttcaggc	420
agaaactgag	cagaggccac	acaagggttag	cttttatgtt	gaaaagagta	aggctcagga	480
agttactaag	gagctatcac	agagggttcct	gaaacgtggg	ctggatgtca	aaataattta	540

(2) INFORMATION FOR SEQ ID NO:230:

(A) LENGTH: 336 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1498156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Leu	His	Ile	Leu	Leu	Tyr	Ser	Ile	Leu	His	Pro	Ala	Leu	Lys	Thr	Ile
1				5					10					15	
Leu	Ala	Ile	Met	Glu	Arg	Leu	Thr	Ser	Pro	Pro	Arg	Leu	Met	Ile	Val
			20					25					30		
Ser	Asp	Leu	Asp	His	Thr	Met	Val	Asp	His	His	Asp	Pro	Glu	Asn	Leu
		35					40					45			
Ser	Leu	Leu	Arg	Phe	Asn	Ser	Leu	Trp	Glu	His	Ala	Tyr	Arg	His	Asp
	50					55					60				
Ser	Leu	Leu	Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu
65					70					75					80
Leu	Arg	Lys	Glu	Lys	Pro	Leu	Leu	Thr	Pro	Asp	Ile	Thr	Ile	Met	Ser
				85					90					95	
Val	Gly	Thr	Glu	Ile	Thr	Tyr	Gly	Asn	Ser	Met	Val	Pro	Asp	His	Gly
			100					105					110		
Trp	Val	Glu	Ala	Leu	Asn	Asn	Lys	Trp	Asp	Leu	Gly	Ile	Val	Lys	Gln
		115					120					125			
Glu	Ala	Ser	Asn	Phe	Pro	Glu	Leu	Lys	Leu	Gln	Ala	Glu	Thr	Glu	Gln
	130					135					140				
Arg	Pro	His	Lys	Val	Ser	Phe	Tyr	Val	Glu	Lys	Ser	Lys	Ala	Gln	Glu
145					150					155					160
Val	Thr	Lys	Glu	Leu	Ser	Gln	Arg	Phe	Leu	Lys	Arg	Gly	Leu	Asp	Val
				165					170					175	
Lys	Ile	Ile	Tyr	Ser	Gly	Gly	Met	Asp	Leu	Asp	Ile	Leu	Pro	Gln	Gly
			180					185					190		
Ala	Gly	Lys	Gly	Gln	Ala	Leu	Ala	Tyr	Leu	Leu	Lys	Lys	Leu	Lys	Thr
		195					200					205			
Glu	Gly	Lys	Leu	Pro	Val	Asn	Thr	Leu	Ala	Cys	Gly	Asp	Ser	Gly	Asn
	210					215					220				
Asp	Ala	Glu	Leu	Phe	Ser	Ile	Pro	Asp	Val	Tyr	Gly	Val	Met	Val	Ser
225					230					235					240
Asn	Ala	Gln	Glu	Glu	Leu	Leu	Lys	Trp	His	Ala	Glu	Asn	Ala	Lys	Asp
				245					250					255	
Asn	Pro	Lys	Val	Ile	His	Ala	Lys	Glu	Arg	Cys	Ala	Gly	Gly	Ile	Ile
			260					265					270		
Gln	Ala	Ile	Gly	His	Phe	Lys	Leu	Gly	Pro	Asn	Leu	Ser	Pro	Arg	Asp
		275					280					285			
Val	Ser	Asp	Phe	Leu	Glu	Ile	Lys	Ala	Glu	Asn	Val	Asn	Pro	Gly	His
	290					295					300				
Glu	Val	Val	Lys	Phe	Phe	Leu	Phe	Tyr	Glu	Lys	Trp	Arg	Arg	Gly	Glu
305					310					315					320
Val	Glu	Asn	Ser	Glu	Ala	Tyr	Thr	Ala	Ser	Pro	Val	Ser	Ile	Ser	Arg

325

330

335

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met	Glu	Arg	Leu	Thr	Ser	Pro	Pro	Arg	Leu	Met	Ile	Val	Ser	Asp	Leu	
1				5					10					15		
Asp	His	Thr	Met	Val	Asp	His	His	Asp	Pro	Glu	Asn	Leu	Ser	Leu	Leu	
			20					25					30			
Arg	Phe	Asn	Ser	Leu	Trp	Glu	His	Ala	Tyr	Arg	His	Asp	Ser	Leu	Leu	
			35				40					45				
Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu	Leu	Arg	Lys	
	50					55					60					
Glu	Lys	Pro	Leu	Leu	Thr	Pro	Asp	Ile	Thr	Ile	Met	Ser	Val	Gly	Thr	
65					70					75					80	
Glu	Ile	Thr	Tyr	Gly	Asn	Ser	Met	Val	Pro	Asp	His	Gly	Trp	Val	Glu	
				85					90					95		
Ala	Leu	Asn	Asn	Lys	Trp	Asp	Leu	Gly	Ile	Val	Lys	Gln	Glu	Ala	Ser	
			100					105						110		
Asn	Phe	Pro	Glu	Leu	Lys	Leu	Gln	Ala	Glu	Thr	Glu	Gln	Arg	Pro	His	
			115				120						125			
Lys	Val	Ser	Phe	Tyr	Val	Glu	Lys	Ser	Lys	Ala	Gln	Glu	Val	Thr	Lys	
	130					135					140					
Glu	Leu	Ser	Gln	Arg	Phe	Leu	Lys	Arg	Gly	Leu	Asp	Val	Lys	Ile	Ile	
145					150					155					160	
Tyr	Ser	Gly	Gly	Met	Asp	Leu	Asp	Ile	Leu	Pro	Gln	Gly	Ala	Gly	Lys	
				165					170					175		
Gly	Gln	Ala	Leu	Ala	Tyr	Leu	Leu	Lys	Lys	Leu	Lys	Thr	Glu	Gly	Lys	
			180					185					190			
Leu	Pro	Val	Asn	Thr	Leu	Ala	Cys	Gly	Asp	Ser	Gly	Asn	Asp	Ala	Glu	
			195				200					205				
Leu	Phe	Ser	Ile	Pro	Asp	Val	Tyr	Gly	Val	Met	Val	Ser	Asn	Ala	Gln	
	210					215					220					
Glu	Glu	Leu	Leu	Lys	Trp	His	Ala	Glu	Asn	Ala	Lys	Asp	Asn	Pro	Lys	
225					230						235				240	
Val	Ile	His	Ala	Lys	Glu	Arg	Cys	Ala	Gly	Gly	Ile	Ile	Gln	Ala	Ile	
				245					250					255		
Gly	His	Phe	Lys	Leu	Gly	Pro	Asn	Leu	Ser	Pro	Arg	Asp	Val	Ser	Asp	
			260					265					270			
Phe	Leu	Glu	Ile	Lys	Ala	Glu	Asn	Val	Asn	Pro	Gly	His	Glu	Val	Val	
			275				280					285				
Lys	Phe	Phe	Leu	Phe	Tyr	Glu	Lys	Trp	Arg	Arg	Gly	Glu	Val	Glu	Asn	
	290					295					300					
Ser	Glu	Ala	Tyr	Thr	Ala	Ser	Pro	Val	Ser	Ile	Ser	Arg				
305					310						315					

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..307  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498158  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```
Met Ile Val Ser Asp Leu Asp His Thr Met Val Asp His His Asp Pro
1          5          10          15
Glu Asn Leu Ser Leu Leu Arg Phe Asn Ser Leu Trp Glu His Ala Tyr
20          25          30
Arg His Asp Ser Leu Leu Val Phe Ser Thr Gly Arg Ser Pro Thr Leu
35          40          45
Tyr Lys Glu Leu Arg Lys Glu Lys Pro Leu Leu Thr Pro Asp Ile Thr
50          55          60
Ile Met Ser Val Gly Thr Glu Ile Thr Tyr Gly Asn Ser Met Val Pro
65          70          75          80
Asp His Gly Trp Val Glu Ala Leu Asn Asn Lys Trp Asp Leu Gly Ile
85          90          95
Val Lys Gln Glu Ala Ser Asn Phe Pro Glu Leu Lys Leu Gln Ala Glu
100         105         110
Thr Glu Gln Arg Pro His Lys Val Ser Phe Tyr Val Glu Lys Ser Lys
115         120         125
Ala Gln Glu Val Thr Lys Glu Leu Ser Gln Arg Phe Leu Lys Arg Gly
130         135         140
Leu Asp Val Lys Ile Ile Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu
145         150         155         160
Pro Gln Gly Ala Gly Lys Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys
165         170         175
Leu Lys Thr Glu Gly Lys Leu Pro Val Asn Thr Leu Ala Cys Gly Asp
180         185         190
Ser Gly Asn Asp Ala Glu Leu Phe Ser Ile Pro Asp Val Tyr Gly Val
195         200         205
Met Val Ser Asn Ala Gln Glu Glu Leu Leu Lys Trp His Ala Glu Asn
210         215         220
Ala Lys Asp Asn Pro Lys Val Ile His Ala Lys Glu Arg Cys Ala Gly
225         230         235         240
Gly Ile Ile Gln Ala Ile Gly His Phe Lys Leu Gly Pro Asn Leu Ser
245         250         255
Pro Arg Asp Val Ser Asp Phe Leu Glu Ile Lys Ala Glu Asn Val Asn
260         265         270
Pro Gly His Glu Val Val Lys Phe Phe Leu Phe Tyr Glu Lys Trp Arg
275         280         285
Arg Gly Glu Val Glu Asn Ser Glu Ala Tyr Thr Ala Ser Pro Val Ser
290         295         300
Ile Ser Arg
305
```

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1220 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1220  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498159  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```
gtaatttctc tttcggtcaa tggtattctt ttagatctcg aacaaaacaa aatctccaga      60
agaaaaaaccc aaattccatg gcgtctaaat cgaagcagca ttttcgttat cagccgcgaa      120
aatctgtgtc acgatcaaca caagctttca cggtgcttat acttcttctc gtagtgattc      180
```



```

tgattcttct ggggtctcggg attttggtcac tacctaattgc taatagaaac tcttccaaga      240
cgaatgattt gaccaacatt gtacgaaaga gtgagacgag ttctggagat gaagaaggga      300
atggtgaacg ttgggttgaa gttatttctt gggagcctcg tgctgttggt tatcacaatt      360
tcttgactaa tgaagaatgt gagcacttga tcagccttgc taaaccgagt atggttaagt      420
caaccgtggt agatgagaaa accggtggga gcaaagatag cagagtgaga actagctcag      480
gaacttttct tagaagagga catgacgaag ttgtcgaggt gattgagaaa aggatttcag      540
atttcacctt cattcctggt gaaaatggtg aaggtcttca agttcttcac taccaagttg      600
ggcagaagta tgagcctcac tatgactatt tcttagatga gttcaacacc aagaatggag      660
gacaacgaat agctactgtg cttatgtacc tctctgatgt cgatgatggt ggcgagactg      720
tgttccctgc agcaagagga aacattagtg ctgtcccatg gtggaacgag ctctcaaaat      780
gtggtaaaga aggactatct gttctaccaa agragcgaga tgctttactt ttctggaaca      840
tgaggcctga tgcattctta gacccttoga gcttgacagg tggatgtcca gtggtgaaag      900
gaaacaaatg gtcattccacg aaatggttcc atgtccacga gttcaagggt taagagmaac      960
caaacaaasa aagctaaaat atgaggaggt ttttcatgga agcttcgaat gtgtgtggat     1020
acagttaaac aggtataatg tgtatttccc ttttgaagtg agagatcctt aggaaattgg     1080
aggctgttct ttcattggggg atatttgaac tttttgtact ttttcttcta aattattttg     1140
aatgatttgt actttacgac atattcgaat ctgagtcttg taacttttaa caactcaata     1200
cgaaccatga attttccggt

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Asn Phe Ser Phe Val Gln Cys Tyr Ser Phe Arg Ser Arg Thr Lys Gln
1          5          10          15
Asn Leu Gln Lys Lys Lys Pro Asn Ser Met Ala Ser Lys Ser Lys Gln
20          25          30
His Leu Arg Tyr Gln Pro Arg Lys Ser Val Ser Arg Ser Thr Gln Ala
35          40          45
Phe Thr Val Leu Ile Leu Leu Val Val Ile Leu Ile Leu Leu Gly
50          55          60
Leu Gly Ile Leu Ser Leu Pro Asn Ala Asn Arg Asn Ser Ser Lys Thr
65          70          75          80
Asn Asp Leu Thr Asn Ile Val Arg Lys Ser Glu Thr Ser Ser Gly Asp
85          90          95
Glu Glu Gly Asn Gly Glu Arg Trp Val Glu Val Ile Ser Trp Glu Pro
100         105         110
Arg Ala Val Val Tyr His Asn Phe Leu Thr Asn Glu Glu Cys Glu His
115         120         125
Leu Ile Ser Leu Ala Lys Pro Ser Met Val Lys Ser Thr Val Val Asp
130         135         140
Glu Lys Thr Gly Gly Ser Lys Asp Ser Arg Val Arg Thr Ser Ser Gly
145         150         155         160
Thr Phe Leu Arg Arg Gly His Asp Glu Val Val Glu Val Ile Glu Lys
165         170         175
Arg Ile Ser Asp Phe Thr Phe Ile Pro Val Glu Asn Gly Glu Gly Leu
180         185         190
Gln Val Leu His Tyr Gln Val Gly Gln Lys Tyr Glu Pro His Tyr Asp
195         200         205
Tyr Phe Leu Asp Glu Phe Asn Thr Lys Asn Gly Gly Gln Arg Ile Ala
210         215         220
Thr Val Leu Met Tyr Leu Ser Asp Val Asp Asp Gly Gly Glu Thr Val
225         230         235         240
Phe Pro Ala Ala Arg Gly Asn Ile Ser Ala Val Pro Trp Trp Asn Glu

```

				245					250					255	
Leu	Ser	Lys	Cys	Gly	Lys	Glu	Gly	Leu	Ser	Val	Leu	Pro	Lys	Xaa	Arg
			260					265					270		
Asp	Ala	Leu	Leu	Phe	Trp	Asn	Met	Arg	Pro	Asp	Ala	Ser	Leu	Asp	Pro
		275				280					285				
Ser	Ser	Leu	His	Gly	Gly	Cys	Pro	Val	Val	Lys	Gly	Asn	Lys	Trp	Ser
	290					295					300				
Ser	Thr	Lys	Trp	Phe	His	Val	His	Glu	Phe	Lys	Val				
305				310						315					

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1498161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Met	Ala	Ser	Lys	Ser	Lys	Gln	His	Leu	Arg	Tyr	Gln	Pro	Arg	Lys	Ser
1			5					10						15	
Val	Ser	Arg	Ser	Thr	Gln	Ala	Phe	Thr	Val	Leu	Ile	Leu	Leu	Leu	Val
			20					25					30		
Val	Ile	Leu	Ile	Leu	Leu	Gly	Leu	Gly	Ile	Leu	Ser	Leu	Pro	Asn	Ala
			35				40					45			
Asn	Arg	Asn	Ser	Ser	Lys	Thr	Asn	Asp	Leu	Thr	Asn	Ile	Val	Arg	Lys
	50					55					60				
Ser	Glu	Thr	Ser	Ser	Gly	Asp	Glu	Glu	Gly	Asn	Gly	Glu	Arg	Trp	Val
	65				70					75				80	
Glu	Val	Ile	Ser	Trp	Glu	Pro	Arg	Ala	Val	Val	Tyr	His	Asn	Phe	Leu
			85					90						95	
Thr	Asn	Glu	Glu	Cys	Glu	His	Leu	Ile	Ser	Leu	Ala	Lys	Pro	Ser	Met
			100					105					110		
Val	Lys	Ser	Thr	Val	Val	Asp	Glu	Lys	Thr	Gly	Gly	Ser	Lys	Asp	Ser
	115					120						125			
Arg	Val	Arg	Thr	Ser	Ser	Gly	Thr	Phe	Leu	Arg	Arg	Gly	His	Asp	Glu
	130					135					140				
Val	Val	Glu	Val	Ile	Glu	Lys	Arg	Ile	Ser	Asp	Phe	Thr	Phe	Ile	Pro
	145				150					155					160
Val	Glu	Asn	Gly	Glu	Gly	Leu	Gln	Val	Leu	His	Tyr	Gln	Val	Gly	Gln
			165					170						175	
Lys	Tyr	Glu	Pro	His	Tyr	Asp	Tyr	Phe	Leu	Asp	Glu	Phe	Asn	Thr	Lys
			180					185					190		
Asn	Gly	Gly	Gln	Arg	Ile	Ala	Thr	Val	Leu	Met	Tyr	Leu	Ser	Asp	Val
		195					200					205			
Asp	Asp	Gly	Gly	Glu	Thr	Val	Phe	Pro	Ala	Ala	Arg	Gly	Asn	Ile	Ser
	210					215					220				
Ala	Val	Pro	Trp	Trp	Asn	Glu	Leu	Ser	Lys	Cys	Gly	Lys	Glu	Gly	Leu
	225				230					235					240
Ser	Val	Leu	Pro	Lys	Xaa	Arg	Asp	Ala	Leu	Leu	Phe	Trp	Asn	Met	Arg
			245						250					255	
Pro	Asp	Ala	Ser	Leu	Asp	Pro	Ser	Ser	Leu	His	Gly	Gly	Cys	Pro	Val
		260					265						270		
Val	Lys	Gly	Asn	Lys	Trp	Ser	Ser	Thr	Lys	Trp	Phe	His	Val	His	Glu
		275					280					285			
Phe	Lys	Val													
	290														

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..180  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498162  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:  
Met Val Lys Ser Thr Val Val Asp Glu Lys Thr Gly Gly Ser Lys Asp  
1 5 10 15  
Ser Arg Val Arg Thr Ser Ser Gly Thr Phe Leu Arg Arg Gly His Asp  
20 25 30  
Glu Val Val Glu Val Ile Glu Lys Arg Ile Ser Asp Phe Thr Phe Ile  
35 40 45  
Pro Val Glu Asn Gly Glu Gly Leu Gln Val Leu His Tyr Gln Val Gly  
50 55 60  
Gln Lys Tyr Glu Pro His Tyr Asp Tyr Phe Leu Asp Glu Phe Asn Thr  
65 70 75 80  
Lys Asn Gly Gly Gln Arg Ile Ala Thr Val Leu Met Tyr Leu Ser Asp  
85 90 95  
Val Asp Asp Gly Gly Glu Thr Val Phe Pro Ala Ala Arg Gly Asn Ile  
100 105 110  
Ser Ala Val Pro Trp Trp Asn Glu Leu Ser Lys Cys Gly Lys Glu Gly  
115 120 125  
Leu Ser Val Leu Pro Lys Xaa Arg Asp Ala Leu Leu Phe Trp Asn Met  
130 135 140  
Arg Pro Asp Ala Ser Leu Asp Pro Ser Ser Leu His Gly Gly Cys Pro  
145 150 155 160  
Val Val Lys Gly Asn Lys Trp Ser Ser Thr Lys Trp Phe His Val His  
165 170 175  
Glu Phe Lys Val  
180

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..496  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

aagagagaaa aaaggttgaa tcgaaacaga tcggaaaatc gtcgagagag agagagagag	60
aagtcaacg acaggcagct aatgctaagg agtttgctga ggaaatggtt cttgaagaca	120
tctctatgca gagagggatt tcgataaacg ctgctcgtaa cttccttggt ggtgggtgctg	180
agaaggattc agacattatt ttctgaggtg tgggctctct ctctctctct ctctctctct	240
ctctctctct ctctctctct ctctctctct ctctctctct ctctctctct ctttgtgcct	300
tctgtgtttg ctcggtttct attttgcgct tcgcgctggt attactctct tcatcagact	360
tatgtttctt caaataaaat ggatttgatg tagatgaaat actgtatcat cttggattgt	420
gctttgatat aaattttttc gagagatttg tgattattac tgttttgagt aattataatt	480
ccctgtttc aagact	

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..48  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498164  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:  
Lys Arg Glu Lys Arg Leu Asn Arg Asn Arg Ser Glu Asn Arg Arg Glu  
1                    5                    10                    15  
Arg Glu Arg Glu Lys Ser Asn Asp Arg Gln Leu Met Leu Arg Ser Leu  
                    20                    25                    30  
Leu Arg Lys Trp Phe Leu Lys Thr Ser Leu Cys Arg Glu Gly Phe Arg  
                    35                    40                    45

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 67 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..67  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498165  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:  
Glu Arg Lys Lys Val Glu Ser Lys Gln Ile Gly Lys Ser Ser Arg Glu  
1                    5                    10                    15  
Arg Glu Arg Glu Val Glu Arg Gln Ala Ala Asn Ala Lys Glu Phe Ala  
                    20                    25                    30  
Glu Glu Met Val Leu Glu Asp Ile Ser Met Gln Arg Gly Ile Ser Ile  
                    35                    40                    45  
Asn Ala Ala Arg Asn Phe Leu Val Gly Gly Ala Glu Lys Asp Ser Asp  
                    50                    55                    60  
Ile Ile Phe  
65

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..33  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498166  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  
Met Val Leu Glu Asp Ile Ser Met Gln Arg Gly Ile Ser Ile Asn Ala  
1                    5                    10                    15  
Ala Arg Asn Phe Leu Val Gly Gly Ala Glu Lys Asp Ser Asp Ile Ile  
                    20                    25                    30  
Phe

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1121 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1121

(D) OTHER INFORMATION: / Ceres Seq. ID 1498167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

aaacccaac	tttcgagttt	rccgatgagt	ctagcctcca	tgatctccgg	ctaaagatca	60
atgaatcgac	gccttcctct	gttcgtttgt	cgattgatta	caacgacggt	gatatcctcg	120
cggtgtttac	tctctcgatt	cgtctgattt	tagtgcgttt	gatcagaaat	cggaaasgaa	180
tcacagaggag	attgttcgta	gattccggtg	gcagcatgaa	tctctccngg	tgtaaaaagg	240
ttaagcgagc	ctctcttggt	gaaaaatata	ttgatggagg	aatctggtga	cacttgtgaa	300
ttgacgattg	tgatcatgac	tgttcatgct	gttatgttag	aatctggatt	tttgtgttgt	360
ttgatcctga	ttcatctatg	cgttttagct	tctcgaagaa	gaatttggtg	tcgcttaact	420
atactctacc	ttctgtgaaa	ggaatagtcg	gtttgaattt	tgagaaggag	gcgatgttgt	480
agtttatgga	tctcttagtg	ttggtagttt	tgttcgtgtg	gtgtctattg	ataaacgtag	540
ctatgtgcac	attgttgatt	tacttatgga	aactttgaaa	tctgatgaag	aagaagatac	600
tttgagcatt	gactgtaagg	tactcgtgtg	gtggagaatg	ataaaagatg	gtattgttac	660
gcctctgttg	gttgatcttt	gctacaaaac	tgggttagaa	cttcacacct	gctttatcag	720
tctacctcga	gagctaaaac	acaagatact	agagtcgctt	cccgggtgtg	atattgggac	780
attggcttgt	gtttcttctg	aactgcgaga	catggcttcg	tagaatgacc	tgtggaagca	840
gaagtgcctg	gaagagtgcc	aagatcttgt	gacagaaggc	aatcatgatg	tggttaactg	900
gaaggagagg	tttgctactt	attggaggga	aaagggaaag	ttctccttca	taagcagggc	960
atttcaaggt	ttttcaggga	gcattggttc	gtcataaatc	ctggaagaag	actaaaaaga	1020
gaccatattg	aatccggtgg	agtgaatggt	tgtttgtatt	caaactttgc	aaataggcaa	1080
ttatagggtt	aagatgggtg	aaagagcatt	ggaaacttag	t		

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Thr	Pro	Thr	Phe	Glu	Phe	Xaa	Asp	Glu	Ser	Ser	Leu	His	Asp	Leu	Arg
1				5					10					15	
Leu	Lys	Ile	Asn	Glu	Ser	Thr	Pro	Ser	Ser	Val	Arg	Leu	Ser	Ile	Asp
			20					25					30		
Tyr	Asn	Asp	Gly	Asp	Ile	Leu	Ala	Ala	Val	Thr	Leu	Ser	Ile	Arg	Leu
			35				40					45			
Ile	Leu	Val	Arg	Leu	Ile	Arg	Asn	Arg	Lys	Xaa	Ile	Ile	Arg	Arg	Leu
			50				55				60				
Phe	Val	Asp	Ser	Gly	Gly	Ser	Met	Asn	Leu	Ser	Xaa	Cys	Lys	Lys	Val
65				70					75					80	
Lys	Arg	Ala	Ser	Leu	Val	Glu	Lys	Tyr	Ile	Asp	Gly	Gly	Ile	Trp	
				85				90						95	

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1498169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Glu Thr Leu Lys Ser Asp Glu Glu Glu Asp Thr Leu Ser Ile Asp

1 5 10 15  
Cys Lys Val Leu Val Trp Trp Arg Met Ile Lys Asp Gly Ile Val Thr  
20 25 30  
Pro Leu Leu Val Asp Leu Cys Tyr Lys Thr Gly Leu Glu Leu Pro Pro  
35 40 45  
Cys Phe Ile Ser Leu Pro Arg Glu Leu Lys His Lys Ile Leu Glu Ser  
50 55 60  
Leu Pro Gly Val Asp Ile Gly Thr Leu Ala Cys Val Ser Ser Glu Leu  
65 70 75 80  
Arg Asp Met Ala Ser  
85

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Ile Lys Asp Gly Ile Val Thr Pro Leu Leu Val Asp Leu Cys Tyr  
1 5 10 15  
Lys Thr Gly Leu Glu Leu Pro Pro Cys Phe Ile Ser Leu Pro Arg Glu  
20 25 30  
Leu Lys His Lys Ile Leu Glu Ser Leu Pro Gly Val Asp Ile Gly Thr  
35 40 45  
Leu Ala Cys Val Ser Ser Glu Leu Arg Asp Met Ala Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..775
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

actctctata cctcctcaag aaaatcaaag cagcagttat ggccgacgta gcaacaaagc 60  
accccatgga agatgaggtg aagaagacgg aggcgtctag tttggtggg aagctagaga 120  
cagacgtgga gatcaaggct tcggctgata agtttcacca catgttcgct gggaaaccac 180  
accatgtctc caaagcaagt ccaggcaaca ttcagggatg tgatctgcac gaaggcgact 240  
ggggcacagt cggctctatc gtcttctgga attacgtwca tgatrgggag gcaaaggtgg 300  
ctaaggagag gattgaggcr gtggagccrg ataagaactt gatcacgttt agggttatag 360  
acggtgatct gatgaaagag tacaagagct tcttgctcac catccagggtg acccckaagc 420  
ytggaggccc tggaagtatt gtgcactggc accttgagta tgagaaaatw agcgaggagg 480  
tagctcatcc ggaaactctc ctccavttct gtgtcgaggt ctccaaagag atcgacgaac 540  
atcttttggc cgaggaatag aggagtacta ctactcttcg tgtttgaatt taaatgcaat 600  
aaataaggac taagagccat gtctttgtga gatatatgaa tgtgagtgtg catcatgaat 660  
gtatgtatac taagatcggt ttacgttggc tactgtaact ttgagaagca atgtgtagta 720  
gctgtgatga agctagtata aatatataat agtatgtta tatatgtttg ctaat

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..185  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498174  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:  
Ser Leu Tyr Leu Leu Lys Lys Ile Lys Ala Ala Val Met Ala Asp Val  
1                    5                    10                    15  
Ala Thr Lys His Pro Met Glu Asp Glu Val Lys Lys Thr Glu Ala Ser  
            20                    25                    30  
Ser Leu Val Gly Lys Leu Glu Thr Asp Val Glu Ile Lys Ala Ser Ala  
            35                    40                    45  
Asp Lys Phe His His Met Phe Ala Gly Lys Pro His His Val Ser Lys  
            50                    55                    60  
Ala Ser Pro Gly Asn Ile Gln Gly Cys Asp Leu His Glu Gly Asp Trp  
65                    70                    75                    80  
Gly Thr Val Gly Ser Ile Val Phe Trp Asn Tyr Xaa His Asp Xaa Glu  
                    85                    90                    95  
Ala Lys Val Ala Lys Glu Arg Ile Glu Xaa Val Glu Xaa Asp Lys Asn  
            100                    105                    110  
Leu Ile Thr Phe Arg Val Ile Asp Gly Asp Leu Met Lys Glu Tyr Lys  
            115                    120                    125  
Ser Phe Leu Leu Thr Ile Gln Val Thr Xaa Lys Xaa Gly Gly Pro Gly  
130                    135                    140  
Ser Ile Val His Trp His Leu Glu Tyr Glu Lys Xaa Ser Glu Glu Val  
145                    150                    155                    160  
Ala His Pro Glu Thr Leu Leu Xaa Phe Cys Val Glu Val Ser Lys Glu  
                    165                    170                    175  
Ile Asp Glu His Leu Leu Ala Glu Glu  
            180                    185  
(2) INFORMATION FOR SEQ ID NO:247:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 173 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..173  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498175  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:  
Met Ala Asp Val Ala Thr Lys His Pro Met Glu Asp Glu Val Lys Lys  
1                    5                    10                    15  
Thr Glu Ala Ser Ser Leu Val Gly Lys Leu Glu Thr Asp Val Glu Ile  
            20                    25                    30  
Lys Ala Ser Ala Asp Lys Phe His His Met Phe Ala Gly Lys Pro His  
            35                    40                    45  
His Val Ser Lys Ala Ser Pro Gly Asn Ile Gln Gly Cys Asp Leu His  
50                    55                    60  
Glu Gly Asp Trp Gly Thr Val Gly Ser Ile Val Phe Trp Asn Tyr Xaa  
65                    70                    75                    80  
His Asp Xaa Glu Ala Lys Val Ala Lys Glu Arg Ile Glu Xaa Val Glu  
            85                    90                    95  
Xaa Asp Lys Asn Leu Ile Thr Phe Arg Val Ile Asp Gly Asp Leu Met  
100                    105                    110  
Lys Glu Tyr Lys Ser Phe Leu Leu Thr Ile Gln Val Thr Xaa Lys Xaa  
115                    120                    125  
Gly Gly Pro Gly Ser Ile Val His Trp His Leu Glu Tyr Glu Lys Xaa  
130                    135                    140

Ser Glu Glu Val Ala His Pro Glu Thr Leu Leu Xaa Phe Cys Val Glu  
145 150 155 160  
Val Ser Lys Glu Ile Asp Glu His Leu Leu Ala Glu Glu  
165 170

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met Glu Asp Glu Val Lys Lys Thr Glu Ala Ser Ser Leu Val Gly Lys  
1 5 10 15  
Leu Glu Thr Asp Val Glu Ile Lys Ala Ser Ala Asp Lys Phe His His  
20 25 30  
Met Phe Ala Gly Lys Pro His His Val Ser Lys Ala Ser Pro Gly Asn  
35 40 45  
Ile Gln Gly Cys Asp Leu His Glu Gly Asp Trp Gly Thr Val Gly Ser  
50 55 60  
Ile Val Phe Trp Asn Tyr Xaa His Asp Xaa Glu Ala Lys Val Ala Lys  
65 70 75 80  
Glu Arg Ile Glu Xaa Val Glu Xaa Asp Lys Asn Leu Ile Thr Phe Arg  
85 90 95  
Val Ile Asp Gly Asp Leu Met Lys Glu Tyr Lys Ser Phe Leu Leu Thr  
100 105 110  
Ile Gln Val Thr Xaa Lys Xaa Gly Gly Pro Gly Ser Ile Val His Trp  
115 120 125  
His Leu Glu Tyr Glu Lys Xaa Ser Glu Glu Val Ala His Pro Glu Thr  
130 135 140  
Leu Leu Xaa Phe Cys Val Glu Val Ser Lys Glu Ile Asp Glu His Leu  
145 150 155 160  
Leu Ala Glu Glu

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..894
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

atTTTgaaaa gTTTctaacc tctaggccac ccactcatgg ctactctggt catgaagctg 60  
gtgagcttct ttctaattct atctactttt tgtctcacta ctgtgaactc ggagccacag 120  
tgccataatt tcaaatcgat cattagtttc ggtgattcta ttgccgacac tggaaacttg 180  
ctgcacctct ccgatacctac caatctccct aaggtcgcggt ttctaccgta cggagaaacc 240  
ttcttccacc atccgaccgg ccgtttctca aacggccggc tcatcatcga ttccattgct 300  
gaatttttgg gttttccgct tgtgcctcct ttttatggat ctcaaaatgc aaattttgag 360  
aaaggagtta attttgcggg tggaggagca acggcactgg aacgttcctt tcttgaagag 420  
agaggcattc attttcctta caccaacggt agtttagccg tacagcttag tagcttcaag 480  
gagagtttgc ctaacttatg tgtctctcct tcagactgca gagatatgat agaaaattct 540  
ttgattctca tgggagaaat tggagggaat gactataact acgcattctg aaggagagac 600  
acataagtta ggcaaactct ccttgaagct acggtggtgg aagacgtgag ggaggaggag 660



gatacgggtgg tgggtgaagga ggaggttacg gaggaagcgg tgggtggtgga ggatggtaat 720  
tcctttaatt aggtttggga ttaccaatga atgttctctc tctcgcttgt tatgcttcta 780  
cttgggttttg ygtgttctct atttgttctt ggttctgctt tagatttgat gtaacagttc 840  
gtgattaggt attttggtat ctggaacgt aatgttaagt cacttgatcat tctc

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Ala Thr Leu Phe Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser  
1 5 10 15  
Thr Phe Cys Leu Thr Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe  
20 25 30  
Lys Ser Ile Ile Ser Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu  
35 40 45  
Leu Ala Leu Ser Asp Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro  
50 55 60  
Tyr Gly Glu Thr Phe Phe His His Pro Thr Gly Arg Phe Ser Asn Gly  
65 70 75 80  
Arg Leu Ile Ile Asp Phe Ile Ala Glu Phe Leu Gly Phe Pro Leu Val  
85 90 95  
Pro Pro Phe Tyr Gly Ser Gln Asn Ala Asn Phe Glu Lys Gly Val Asn  
100 105 110  
Phe Ala Val Gly Gly Ala Thr Ala Leu Glu Arg Ser Phe Leu Glu Glu  
115 120 125  
Arg Gly Ile His Phe Pro Tyr Thr Asn Val Ser Leu Ala Val Gln Leu  
130 135 140  
Ser Ser Phe Lys Glu Ser Leu Pro Asn Leu Cys Val Ser Pro Ser Asp  
145 150 155 160  
Cys Arg Asp Met Ile Glu Asn Ser Leu Ile Leu Met Gly Glu Ile Gly  
165 170 175  
Gly Asn Asp Tyr Asn Tyr Ala Phe  
180

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser Thr Phe Cys Leu Thr  
1 5 10 15  
Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe Lys Ser Ile Ser  
20 25 30  
Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu Leu Ala Leu Ser Asp  
35 40 45  
Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro Tyr Gly Glu Thr Phe  
50 55 60  
Phe His His Pro Thr Gly Arg Phe Ser Asn Gly Arg Leu Ile Ile Asp

```

65          70          75          80
Phe Ile Ala Glu Phe Leu Gly Phe Pro Leu Val Pro Pro Phe Tyr Gly
          85          90          95
Ser Gln Asn Ala Asn Phe Glu Lys Gly Val Asn Phe Ala Val Gly Gly
          100         105         110
Ala Thr Ala Leu Glu Arg Ser Phe Leu Glu Glu Arg Gly Ile His Phe
          115         120         125
Pro Tyr Thr Asn Val Ser Leu Ala Val Gln Leu Ser Ser Phe Lys Glu
          130         135         140
Ser Leu Pro Asn Leu Cys Val Ser Pro Ser Asp Cys Arg Asp Met Ile
145         150         155         160
Glu Asn Ser Leu Ile Leu Met Gly Glu Ile Gly Gly Asn Asp Tyr Asn
          165         170         175
Tyr Ala Phe
```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

agtcgtctag ggtttgtttt tcgtttcttc tccgattggt cagaggaatt gcgaattaag      60
ataaagatga ggccagtgtt cgtcggcaat ttcgagtatg aaactcgcca gtcggatctg      120
gaacggttgt tcgacaagta tgggagagtc gaccgagtgg acatgaaatc tggatatgct      180
tttgtgtact ttgaggatga acgtgatgct gaagacgcta ttcgcaaact cgacaatttt      240
ccttttggtat atgagaaacg caggttatca gttgaatggg caaagggtga acgtggcagg      300
cctcgtggtg acgcgaaaac cccttcaaat ctgaagccta caaagacact gtttgtcatt      360
aactttgacc ccattagaac aaaagagcac gacattgaaa aacactttga gccctatggt      420
aaggtcacca acgtgcgtat cagacgcaac ttctcatttg ttcagtttga aacacaagag      480
gatgctacaa aagcccttga agctactcaa agaagcaaaa tattggatag ggttgtttcc      540
gtggagtatg cgttgaaaga tgacgatgaa agagatgatc gaaatggtgg tcgtagcccg      600
agaaggtctc ttagtcctgt gtatcgtagg cgatcatgta tgatgtactg tcgttatttt      660
aaagaaaatt tggcaccttt tgtataaaca gaatttctta tacctcgagc tttgtgttta      720
cgt
```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Ser Arg Leu Gly Phe Val Phe Arg Phe Phe Ser Asp Cys Ser Glu Glu
1          5          10          15
Leu Arg Ile Lys Ile Lys Met Arg Pro Val Phe Val Gly Asn Phe Glu
          20          25          30
Tyr Glu Thr Arg Gln Ser Asp Leu Glu Arg Leu Phe Asp Lys Tyr Gly
          35          40          45
Arg Val Asp Arg Val Asp Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe
          50          55          60
Glu Asp Glu Arg Asp Ala Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..174
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala
1          5          10          15
Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys
20          25          30
Arg Arg Leu Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg
35          40          45
Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe
50          55          60
Val Ile Asn Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys
65          70          75          80
His Phe Glu Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn
85          90          95
Phe Ser Phe Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu
100         105         110
Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu
115         120         125
Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp Asp Arg Asn Gly Gly Arg
130         135         140
Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met
145         150         155         160
Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val
165         170
```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1051
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
aaaaaacaga aaaaattcgt ggaaacgcc aataacgagat ctagcacaaa ctctagtgtg 60
ggtgtagaag aagacaaaag caaggagctt cataataaaa ccctagagat atttgtttct 120
ccaatttcaa aagacgagac gtgaagaaga cgatcgaaga tgaacatttt cagattagct 180
ggtgatatga ctacacctagc cagtgttctt gtcttgcttc tcaagatcca caccatcaaa 240
tcctgcgctg gtgtttcatt gaagactcaa gaactctatg ccattgtctt tgcgacgcgt 300
tatttgagata ttttcacgag ttttgtgtct ctgtacaaca cctctatgaa gttgggtgtc 360
ttaggaagtt ctttttcgat tgtgtggtac atgaagtatc ataaggccgt ccacaggact 420
tacgacagag agcaagatac gtttcgctat tggttccttg tgcttccttg ctttctctta 480
gctcttctga ttcatgaaaa gtttaccttt cttgaggtat tgtggacgtt ttcattgtac 540
ttggaggctg ttgccatatt acctcagctt gtcttgttgc aaaggactag aaatattgac 600
aacttgaccg gacaatatat atttctcctt ggggggtacc gtggattata catcctcaac 660
tggatctacc gttacttcac tgagcgcgac tttgttcaat ggataacatg gatcgccggg 720
tttgttcaaa cactgctcta tgccgacttc ttctattatt atttcctaag ctggaagaac 780
aacaaaaagc tccaattacc agcttaattt ctaaagtctt aatgctcggg aaccctacgg 840
attcgatttg gtgcccagca aaacatctac cggaatgtta ccaatttact ctgttggttg 900
ttattagagg agaacgagca tagatgtgta aactccagca atctaactta ttacactttc 960
tttagacttt ctctgtctct atcttttttt ttggtcgact tagtggttact aaatatttctg 1020
```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..215
(D) OTHER INFORMATION: / Ceres Seq. ID 1498191
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ile | Phe | Arg | Leu | Ala | Gly | Asp | Met | Thr | His | Leu | Ala | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Leu | Leu | Leu | Lys | Ile | His | Thr | Ile | Lys | Ser | Cys | Ala | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Lys | Thr | Gln | Glu | Leu | Tyr | Ala | Ile | Val | Phe | Ala | Thr | Arg | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Ile | Phe | Thr | Ser | Phe | Val | Ser | Leu | Tyr | Asn | Thr | Ser | Met | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Phe | Leu | Gly | Ser | Ser | Phe | Ser | Ile | Val | Trp | Tyr | Met | Lys | Tyr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Lys | Ala | Val | His | Arg | Thr | Tyr | Asp | Arg | Glu | Gln | Asp | Thr | Phe | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Trp | Phe | Leu | Val | Leu | Pro | Cys | Phe | Leu | Leu | Ala | Leu | Leu | Ile | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | Phe | Thr | Phe | Leu | Glu | Val | Leu | Trp | Thr | Phe | Ser | Leu | Tyr | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Ala | Val | Ala | Ile | Leu | Pro | Gln | Leu | Val | Leu | Leu | Gln | Arg | Thr | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Ile | Asp | Asn | Leu | Thr | Gly | Gln | Tyr | Ile | Phe | Leu | Leu | Gly | Gly | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Gly | Leu | Tyr | Ile | Leu | Asn | Trp | Ile | Tyr | Arg | Tyr | Phe | Thr | Glu | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| His | Phe | Val | His | Trp | Ile | Thr | Trp | Ile | Ala | Gly | Phe | Val | Gln | Thr | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Tyr | Ala | Asp | Phe | Phe | Tyr | Tyr | Tyr | Phe | Leu | Ser | Trp | Lys | Asn | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Lys | Leu | Gln | Leu | Pro | Ala |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- ```
(      (A) LENGTH: 206 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..206
      (D) OTHER INFORMATION: / Ceres Seq. ID 1498192
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1															
Met	Thr	His	Leu	Ala	Ser	Val	Leu	Val	Leu	Leu	Lys	Ile	His	Thr	
1				5					10				15		
Ile	Lys	Ser	Cys	Ala	Gly	Val	Ser	Leu	Lys	Thr	Gln	Glu	Leu	Tyr	Ala
			20					25					30		
Ile	Val	Phe	Ala	Thr	Arg	Tyr	Leu	Asp	Ile	Phe	Thr	Ser	Phe	Val	Ser
		35					40					45			
Leu	Tyr	Asn	Thr	Ser	Met	Lys	Leu	Val	Phe	Leu	Gly	Ser	Ser	Phe	Ser
	50					55					60				

Ile Val Trp Tyr Met Lys Tyr His Lys Ala Val His Arg Thr Tyr Asp  
65 70 75 80  
Arg Glu Gln Asp Thr Phe Arg His Trp Phe Leu Val Leu Pro Cys Phe  
85 90 95  
Leu Leu Ala Leu Leu Ile His Glu Lys Phe Thr Phe Leu Glu Val Leu  
100 105 110  
Trp Thr Phe Ser Leu Tyr Leu Glu Ala Val Ala Ile Leu Pro Gln Leu  
115 120 125  
Val Leu Leu Gln Arg Thr Arg Asn Ile Asp Asn Leu Thr Gly Gln Tyr  
130 135 140  
Ile Phe Leu Leu Gly Gly Tyr Arg Gly Leu Tyr Ile Leu Asn Trp Ile  
145 150 155 160  
Tyr Arg Tyr Phe Thr Glu Pro His Phe Val His Trp Ile Thr Trp Ile  
165 170 175  
Ala Gly Phe Val Gln Thr Leu Leu Tyr Ala Asp Phe Phe Tyr Tyr Tyr  
180 185 190  
Phe Leu Ser Trp Lys Asn Asn Lys Lys Leu Gln Leu Pro Ala  
195 200 205

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1498193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met Lys Leu Val Phe Leu Gly Ser Ser Phe Ser Ile Val Trp Tyr Met  
1 5 10 15  
Lys Tyr His Lys Ala Val His Arg Thr Tyr Asp Arg Glu Gln Asp Thr  
20 25 30  
Phe Arg His Trp Phe Leu Val Leu Pro Cys Phe Leu Leu Ala Leu Leu  
35 40 45  
Ile His Glu Lys Phe Thr Phe Leu Glu Val Leu Trp Thr Phe Ser Leu  
50 55 60  
Tyr Leu Glu Ala Val Ala Ile Leu Pro Gln Leu Val Leu Leu Gln Arg  
65 70 75 80  
Thr Arg Asn Ile Asp Asn Leu Thr Gly Gln Tyr Ile Phe Leu Leu Gly  
85 90 95  
Gly Tyr Arg Gly Leu Tyr Ile Leu Asn Trp Ile Tyr Arg Tyr Phe Thr  
100 105 110  
Glu Pro His Phe Val His Trp Ile Thr Trp Ile Ala Gly Phe Val Gln  
115 120 125  
Thr Leu Leu Tyr Ala Asp Phe Phe Tyr Tyr Tyr Phe Leu Ser Trp Lys  
130 135 140  
Asn Asn Lys Lys Leu Gln Leu Pro Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 947 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..947

(D) OTHER INFORMATION: / Ceres Seq. ID 1498194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

aatgttgctt	taaaaccaat	gctcctcttc	ttgttcttca	tataaaccac	atatacctctc	60
ctccatatct	taacaatttc	atagcaaacc	ctaaaattga	gaaagagata	gagagagaaa	120
gatgggtaga	ggaaagatcg	agataaagag	gatagagaac	gcaaacaaca	gagtgggtgac	180
gttctcaaag	aggaggaatg	gattgggtgaa	gaaggctaaa	gagatcacag	ttctttgtga	240
tgcaaaagtt	gccctcataa	tccttgcaag	taatggtaag	atgattgatt	actgttgtcc	300
ttccatggat	cttgggtgcta	tgttggacca	ataccagaag	ttatctggca	agaaactatg	360
ggatgctaag	catgagaacc	ttagcaatga	gattgatagg	atcaagaaag	agaatgatag	420
cttacaactg	gagctcaggc	atttgaaggg	agaagatata	cagtctctca	acttgaaaaa	480
tctgatggct	gtcagcacg	ccattgaaca	tggcctcgac	aaagtccgag	accaccagat	540
ggagatcctt	atatcaaaga	ggagaaatga	gaagatgatg	gcggaggagc	aacggcaact	600
cactttccag	ctgcaacaac	aggagatggc	tatagcaagc	aacgcaagag	gaatgatgat	660
gagagatcat	gatgggcagt	ttggatatag	agtgcaaccg	attcagccaa	atcttcagga	720
aaagattatg	tcttttgtca	tcgattgatc	atcgagattt	tataatctca	tcctgatcaa	780
ctcctatcta	taatatcgct	gtcttttagtt	tgtctttatc	aatctgtgtg	tcctaatctc	840
gagcaacata	tatactcgct	atcagacttt	ttacttaagc	tatatgtgtg	ttgtttgctt	900
atgacctcta	tgtattgggt	gtgttggtgtg	cttaaacgtt	tcgmact		

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met	Gly	Arg	Gly	Lys	Ile	Glu	Ile	Lys	Arg	Ile	Glu	Asn	Ala	Asn	Asn	
1				5				10						15		
Arg	Val	Val	Thr	Phe	Ser	Lys	Arg	Arg	Asn	Gly	Leu	Val	Lys	Lys	Ala	
			20					25					30			
Lys	Glu	Ile	Thr	Val	Leu	Cys	Asp	Ala	Lys	Val	Ala	Leu	Ile	Ile	Phe	
			35					40					45			
Ala	Ser	Asn	Gly	Lys	Met	Ile	Asp	Tyr	Cys	Cys	Pro	Ser	Met	Asp	Leu	
			50					55					60			
Gly	Ala	Met	Leu	Asp	Gln	Tyr	Gln	Lys	Leu	Ser	Gly	Lys	Lys	Leu	Trp	
65					70					75					80	
Asp	Ala	Lys	His	Glu	Asn	Leu	Ser	Asn	Glu	Ile	Asp	Arg	Ile	Lys	Lys	
			85							90					95	
Glu	Asn	Asp	Ser	Leu	Gln	Leu	Glu	Leu	Arg	His	Leu	Lys	Gly	Glu	Asp	
			100						105					110		
Ile	Gln	Ser	Leu	Asn	Leu	Lys	Asn	Leu	Met	Ala	Val	Glu	His	Ala	Ile	
			115						120					125		
Glu	His	Gly	Leu	Asp	Lys	Val	Arg	Asp	His	Gln	Met	Glu	Ile	Leu	Ile	
			130											140		
Ser	Lys	Arg	Arg	Asn	Glu	Lys	Met	Met	Ala	Glu	Glu	Gln	Arg	Gln	Leu	
145						150							155		160	
Thr	Phe	Gln	Leu	Gln	Gln	Gln	Glu	Met	Ala	Ile	Ala	Ser	Asn	Ala	Arg	
						165								170		
Gly	Met	Met	Met	Arg	Asp	His	Asp	Gly	Gln	Phe	Gly	Tyr	Arg	Val	Gln	
						180								185		
Pro	Ile	Gln	Pro	Asn	Leu	Gln	Glu	Lys	Ile	Met	Ser	Leu	Val	Ile	Asp	
						195								200		
															205	

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..155  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498196  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met	Ile	Asp	Tyr	Cys	Cys	Pro	Ser	Met	Asp	Leu	Gly	Ala	Met	Leu	Asp
1				5					10					15	
Gln	Tyr	Gln	Lys	Leu	Ser	Gly	Lys	Lys	Leu	Trp	Asp	Ala	Lys	His	Glu
			20					25					30		
Asn	Leu	Ser	Asn	Glu	Ile	Asp	Arg	Ile	Lys	Lys	Glu	Asn	Asp	Ser	Leu
		35					40					45			
Gln	Leu	Glu	Leu	Arg	His	Leu	Lys	Gly	Glu	Asp	Ile	Gln	Ser	Leu	Asn
	50					55				60					
Leu	Lys	Asn	Leu	Met	Ala	Val	Glu	His	Ala	Ile	Glu	His	Gly	Leu	Asp
65					70					75				80	
Lys	Val	Arg	Asp	His	Gln	Met	Glu	Ile	Leu	Ile	Ser	Lys	Arg	Arg	Asn
			85						90				95		
Glu	Lys	Met	Met	Ala	Glu	Glu	Gln	Arg	Gln	Leu	Thr	Phe	Gln	Leu	Gln
			100					105					110		
Gln	Gln	Glu	Met	Ala	Ile	Ala	Ser	Asn	Ala	Arg	Gly	Met	Met	Met	Arg
		115					120					125			
Asp	His	Asp	Gly	Gln	Phe	Gly	Tyr	Arg	Val	Gln	Pro	Ile	Gln	Pro	Asn
	130					135					140				
Leu	Gln	Glu	Lys	Ile	Met	Ser	Leu	Val	Ile	Asp					
145					150					155					

- (2) INFORMATION FOR SEQ ID NO:263:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498197  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met	Asp	Leu	Gly	Ala	Met	Leu	Asp	Gln	Tyr	Gln	Lys	Leu	Ser	Gly	Lys
1				5					10					15	
Lys	Leu	Trp	Asp	Ala	Lys	His	Glu	Asn	Leu	Ser	Asn	Glu	Ile	Asp	Arg
			20					25					30		
Ile	Lys	Lys	Glu	Asn	Asp	Ser	Leu	Gln	Leu	Glu	Leu	Arg	His	Leu	Lys
		35					40					45			
Gly	Glu	Asp	Ile	Gln	Ser	Leu	Asn	Leu	Lys	Asn	Leu	Met	Ala	Val	Glu
	50					55				60					
His	Ala	Ile	Glu	His	Gly	Leu	Asp	Lys	Val	Arg	Asp	His	Gln	Met	Glu
65					70					75				80	
Ile	Leu	Ile	Ser	Lys	Arg	Arg	Asn	Glu	Lys	Met	Met	Ala	Glu	Glu	Gln
			85						90				95		
Arg	Gln	Leu	Thr	Phe	Gln	Leu	Gln	Gln	Glu	Met	Ala	Ile	Ala	Ser	
		100					105					110			
Asn	Ala	Arg	Gly	Met	Met	Met	Arg	Asp	His	Asp	Gly	Gln	Phe	Gly	Tyr
	115					120						125			
Arg	Val	Gln	Pro	Ile	Gln	Pro	Asn	Leu	Gln	Glu	Lys	Ile	Met	Ser	Leu
	130					135					140				
Val	Ile	Asp													
145															

- (2) INFORMATION FOR SEQ ID NO:264:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1145  
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498198  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```

atttcaaacc acacattcaa actaactctg caaaagaaaa aaaaactcag agcagaggag      60
atcgagagag acaaagagag acaaagagag agagagagag agagagagag agagagagag      120
agagatcttc aacaagcaat gtctatatcc atggcggttat tctctccgcc gatctcttcc      180
tcacttcaaa accctaattc catccccaag atctcaacct ctcttctctc caccaaacgt      240
ttctctctaa tctccgtccc tagagcttcc tccgacaatg gtacgacttc ccccgctcgtg      300
aaaattccga agcctgcgtc tgtagctgta gaggaagttc cgggttaaatac tccggcgga      360
agctcctccg cttctgaaaa cggcgccggtt ggaggtgaag cgactgattc gactactgag      420
acggtaatca aatatcaaaa tgcgaagtgg gttaatggaa cttgggatct gaaacagttc      480
gagaaagatg gcaaaactga ttgggattct gttatcgttt ctgaggcaaa gaggagaaaa      540
tggcttgaag ataaccggga aacaacgagt aacgacgagc ttgttgtctt cgatacttcg      600
attattccat ggtgggcatg gatgaagaga taccatctac ctgaagctga acttctcaat      660
ggtcgtgctg cgatgatagg gttcttcatg gcttactttg ttgatagtct taccggagta      720
ggacttggtg atcaaatggg gaatttcttc tgcaaaacac tcttgtttgt ggctgtagct      780
ggagttctct tcatccgtaa gaatgaagat ttagacaaac ttaaggatct gtccgatgag      840
actacgttat atgacaaaca atggcaagct gcatggaaag agccagattc atcaacagtt      900
tcttcaaaga agtgaacaag ttcttacaat ctttcatttt cctttttttg ttatgcaata      960
atctgtgaat cagtgaagat ttatctctac tgaactactg atcttcagat ttgttaatct      1020
ttctgcttta aaaatctcta tgaagtagtc tcaaagataa tgtatcgaag gtctttgact      1080
tgtaaagcag acctatttcg ttttgacgct tgataattta atcaataaga gatttttttt      1140
ttaat
  
```

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: peptide  
 (B) LOCATION: 1..304  
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498199  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```

Ile Ser Asn His Thr Phe Lys Leu Thr Leu Gln Lys Lys Lys Leu
1      5      10      15
Arg Ala Glu Glu Ile Glu Arg Asp Lys Glu Arg Gln Arg Glu Arg Glu
20     25     30
Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Leu Gln Gln Ala Met Ser
35     40     45
Ile Ser Met Ala Leu Phe Ser Pro Pro Ile Ser Ser Ser Leu Gln Asn
50     55     60
Pro Asn Leu Ile Pro Lys Ile Ser Thr Ser Leu Ser Thr Lys Arg
65     70     75     80
Phe Ser Leu Ile Ser Val Pro Arg Ala Ser Ser Asp Asn Gly Thr Thr
85     90     95
Ser Pro Val Val Lys Ile Pro Lys Pro Ala Ser Val Ala Val Glu Glu
100    105    110
Val Pro Val Lys Ser Pro Ala Glu Ser Ser Ser Ala Ser Glu Asn Gly
115    120    125
Ala Val Gly Gly Glu Ala Thr Asp Ser Ser Thr Glu Thr Val Ile Lys
130    135    140
  
```

Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys	Gln	Phe
145					150					155					160
Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser	Glu	Ala
				165					170					175	
Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser	Asn	Asp
			180					185					190		
Glu	Leu	Val	Val	Phe	Asp	Thr	Ser	Ile	Ile	Pro	Trp	Trp	Ala	Trp	Met
		195					200					205			
Lys	Arg	Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu	Leu	Asn	Gly	Arg	Ala	Ala
	210					215					220				
Met	Ile	Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val	Asp	Ser	Leu	Thr	Gly	Val
225					230					235					240
Gly	Leu	Val	Asp	Gln	Met	Gly	Asn	Phe	Phe	Cys	Lys	Thr	Leu	Leu	Phe
				245					250					255	
Val	Ala	Val	Ala	Gly	Val	Leu	Phe	Ile	Arg	Lys	Asn	Glu	Asp	Leu	Asp
			260					265					270		
Lys	Leu	Lys	Asp	Leu	Phe	Asp	Glu	Thr	Thr	Leu	Tyr	Asp	Lys	Gln	Trp
		275				280						285			
Gln	Ala	Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser	Thr	Val	Ser	Ser	Lys	Lys
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..258

(D) OTHER INFORMATION: / Ceres Seq. ID 1498200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met	Ser	Ile	Ser	Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ser	Ser	Leu
1				5					10					15	
Gln	Asn	Pro	Asn	Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser	Leu	Leu	Ser	Thr
			20					25					30		
Lys	Arg	Phe	Ser	Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser	Ser	Asp	Asn	Gly
		35					40					45			
Thr	Thr	Ser	Pro	Val	Val	Lys	Ile	Pro	Lys	Pro	Ala	Ser	Val	Ala	Val
		50				55					60				
Glu	Glu	Val	Pro	Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser	Ser	Ala	Ser	Glu
65					70				75					80	
Asn	Gly	Ala	Val	Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Val
			85					90					95		
Ile	Lys	Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys
		100					105					110			
Gln	Phe	Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser
		115					120				125				
Glu	Ala	Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser
		130				135					140				
Asn	Asp	Glu	Leu	Val	Val	Phe	Asp	Thr	Ser	Ile	Ile	Pro	Trp	Trp	Ala
145					150					155					160
Trp	Met	Lys	Arg	Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu	Leu	Asn	Gly	Arg
			165					170					175		
Ala	Ala	Met	Ile	Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val	Asp	Ser	Leu	Thr
		180						185					190		
Gly	Val	Gly	Leu	Val	Asp	Gln	Met	Gly	Asn	Phe	Phe	Cys	Lys	Thr	Leu
		195				200						205			
Leu	Phe	Val	Ala	Val	Ala	Gly	Val	Leu	Phe	Ile	Arg	Lys	Asn	Glu	Asp

210		215		220											
Leu	Asp	Lys	Leu	Lys	Asp	Leu	Phe	Asp	Glu	Thr	Thr	Leu	Tyr	Asp	Lys
225			230						235						240
Gln	Trp	Gln	Ala	Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser	Thr	Val	Ser	Ser
			245						250						255
Lys	Lys														

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ser	Ser	Leu	Gln	Asn	Pro	Asn
1				5					10					15	
Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser	Leu	Leu	Ser	Thr	Lys	Arg	Phe	Ser
			20					25					30		
Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser	Ser	Asp	Asn	Gly	Thr	Thr	Ser	Pro
			35				40				45				
Val	Val	Lys	Ile	Pro	Lys	Pro	Ala	Ser	Val	Ala	Val	Glu	Glu	Val	Pro
			50			55				60					
Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser	Ser	Ala	Ser	Glu	Asn	Gly	Ala	Val
65					70					75				80	
Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Val	Ile	Lys	Tyr	Gln
				85				90						95	
Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys	Gln	Phe	Glu	Lys
			100					105					110		
Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser	Glu	Ala	Lys	Arg
			115				120					125			
Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser	Asn	Asp	Glu	Leu
			130				135					140			
Val	Val	Phe	Asp	Thr	Ser	Ile	Ile	Pro	Trp	Trp	Ala	Trp	Met	Lys	Arg
145					150					155				160	
Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu	Leu	Asn	Gly	Arg	Ala	Ala	Met	Ile
				165					170					175	
Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val	Asp	Ser	Leu	Thr	Gly	Val	Gly	Leu
			180				185					190			
Val	Asp	Gln	Met	Gly	Asn	Phe	Phe	Cys	Lys	Thr	Leu	Leu	Phe	Val	Ala
			195				200					205			
Val	Ala	Gly	Val	Leu	Phe	Ile	Arg	Lys	Asn	Glu	Asp	Leu	Asp	Lys	Leu
			210			215					220				
Lys	Asp	Leu	Phe	Asp	Glu	Thr	Thr	Leu	Tyr	Asp	Lys	Gln	Trp	Gln	Ala
225					230					235					240
Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser	Thr	Val	Ser	Ser	Lys	Lys		
				245					250						

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1498202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

aaaaaagttt	ctgagagatt	gattaaaata	tttatttgat	tacagatctg	ctctgctgct	60
atagaattgc	ggattctagt	gcaaatagaa	gggaagttgt	cggcgaaagg	tcacatttta	120
ttattgacaa	gatgattcaa	atggacggtg	gagataggct	gagagtgcg	ttattagatc	180
gaatgtcaac	ggtggagaat	ggccggagct	cagtgcacttt	agaagataatt	ctgatggctg	240
aaacgagcag	tttccgatct	cttactacgc	cgacaactcc	ggtgaggaat	cactctagta	300
gtagtttact	tgacgtgatg	agaagagagc	gtcgccgtga	taaaaccgct	tggaaatctc	360
tccgggata	gctcyktctt	aaacgcaccg	ctactggttg	gatctcgtct	aatcctatcc	420
ctaccttgga	taatcatatt	cttactccgg	ataacgata	ccaccgattt	aaccgccttg	480
gattcctcct	tactaactcg	gagacaaacc	ggagcagtcg	tgacgtcagc	gacgcagcag	540
aggaagtggc	ggagcgagaa	ggaaggctcc	ggctaggcac	cgtgttgccg	gcggagagag	600
aggaatgca	accaccgagg	atgtctctaa	tggagttggt	ggagccaccg	tctcaaccac	660
cgcccattaa	gcattctcgtc	aataagtttt	aattactttg	gtgatttgta	tgagcgagct	720
ctctttgcgc	tgctgactct	ctctatttat	ctctgcttct	tgcttgtaaa	taaaatgcgt	780
tctattgagc						

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met	Ile	Gln	Met	Asp	Gly	Gly	Asp	Arg	Leu	Arg	Val	Thr	Leu	Leu	Asp
1			5					10					15		
Arg	Met	Ser	Thr	Val	Glu	Asn	Gly	Arg	Ser	Ser	Val	Thr	Leu	Glu	Asp
			20					25					30		
Ile	Leu	Met	Ala	Glu	Thr	Ser	Ser	Phe	Arg	Ser	Leu	Thr	Thr	Pro	Thr
			35					40				45			
Thr	Pro	Val	Arg	Asn	His	Ser	Ser	Ser	Ser	Leu	Leu	Asp	Val	Met	Arg
			50				55				60				
Arg	Glu	Arg	Arg	Arg	Asp	Lys	Thr	Ala	Trp	Lys	Ser	Leu	Arg	Asp	Xaa
65					70					75				80	
Leu	Xaa	Leu	Lys	Arg	Thr	Ala	Thr	Gly	Trp	Ile	Ser	Ser	Asn	Pro	Ile
			85					90					95		
Pro	Thr	Leu	Asp	Asn	His	Ile	Leu	Thr	Pro	Asp	Asn	Asp	Ser	His	Arg
			100					105				110			
Phe	Asn	Arg	Leu	Gly	Phe	Leu	Leu	Thr	Asn	Ser	Glu	Thr	Asn	Arg	Ser
			115				120					125			
Ser	Arg	Asp	Val	Ser	Asp	Ala	Glu	Glu	Val	Ala	Glu	Arg	Glu	Gly	
			130				135				140				
Arg	Leu	Arg	Leu	Gly	Thr	Val	Leu	Ala	Ala	Glu	Arg	Glu	Glu	Met	Gln
145				150						155				160	
Pro	Pro	Arg	Met	Ser	Leu	Met	Glu	Leu	Leu	Glu	Pro	Pro	Ser	Gln	Pro
			165					170						175	
Pro	Pro	Ile	Lys	His	Leu	Val	Asn	Lys	Phe						
			180					185							

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```
Met Asp Gly Gly Asp Arg Leu Arg Val Thr Leu Leu Asp Arg Met Ser
1          5          10          15
Thr Val Glu Asn Gly Arg Ser Ser Val Thr Leu Glu Asp Ile Leu Met
          20          25          30
Ala Glu Thr Ser Ser Phe Arg Ser Leu Thr Thr Pro Thr Thr Pro Val
          35          40          45
Arg Asn His Ser Ser Ser Ser Leu Leu Asp Val Met Arg Arg Glu Arg
          50          55          60
Arg Arg Asp Lys Thr Ala Trp Lys Ser Leu Arg Asp Xaa Leu Xaa Leu
          65          70          75          80
Lys Arg Thr Ala Thr Gly Trp Ile Ser Ser Asn Pro Ile Pro Thr Leu
          85          90          95
Asp Asn His Ile Leu Thr Pro Asp Asn Asp Ser His Arg Phe Asn Arg
          100         105         110
Leu Gly Phe Leu Leu Thr Asn Ser Glu Thr Asn Arg Ser Ser Arg Asp
          115         120         125
Val Ser Asp Ala Ala Glu Glu Val Ala Glu Arg Glu Gly Arg Leu Arg
          130         135         140
Leu Gly Thr Val Leu Ala Ala Glu Arg Glu Glu Met Gln Pro Pro Arg
          145         150         155         160
Met Ser Leu Met Glu Leu Leu Glu Pro Pro Ser Gln Pro Pro Pro Ile
          165         170         175
Lys His Leu Val Asn Lys Phe
          180
```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1498205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```
Met Ser Thr Val Glu Asn Gly Arg Ser Ser Val Thr Leu Glu Asp Ile
1          5          10          15
Leu Met Ala Glu Thr Ser Ser Phe Arg Ser Leu Thr Thr Pro Thr Thr
          20          25          30
Pro Val Arg Asn His Ser Ser Ser Ser Leu Leu Asp Val Met Arg Arg
          35          40          45
Glu Arg Arg Arg Asp Lys Thr Ala Trp Lys Ser Leu Arg Asp Xaa Leu
          50          55          60
Xaa Leu Lys Arg Thr Ala Thr Gly Trp Ile Ser Ser Asn Pro Ile Pro
          65          70          75          80
Thr Leu Asp Asn His Ile Leu Thr Pro Asp Asn Asp Ser His Arg Phe
          85          90          95
Asn Arg Leu Gly Phe Leu Leu Thr Asn Ser Glu Thr Asn Arg Ser Ser
          100         105         110
Arg Asp Val Ser Asp Ala Ala Glu Val Ala Glu Arg Glu Gly Arg
          115         120         125
Leu Arg Leu Gly Thr Val Leu Ala Ala Glu Arg Glu Glu Met Gln Pro
          130         135         140
Pro Arg Met Ser Leu Met Glu Leu Leu Glu Pro Pro Ser Gln Pro Pro
          145         150         155         160
Pro Ile Lys His Leu Val Asn Lys Phe
          165
```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1609
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```
ccatagtacc agttctgaaa tctcactttc acagtttgtg tctgtgcgat aatggccatg      60
gcagagctct caacccccaa aacgacgtcg ctttttctca actcttcgtc tcggcttcgt      120
ctctcttcaa aattgcacct ttcaaaccac ttctgccatc ttcttcttcc acctctccac      180
acaacaactc ccaactccaa aatctcttgc tccgtttctc aaaatagcca agctcctggt      240
gctgtgcaag aaaatggatt ggtgaagacg aagaaagagt gttatggagt gttctgcctc      300
acctatgata ttaaagctga agaagagaca agatcatgga agaagttaat taatattgca      360
gtttcagggt ctgcaggaat gatttctaac catcttctct tcaaacttgc ttcaggggaa      420
gtatttggtc cagatcaacc cattgcattg aaactgctag gatcagagag atcaattcaa      480
gctcttgaa ggtgtgcaat ggaactggag gattcattgt tcccattggt gagagaagtt      540
gatataggaa cagatccaaa tgaagtgttc caagatgtgg agtgggctat tctgattgga      600
gcaaaacctc gagggccttg aatggaacgt gctgacttgt tggacatcaa tggccaaatc      660
tttgctgagc agggcaaagc tctgaacaaa gctgcctctc ctaacgtcaa ggttcttgta      720
gtgggaaacc cttgcaacac caatgccttg atttgtctta aaaatgctcc caacattcct      780
gcaaagaact tccatgccct cagcagggtta gacgaaaatc gtgccaaatg ccagcttgct      840
cttaaagccg gtgttttcta tgacaaagtg tctaatatga ccatatgggg aaatcactcc      900
acgactcagg tgccagactt cttaaagtgc agaattaatg gcctgcctgt gaaggaggtt      960
attacagatc acaaagtgtt agaagaggga ttcactgaga gtgtgcagaa gagagggtgg      1020
ttattaattc agaaatgggg tcgatcttct gctgcttcta ctgctgtttc cattgttgat      1080
gctataaagt ctcttgtrac tctactcctt gaggktgatt ggttttcgac tgggggtgtac      1140
acggatggaa atccttatgg tattgaagag ggccttgtct tcagtatgcc atgccggtcg      1200
aaggagatg gagattatga acttgtcaag gatgtagaaa ttgatgacta ccttcgccaa      1260
cgaatcgcca agtcggaagc ggaactgttg gctgagaaga gatgtgttgc acacctcact      1320
ggagagggca ttgcctactg tgatcttggg ccggtagata ctatgcttcc tgggggaagt      1380
tgatttttgc aggacgttga acatctcaag taagcattct cttccgggtt gttagctgta      1440
cagagcacag ccacattact tatgatgatt gttcagaata agaaaatgaa actcttattt      1500
cttatttaca tgcactctga tgtatttttt cttgagcaat gctccaaaag tcatatacag      1560
tagtatttgt aaacacttga aacgtttcta tgctttattc cagtttccag
```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
Met Ala Met Ala Glu Leu Ser Thr Pro Lys Thr Thr Ser Pro Phe Leu
1          5          10          15
Asn Ser Ser Ser Arg Leu Arg Leu Ser Ser Lys Leu His Leu Ser Asn
20          25          30
His Phe Arg His Leu Leu Leu Pro Pro Leu His Thr Thr Thr Pro Asn
35          40          45
Ser Lys Ile Ser Cys Ser Val Ser Gln Asn Ser Gln Ala Pro Val Ala
50          55          60
Val Gln Glu Asn Gly Leu Val Lys Thr Lys Lys Glu Cys Tyr Gly Val
65          70          75          80
```

Phe	Cys	Leu	Thr	Tyr	Asp	Leu	Lys	Ala	Glu	Glu	Glu	Thr	Arg	Ser	Trp
				85					90					95	
Lys	Lys	Leu	Ile	Asn	Ile	Ala	Val	Ser	Gly	Ala	Ala	Gly	Met	Ile	Ser
			100					105					110		
Asn	His	Leu	Leu	Phe	Lys	Leu	Ala	Ser	Gly	Glu	Val	Phe	Gly	Pro	Asp
			115				120					125			
Gln	Pro	Ile	Ala	Leu	Lys	Leu	Leu	Gly	Ser	Glu	Arg	Ser	Ile	Gln	Ala
			130				135					140			
Leu	Glu	Gly	Val	Ala	Met	Glu	Leu	Glu	Asp	Ser	Leu	Phe	Pro	Leu	Leu
			145		150					155					160
Arg	Glu	Val	Asp	Ile	Gly	Thr	Asp	Pro	Asn	Glu	Val	Phe	Gln	Asp	Val
			165						170					175	
Glu	Trp	Ala	Ile	Leu	Ile	Gly	Ala	Lys	Pro	Arg	Gly	Pro	Gly	Met	Glu
			180					185						190	
Arg	Ala	Asp	Leu	Leu	Asp	Ile	Asn	Gly	Gln	Ile	Phe	Ala	Glu	Gln	Gly
			195				200					205			
Lys	Ala	Leu	Asn	Lys	Ala	Ala	Ser	Pro	Asn	Val	Lys	Val	Leu	Val	Val
			210			215					220				
Gly	Asn	Pro	Cys	Asn	Thr	Asn	Ala	Leu	Ile	Cys	Leu	Lys	Asn	Ala	Pro
			225		230					235					240
Asn	Ile	Pro	Ala	Lys	Asn	Phe	His	Ala	Leu	Thr	Arg	Leu	Asp	Glu	Asn
			245					250						255	
Arg	Ala	Lys	Cys	Gln	Leu	Ala	Leu	Lys	Ala	Gly	Val	Phe	Tyr	Asp	Lys
			260				265						270		
Val	Ser	Asn	Met	Thr	Ile	Trp	Gly	Asn	His	Ser	Thr	Thr	Gln	Val	Pro
			275				280						285		
Asp	Phe	Leu	Asn	Ala	Arg	Ile	Asn	Gly	Leu	Pro	Val	Lys	Glu	Val	Ile
			290		295						300				
Thr	Asp	His	Lys	Trp	Leu	Glu	Glu	Gly	Phe	Thr	Glu	Ser	Val	Gln	Lys
			305		310					315					320
Arg	Gly	Gly	Leu	Leu	Ile	Gln	Lys	Trp	Gly	Arg	Ser	Ser	Ala	Ala	Ser
			325					330						335	
Thr	Ala	Val	Ser	Ile	Val	Asp	Ala	Ile	Lys	Ser	Leu	Xaa	Thr	Pro	Thr
			340				345						350		
Pro	Glu	Xaa	Asp	Trp	Phe	Ser	Thr	Gly	Val	Tyr	Thr	Asp	Gly	Asn	Pro
			355				360					365			
Tyr	Gly	Ile	Glu	Glu	Gly	Leu	Val	Phe	Ser	Met	Pro	Cys	Arg	Ser	Lys
			370			375					380				
Gly	Asp	Gly	Asp	Tyr	Glu	Leu	Val	Lys	Asp	Val	Glu	Ile	Asp	Asp	Tyr
			385		390					395					400
Leu	Arg	Gln	Arg	Ile	Ala	Lys	Ser	Glu	Ala	Glu	Leu	Leu	Ala	Glu	Lys
			405						410					415	
Arg	Cys	Val	Ala	His	Leu	Thr	Gly	Glu	Gly	Ile	Ala	Tyr	Cys	Asp	Leu
			420					425					430		
Gly	Pro	Val	Asp	Thr	Met	Leu	Pro	Gly	Glu	Val					
			435				440								

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..441
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met	Ala	Glu	Leu	Ser	Thr	Pro	Lys	Thr	Thr	Ser	Pro	Phe	Leu	Asn	Ser
1				5				10						15	
Ser	Ser	Arg	Leu	Arg	Leu	Ser	Ser	Lys	Leu	His	Leu	Ser	Asn	His	Phe

(ix) FEATURE:



(A) NAME/KEY: peptide

(B) LOCATION: 1..334

(D) OTHER INFORMATION: / Ceres Seq. ID 1498209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met	Ile	Ser	Asn	His	Leu	Leu	Phe	Lys	Leu	Ala	Ser	Gly	Glu	Val	Phe
1				5					10					15	
Gly	Pro	Asp	Gln	Pro	Ile	Ala	Leu	Lys	Leu	Leu	Gly	Ser	Glu	Arg	Ser
			20					25					30		
Ile	Gln	Ala	Leu	Glu	Gly	Val	Ala	Met	Glu	Leu	Glu	Asp	Ser	Leu	Phe
		35					40					45			
Pro	Leu	Leu	Arg	Glu	Val	Asp	Ile	Gly	Thr	Asp	Pro	Asn	Glu	Val	Phe
	50						55				60				
Gln	Asp	Val	Glu	Trp	Ala	Ile	Leu	Ile	Gly	Ala	Lys	Pro	Arg	Gly	Pro
65					70				75					80	
Gly	Met	Glu	Arg	Ala	Asp	Leu	Leu	Asp	Ile	Asn	Gly	Gln	Ile	Phe	Ala
				85					90					95	
Glu	Gln	Gly	Lys	Ala	Leu	Asn	Lys	Ala	Ala	Ser	Pro	Asn	Val	Lys	Val
			100					105					110		
Leu	Val	Val	Gly	Asn	Pro	Cys	Asn	Thr	Asn	Ala	Leu	Ile	Cys	Leu	Lys
	115						120					125			
Asn	Ala	Pro	Asn	Ile	Pro	Ala	Lys	Asn	Phe	His	Ala	Leu	Thr	Arg	Leu
	130					135					140				
Asp	Glu	Asn	Arg	Ala	Lys	Cys	Gln	Leu	Ala	Leu	Lys	Ala	Gly	Val	Phe
145					150				155					160	
Tyr	Asp	Lys	Val	Ser	Asn	Met	Thr	Ile	Trp	Gly	Asn	His	Ser	Thr	Thr
			165						170					175	
Gln	Val	Pro	Asp	Phe	Leu	Asn	Ala	Arg	Ile	Asn	Gly	Leu	Pro	Val	Lys
			180					185					190		
Glu	Val	Ile	Thr	Asp	His	Lys	Trp	Leu	Glu	Glu	Gly	Phe	Thr	Glu	Ser
	195						200					205			
Val	Gln	Lys	Arg	Gly	Gly	Leu	Leu	Ile	Gln	Lys	Trp	Gly	Arg	Ser	Ser
	210					215					220				
Ala	Ala	Ser	Thr	Ala	Val	Ser	Ile	Val	Asp	Ala	Ile	Lys	Ser	Leu	Xaa
225					230				235					240	
Thr	Pro	Thr	Pro	Glu	Xaa	Asp	Trp	Phe	Ser	Thr	Gly	Val	Tyr	Thr	Asp
			245					250					255		
Gly	Asn	Pro	Tyr	Gly	Ile	Glu	Glu	Gly	Leu	Val	Phe	Ser	Met	Pro	Cys
	260					265						270			
Arg	Ser	Lys	Gly	Asp	Gly	Asp	Tyr	Glu	Leu	Val	Lys	Asp	Val	Glu	Ile
	275					280						285			
Asp	Asp	Tyr	Leu	Arg	Gln	Arg	Ile	Ala	Lys	Ser	Glu	Ala	Glu	Leu	Leu
	290					295					300				
Ala	Glu	Lys	Arg	Cys	Val	Ala	His	Leu	Thr	Gly	Glu	Gly	Ile	Ala	Tyr
305					310				315					320	
Cys	Asp	Leu	Gly	Pro	Val	Asp	Thr	Met	Leu	Pro	Gly	Glu	Val		
			325					330							

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1500 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1500

(D) OTHER INFORMATION: / Ceres Seq. ID 1498210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

atctcttggt	ctctccgcc	atctctgctc	tcttttat	ttccagaaag	tttttttt	60
tttcccgaa	tccgttaat	tcattgggg	ttccattga	agcaatggc	acggctttc	120
ctcccacta	gctcactgc	acggttcct	tgcatggat	ccatgaga	cgtctcttc	180

tcccgatccg	attggctcct	ccttcttctt	tcctcggatc	cacccgttcc	ctctcccttc	240
gcagactcaa	tcactccaac	gccacccgtc	gatctcccgt	cgctctctgtc	caggaagttg	300
tcaaggagaa	gcaatccacc	aataatacca	gcctgttgat	aaccaaagag	gaaggattgg	360
agttgtatga	agatatgata	ctaggtagat	ctttcgaaga	catgtgtgct	caaagtatt	420
accgaggcaa	gatgtttggt	tttgttctact	tgtacaatgg	ccaagaggct	gtttctactg	480
gctttatcaa	gctccttacc	aagtctgact	ctgtcgttag	tacctaccgt	gaccatgtcc	540
atgccctcag	caaaggtgtc	tctgctcgtg	ctgttatgag	cgagctcttc	ggcaagggtta	600
ctggatgctg	cagaggccaa	ggtggatcca	tgcacatgtt	ctccaaagaa	cacaacatgc	660
ttggtggctt	tgtcttttatt	ggtgaaggca	ttcctgtcgc	cactggtgct	gccttttagct	720
ccaagtacag	gaggggaagtc	ttgaaacagg	attgtgatga	tgtcactgtc	gccttttttcg	780
gagatggaac	ttgtaacaac	ggacagttct	tcgagtgtct	caacatggct	gctctctata	840
aactgcctat	tatctttgtt	gtcgagaata	acttgtgggc	cattgggatg	tctcacttga	900
gagccacttc	tgaccccgag	atttgggaaga	aaggtcctgc	atttgggatg	cctggtgttc	960
atgttgacgg	tatggatgtc	ttgaaggtca	gggaagtcgc	taaagaggct	gtcactagag	1020
ctagaagagg	agaaggtcca	accttggttg	aatgtgagac	ttatagattt	agaggacact	1080
ccttggtctga	tcccgatgag	ctccgtgatg	ctgctgagaa	agccaaatac	gcggctagag	1140
acccaatcgc	agcattgaag	aagtatttga	tagagaacaa	gcttgcaaag	gaagcagagc	1200
taaagtcaat	agagaaaaag	atagacgagt	tgggtggagga	agcggttgag	tttgacagacg	1260
ctagtccaca	gccccgtcgc	agtcagttgc	tagagaatgt	gtttgctgat	ccaaaaggat	1320
ttggaattgg	acctgatgga	cggtagacat	gtgaggacc	caagtttacc	gaaggcacag	1380
ctcaagtctg	agaagacaag	tttaaccata	atctgtctac	tgtctcttcg	atgtattcta	1440
tatatcttat	taagttaaatt	gctacagaga	atcagtttga	atcatttgca	ctttttgctg	1500

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1498211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Leu	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ala	Leu	Phe	Tyr	Phe	Pro	Arg	Lys
1			5					10					15		
Phe	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu	Gly	Phe	Pro	Leu
			20					25					30		
Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val
		35				40						45			
Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu
	50				55						60				
Ala	Pro	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg
65					70					75				80	
Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val
			85					90						95	
Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu
		100					105					110			
Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly
		115				120						125			
Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met
	130				135						140				
Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly
145					150					155				160	
Phe	Ile	Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	Ser	Thr	Tyr	Arg
			165					170						175	
Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala	Arg	Ala	Val	Met
		180					185					190			
Ser	Glu	Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg	Gly	Gln	Gly	Gly
		195				200						205			

```

Ser Met His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala
  210                      215                      220
Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser
  225                      230                      235                      240
Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val
                      245                      250                      255
Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys
                      260                      265                      270
Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu
  275                      280                      285
Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp
  290                      295                      300
Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His
  305                      310                      315                      320
Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala
                      325                      330                      335
Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu
                      340                      345                      350
Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg
  355                      360                      365
Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala
  370                      375                      380
Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu
  385                      390                      395                      400
Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu
                      405                      410                      415
Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn
                      420                      425                      430
Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr
  435                      440                      445
Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val
  450                      455                      460

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1498212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Ala Thr Ala Phe Ala Pro Thr Lys Leu Thr Ala Thr Val Pro Leu
  1                      5                      10                      15
His Gly Ser His Glu Asn Arg Leu Leu Leu Pro Ile Arg Leu Ala Pro
  20                      25                      30
Pro Ser Ser Phe Leu Gly Ser Thr Arg Ser Leu Ser Leu Arg Arg Leu
  35                      40                      45
Asn His Ser Asn Ala Thr Arg Arg Ser Pro Val Val Ser Val Gln Glu
  50                      55                      60
Val Val Lys Glu Lys Gln Ser Thr Asn Asn Thr Ser Leu Leu Ile Thr
  65                      70                      75                      80
Lys Glu Glu Gly Leu Glu Leu Tyr Glu Asp Met Ile Leu Gly Arg Ser
                      85                      90                      95
Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr Arg Gly Lys Met Phe Gly
                      100                      105                      110
Phe Val His Leu Tyr Asn Gly Gln Glu Ala Val Ser Thr Gly Phe Ile
                      115                      120                      125
Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His

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130	135	140
Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met Ser Glu		
145	150	155
Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly Ser Met		
165	170	175
His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala Phe Ile		
180	185	190
Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser Lys Tyr		
195	200	205
Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val Ala Phe		
210	215	220
Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys Leu Asn		
225	230	235
Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu Asn Asn		
245	250	255
Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp Pro Glu		
260	265	270
Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His Val Asp		
275	280	285
Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala Val Thr		
290	295	300
Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu Thr Tyr		
305	310	315
Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg Asp Ala		
325	330	335
Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala Leu Lys		
340	345	350
Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu Lys Ser		
355	360	365
Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu Phe Ala		
370	375	380
Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn Val Phe		
385	390	395
Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr Arg Cys		
405	410	415
Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val		
420	425	

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr		
1	5	10
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala		
20	25	30
Val Ser Thr Gly Phe Ile Lys Leu Thr Lys Ser Asp Ser Val Val		
35	40	45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala		
50	55	60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg		
65	70	75
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu		
85	90	95

(2) INFORMATION FOR SEQ ID NO:280:

(A) LENGTH: 1126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1126

(D) OTHER INFORMATION: / Ceres Seq. ID 1498214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

aaaaataattt	gaaaggaata	tgaatatctc	gttgaagaag	acttgctcct	gaaatccttt	60
ggaccgaaac	tcgtaaaatt	atttcctctc	aatttctctg	aaatctattc	accgtctcct	120
ttgtctcctc	ctocaaatcg	atcggtcctc	gtcgtcgtct	gattttctct	acgattgctt	180
tttctgtcta	gctcgataag	aaaaaacaaa	actaattttt	gaagagtttt	tttttttggg	240
tttgggagcg	atgggtcaag	cttttcgtaa	gctattcgat	actttctctg	gcaatcaaga	300
aatgaggggc	gttatgcttg	ggctggatgc	tgctggcaaa	tcaactattc	tcatacagct	360
tcataattggg	gaagttttgt	ctactgttcc	caccattgga	atcaatgttg	agaaagtcca	420
gtacaagaat	gtgatgttca	cagtttggga	tgttggtggc	caagagaaac	tgagacctct	480
ttggaggcat	tacttcaata	atactgatgg	acttatatac	gtgggtggatt	ccttagatcg	540
agagaggatc	gggaaagcaa	agcaagaatt	tcaggagatc	ataaaagacc	cattcatgct	600
aaacagtatc	attctggtgt	ttgcaaacaa	acaggacatg	agaggagcca	tgtcaccgag	660
agaagtatgt	gaagggttag	gcttatttga	tctcaagaac	aggaaatggc	acatacaagg	720
tacttgctgt	cttcgtggag	acgggcttta	tgaaggcttg	gactggttat	catctactct	780
taaggatggt	aaagccgctg	gattcacatc	ggttggccac	tcgttttaaa	tcttcacggt	840
atactttgat	atcaatggcc	agtgtcttct	tcttggtctt	atcacgaaat	cagaatctct	900
gaagactttt	tttgtttaagg	aaagaatgat	cttctcattg	tggcaatatt	agactccatt	960
agactatttt	tgaatttttg	tcatgctgcc	atgaaagctt	ctttgtatat	tctgctgatg	1020

aagagttgta tcatctgaaa aaccttctct ttgggggtcat ctttgtccga ttaagacttt 1080  
ggtagatgta tatacattcc ttcgaaatca tgatatattt ttttat

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1498215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met	Gly	Gln	Ala	Phe	Arg	Lys	Leu	Phe	Asp	Thr	Phe	Phe	Gly	Asn	Gln
1			5						10					15	
Glu	Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr
			20					25					30		
Ile	Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr
		35					40					45			
Ile	Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr
	50					55				60					
Val	Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Pro	Leu	Trp	Arg	His
65					70				75					80	
Tyr	Phe	Asn	Asn	Thr	Asp	Gly	Leu	Ile	Tyr	Val	Val	Asp	Ser	Leu	Asp
				85					90				95		
Arg	Glu	Arg	Ile	Gly	Lys	Ala	Lys	Gln	Glu	Phe	Gln	Glu	Ile	Ile	Lys
			100					105				110			
Asp	Pro	Phe	Met	Leu	Asn	Ser	Ile	Ile	Leu	Val	Phe	Ala	Asn	Lys	Gln
		115					120					125			
Asp	Met	Arg	Gly	Ala	Met	Ser	Pro	Arg	Glu	Val	Cys	Glu	Gly	Leu	Gly
	130					135					140				
Leu	Phe	Asp	Leu	Lys	Asn	Arg	Lys	Trp	His	Ile	Gln	Gly	Thr	Cys	Ala
145					150					155				160	
Leu	Arg	Gly	Asp	Gly	Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Ser	Thr
			165					170					175		
Leu	Lys	Asp	Val	Lys	Ala	Ala	Gly	Phe	Thr	Ser	Val	Gly	His	Ser	Phe
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile
1			5						10					15	
Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile
			20					25				30			
Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val
		35					40					45			
Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Pro	Leu	Trp	Arg	His	Tyr
	50					55					60				
Phe	Asn	Asn	Thr	Asp	Gly	Leu	Ile	Tyr	Val	Val	Asp	Ser	Leu	Asp	Arg

65					70					75					80
Glu	Arg	Ile	Gly	Lys	Ala	Lys	Gln	Glu	Phe	Gln	Glu	Ile	Ile	Lys	Asp
				85					90					95	
Pro	Phe	Met	Leu	Asn	Ser	Ile	Ile	Leu	Val	Phe	Ala	Asn	Lys	Gln	Asp
				100				105					110		
Met	Arg	Gly	Ala	Met	Ser	Pro	Arg	Glu	Val	Cys	Glu	Gly	Leu	Gly	Leu
		115					120				125				
Phe	Asp	Leu	Lys	Asn	Arg	Lys	Trp	His	Ile	Gln	Gly	Thr	Cys	Ala	Leu
	130					135				140					
Arg	Gly	Asp	Gly	Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Ser	Thr	Leu
145					150					155					160
Lys	Asp	Val	Lys	Ala	Gly	Phe	Thr	Ser	Val	Gly	His	Ser	Phe		
			165				170						175		

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile	Leu	Tyr	Lys	Leu
1				5				10					15		
His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile	Gly	Phe	Asn	Val
		20						25					30		
Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val	Trp	Asp	Val	Gly
		35				40					45				
Gly	Gln	Glu	Lys	Leu	Arg	Pro	Leu	Trp	Arg	His	Tyr	Phe	Asn	Asn	Thr
	50					55				60					
Asp	Gly	Leu	Ile	Tyr	Val	Val	Asp	Ser	Leu	Asp	Arg	Glu	Arg	Ile	Gly
65					70				75					80	
Lys	Ala	Lys	Gln	Glu	Phe	Gln	Glu	Ile	Ile	Lys	Asp	Pro	Phe	Met	Leu
			85						90					95	
Asn	Ser	Ile	Ile	Leu	Val	Phe	Ala	Asn	Lys	Gln	Asp	Met	Arg	Gly	Ala
		100						105					110		
Met	Ser	Pro	Arg	Glu	Val	Cys	Glu	Gly	Leu	Gly	Leu	Phe	Asp	Leu	Lys
		115					120					125			
Asn	Arg	Lys	Trp	His	Ile	Gln	Gly	Thr	Cys	Ala	Leu	Arg	Gly	Asp	Gly
	130					135				140					
Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Ser	Thr	Leu	Lys	Asp	Val	Lys
145					150					155					160
Ala	Ala	Gly	Phe	Thr	Ser	Val	Gly	His	Ser	Phe					
			165				170								

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1056
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

aaaaaaaaa accaaagcaa aaaaatggct ttgaaactca cttctccgcc ttcagttttc  
tcacaatcaa ggagattatc ttctttcttcg ttaattccga taagggtcaaa atccacattc

60  
120

accggatttc gatcgagaac cgggtgtttat ttaagcaaaa cgacggcgct tcagtcgtct	180
acaaaactga gtgtggcggc ggagagtcct gcggcgacaa ttgcgacgga tgattggggg	240
aaagtatcgg cggttctgtt tgatatggac ggtgtgcttt gtaacagtga agatctttct	300
agacgcgcg ccgtggatgt ttttacggag atgggagttg aagtcactgt ggacgatttc	360
gttcctttta tgggaacagg tgaagccaag tttttaggag gtgttgcttc agtcaaagaa	420
gttaaaggat ttgatccaga tgcagctaaa aagagattct ttgaaatata tctcgataag	480
tatgcgaagc cagaatctgg gattggattt ccaggagcat tggagcttgt tactgagtgt	540
aagaacaaag gccttaaagt cgctgttgca tctagtgtcg accgtatcaa agttgatgcg	600
aatctgaaag ctgctggttt gtctttgacc atgtttgatg ccattgtttc agcagatgcc	660
tttgagaatt tgaaaccagc tccagatatt ttcttggtcg ctgcaaagat cttaggtgtg	720
cctaccagcg agtgtgttgt tattgaagat gcgcttgctg gagtccaagc cgcacaagct	780
gcgaacatga gatgtatagc cgtaaaaact actttatctg aagcaattct taaggatgct	840
ggtccttcaa tgatacgaga cgatattgga aacatctcaa tcaatgacat tctcactggt	900
ggctcagatt ctaccagtat gtagtctcaa agaaattcga tggaaaatat cgttcttttc	960
atgtgtattt tatttcttgt ttactccttt tgaaaacttt tgaataaagg ggctttcttt	1020
gtaacgagat tacacattta aaacaatctt ttctgt	

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Lys	Lys	Lys	Asn	Gln	Ser	Lys	Lys	Met	Ala	Leu	Lys	Leu	Thr	Ser	Pro
1			5					10						15	
Pro	Ser	Val	Phe	Ser	Gln	Ser	Arg	Arg	Leu	Ser	Ser	Ser	Ser	Leu	Ile
			20					25					30		
Pro	Ile	Arg	Ser	Lys	Ser	Thr	Phe	Thr	Gly	Phe	Arg	Ser	Arg	Thr	Gly
			35				40					45			
Val	Tyr	Leu	Ser	Lys	Thr	Thr	Ala	Leu	Gln	Ser	Ser	Thr	Lys	Leu	Ser
			50				55				60				
Val	Ala	Ala	Glu	Ser	Pro	Ala	Ala	Thr	Ile	Ala	Thr	Asp	Asp	Trp	Gly
65					70					75				80	
Lys	Val	Ser	Ala	Val	Leu	Phe	Asp	Met	Asp	Gly	Val	Leu	Cys	Asn	Ser
				85				90						95	
Glu	Asp	Leu	Ser	Arg	Arg	Ala	Ala	Val	Asp	Val	Phe	Thr	Glu	Met	Gly
			100					105					110		
Val	Glu	Val	Thr	Val	Asp	Asp	Phe	Val	Pro	Phe	Met	Gly	Thr	Gly	Glu
			115				120					125			
Ala	Lys	Phe	Leu	Gly	Gly	Val	Ala	Ser	Val	Lys	Glu	Val	Lys	Gly	Phe
			130				135					140			
Asp	Pro	Asp	Ala	Ala	Lys	Lys	Arg	Phe	Phe	Glu	Ile	Tyr	Leu	Asp	Lys
145					150					155				160	
Tyr	Ala	Lys	Pro	Glu	Ser	Gly	Ile	Gly	Phe	Pro	Gly	Ala	Leu	Glu	Leu
			165					170						175	
Val	Thr	Glu	Cys	Lys	Asn	Lys	Gly	Leu	Lys	Val	Ala	Val	Ala	Ser	Ser
			180					185					190		
Ala	Asp	Arg	Ile	Lys	Val	Asp	Ala	Asn	Leu	Lys	Ala	Ala	Gly	Leu	Ser
			195				200						205		
Leu	Thr	Met	Phe	Asp	Ala	Ile	Val	Ser	Ala	Asp	Ala	Phe	Glu	Asn	Leu
			210				215					220			
Lys	Pro	Ala	Pro	Asp	Ile	Phe	Leu	Ala	Ala	Ala	Lys	Ile	Leu	Gly	Val
225					230					235				240	
Pro	Thr	Ser	Glu	Cys	Val	Val	Ile	Glu	Asp	Ala	Leu	Ala	Gly	Val	Gln
			245					250						255	
Ala	Ala	Gln	Ala	Ala	Asn	Met	Arg	Cys	Ile	Ala	Val	Lys	Thr	Thr	Leu



260 265 270  
Ser Glu Ala Ile Leu Lys Asp Ala Gly Pro Ser Met Ile Arg Asp Asp  
275 280 285  
Ile Gly Asn Ile Ser Ile Asn Asp Ile Leu Thr Gly Gly Ser Asp Ser  
290 295 300  
Thr Ser Met  
305

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..299

(D) OTHER INFORMATION: / Ceres Seq. ID 1498220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Ala Leu Lys Leu Thr Ser Pro Pro Ser Val Phe Ser Gln Ser Arg  
1 5 10 15  
Arg Leu Ser Ser Ser Ser Leu Ile Pro Ile Arg Ser Lys Ser Thr Phe  
20 25 30  
Thr Gly Phe Arg Ser Arg Thr Gly Val Tyr Leu Ser Lys Thr Thr Ala  
35 40 45  
Leu Gln Ser Ser Thr Lys Leu Ser Val Ala Ala Glu Ser Pro Ala Ala  
50 55 60  
Thr Ile Ala Thr Asp Asp Trp Gly Lys Val Ser Ala Val Leu Phe Asp  
65 70 75 80  
Met Asp Gly Val Leu Cys Asn Ser Glu Asp Leu Ser Arg Arg Ala Ala  
85 90 95  
Val Asp Val Phe Thr Glu Met Gly Val Glu Val Thr Val Asp Asp Phe  
100 105 110  
Val Pro Phe Met Gly Thr Gly Glu Ala Lys Phe Leu Gly Gly Val Ala  
115 120 125  
Ser Val Lys Glu Val Lys Gly Phe Asp Pro Asp Ala Ala Lys Lys Arg  
130 135 140  
Phe Phe Glu Ile Tyr Leu Asp Lys Tyr Ala Lys Pro Glu Ser Gly Ile  
145 150 155 160  
Gly Phe Pro Gly Ala Leu Glu Leu Val Thr Glu Cys Lys Asn Lys Gly  
165 170 175  
Leu Lys Val Ala Val Ala Ser Ser Ala Asp Arg Ile Lys Val Asp Ala  
180 185 190  
Asn Leu Lys Ala Ala Gly Leu Ser Leu Thr Met Phe Asp Ala Ile Val  
195 200 205  
Ser Ala Asp Ala Phe Glu Asn Leu Lys Pro Ala Pro Asp Ile Phe Leu  
210 215 220  
Ala Ala Ala Lys Ile Leu Gly Val Pro Thr Ser Glu Cys Val Val Ile  
225 230 235 240  
Glu Asp Ala Leu Ala Gly Val Gln Ala Ala Gln Ala Ala Asn Met Arg  
245 250 255  
Cys Ile Ala Val Lys Thr Thr Leu Ser Glu Ala Ile Leu Lys Asp Ala  
260 265 270  
Gly Pro Ser Met Ile Arg Asp Asp Ile Gly Asn Ile Ser Ile Asn Asp  
275 280 285  
Ile Leu Thr Gly Gly Ser Asp Ser Thr Ser Met  
290 295

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..219  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498221  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
Met Asp Gly Val Leu Cys Asn Ser Glu Asp Leu Ser Arg Arg Ala Ala
1          5          10          15
Val Asp Val Phe Thr Glu Met Gly Val Glu Val Thr Val Asp Asp Phe
20          25          30
Val Pro Phe Met Gly Thr Gly Glu Ala Lys Phe Leu Gly Gly Val Ala
35          40          45
Ser Val Lys Glu Val Lys Gly Phe Asp Pro Asp Ala Ala Lys Lys Arg
50          55          60
Phe Phe Glu Ile Tyr Leu Asp Lys Tyr Ala Lys Pro Glu Ser Gly Ile
65          70          75          80
Gly Phe Pro Gly Ala Leu Glu Leu Val Thr Glu Cys Lys Asn Lys Gly
85          90          95
Leu Lys Val Ala Val Ala Ser Ser Ala Asp Arg Ile Lys Val Asp Ala
100         105         110
Asn Leu Lys Ala Ala Gly Leu Ser Leu Thr Met Phe Asp Ala Ile Val
115         120         125
Ser Ala Asp Ala Phe Glu Asn Leu Lys Pro Ala Pro Asp Ile Phe Leu
130         135         140
Ala Ala Ala Lys Ile Leu Gly Val Pro Thr Ser Glu Cys Val Val Ile
145         150         155         160
Glu Asp Ala Leu Ala Gly Val Gln Ala Ala Gln Ala Ala Asn Met Arg
165         170         175
Cys Ile Ala Val Lys Thr Thr Leu Ser Glu Ala Ile Leu Lys Asp Ala
180         185         190
Gly Pro Ser Met Ile Arg Asp Asp Ile Gly Asn Ile Ser Ile Asn Asp
195         200         205
Ile Leu Thr Gly Gly Ser Asp Ser Thr Ser Met
210         215
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..643  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
aaaaaaaaatca aacccaccat tcaaacaaaa cacaaaaaaca aaaaaaaaaa catttcccca      60
aaaaaaaaaaaa aacagaggat gaaacaaaac cagagcaagt ttttgagaat aatctcaacg      120
cctctaagag ctttaggcaa ggcacgtgat ttctacgtga gaagcatcac cggttgcgca      180
gctcggactc aatattcctc ctccgcctcc gtctccgctc cttttccaag aagccggagc      240
tcctcctccg ccgccttctc ctccctccgca tcatcccgga gaaccaccga ttctgggata      300
gatgaagatt acagcgagct agtgagagct gcgtcgggtga ggagtttagg gcacaagaat      360
gagatagaca tgttgataca agagaagctg caacagcaga agcaacagaa gcaaggaggg      420
ttgcctaaga gctcagatgc tgggatggcg aggatagagg aagaggaaga aacagaggaa      480
ggatctgtga atccgaaggt gaagaagact aagaaagtct ctgatctttt gtatcctcgt      540
agcaaattctt acgccgttac tactagtacc cctatcttgt aacttctctt cttatttttt      600
cttctttctta attttagtat tttgtggatt gattatcatt ttc
```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..193
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Lys Lys Ile Lys Pro Thr Ile Gln Thr Lys His Lys Asn Lys Lys Lys  
1 5 10 15  
Asn Ile Ser Pro Lys Lys Lys Lys Gln Arg Met Lys Gln Asn Gln Ser  
20 25 30  
Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu Arg Ala Leu Gly Lys Ala  
35 40 45  
Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly Cys Ala Ala Arg Thr Gln  
50 55 60  
Tyr Ser Ser Ser Ala Ser Val Ser Ala Pro Phe Pro Arg Ser Arg Ser  
65 70 75 80  
Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala Ser Ser Arg Arg Thr Thr  
85 90 95  
Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu Leu Val Arg Ala Ala Ser  
100 105 110  
Val Arg Ser Leu Gly His Lys Asn Glu Ile Asp Met Leu Ile Gln Glu  
115 120 125  
Lys Leu Gln Gln Gln Lys Gln Gln Lys Gln Gly Gly Leu Pro Lys Ser  
130 135 140  
Ser Ser Ala Gly Met Ala Arg Ile Glu Glu Glu Glu Thr Glu Glu  
145 150 155 160  
Gly Ser Val Asn Pro Lys Val Lys Lys Thr Lys Lys Val Ser Asp Leu  
165 170 175  
Leu Tyr Pro Arg Ser Lys Ser Tyr Ala Val Thr Thr Ser Thr Pro Ile  
180 185 190  
Leu

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1498225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met Lys Gln Asn Gln Ser Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu  
1 5 10 15  
Arg Ala Leu Gly Lys Ala Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly  
20 25 30  
Cys Ala Ala Arg Thr Gln Tyr Ser Ser Ser Ala Ser Val Ser Ala Pro  
35 40 45  
Phe Pro Arg Ser Arg Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala  
50 55 60  
Ser Ser Arg Arg Thr Thr Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu  
65 70 75 80  
Leu Val Arg Ala Ala Ser Val Arg Ser Leu Gly His Lys Asn Glu Ile  
85 90 95  
Asp Met Leu Ile Gln Glu Lys Leu Gln Gln Gln Lys Gln Gln Lys Gln

100 105 110  
Gly Gly Leu Pro Lys Ser Ser Ser Ala Gly Met Ala Arg Ile Glu Glu  
115 120 125  
Glu Glu Glu Thr Glu Glu Gly Ser Val Asn Pro Lys Val Lys Lys Thr  
130 135 140  
Lys Lys Val Ser Asp Leu Leu Tyr Pro Arg Ser Lys Ser Tyr Ala Val  
145 150 155 160  
Thr Thr Ser Thr Pro Ile Leu  
165

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

attacttctc cactgaatgc atttactctc ctaatgcata tcgtgggttt gcccgtagt	60
tcatacaaaga tttggaaaga ataaggccaa gggcgattct ggacatcata aagtctggtg	120
aagatttttag aattgcaaca accacaaaga tgcctgagca agggacgtgt gagcgatgcg	180
ggtatatattc tagccagaaa tgggtgtaaag cttgtgtttt gctggaagga ctgaaccgtg	240
gtttgcctaa gatgggtatt ggaagacctc gaggcgtaaa tggatgatcat aataaggaaa	300
caaagaagcc tggatctgta gcaaaatcta tagagagcaa acaatgtgga tctctggatt	360
tctaaaattt tgagaaaaaa gctacaaaat cgtatgagtc atagtgaatg atttgattat	420
atagaaaaag aaaagatttt ttttttcctt tcataaaactt cttgtagaac ttaattgtac	480
ttttgggttt cttttttggt t	

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Tyr Phe Ser Thr Glu Cys Ile Tyr Ser Pro Asn Ala Tyr Arg Gly Phe	
1 5 10 15	
Ala Arg Glu Phe Ile Lys Asp Leu Glu Arg Ile Arg Pro Arg Ala Ile	
20 25 30	
Leu Asp Ile Ile Lys Ser Gly Glu Asp Phe Arg Ile Ala Thr Thr Thr	
35 40 45	
Lys Met Pro Glu Gln Gly Thr Cys Glu Arg Cys Gly Tyr Ile Ser Ser	
50 55 60	
Gln Lys Trp Cys Lys Ala Cys Val Leu Leu Glu Gly Leu Asn Arg Gly	
65 70 75 80	
Leu Pro Lys Met Gly Ile Gly Arg Pro Arg Gly Val Asn Gly Asp His	
85 90 95	
Asn Lys Glu Thr Lys Lys Pro Gly Ser Val Ala Lys Ser Ile Glu Ser	
100 105 110	
Lys Gln Cys Gly Ser Leu Asp Phe	
115 120	

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..71  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498228  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:  
Met Pro Glu Gln Gly Thr Cys Glu Arg Cys Gly Tyr Ile Ser Ser Gln  
1                  5                  10                  15  
Lys Trp Cys Lys Ala Cys Val Leu Leu Glu Gly Leu Asn Arg Gly Leu  
                  20                  25                  30  
Pro Lys Met Gly Ile Gly Arg Pro Arg Gly Val Asn Gly Asp His Asn  
                  35                  40                  45  
Lys Glu Thr Lys Lys Pro Gly Ser Val Ala Lys Ser Ile Glu Ser Lys  
50                  55                  60  
Gln Cys Gly Ser Leu Asp Phe  
65                  70  
(2) INFORMATION FOR SEQ ID NO:294:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 567 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..567  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498244  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:  
aaaaacacaa caaaatggga aacttcatat gcgtaacgga aaaaacgacg acgtcgtggn 60  
tcaggagacg ataatggatc atataacaag agaaggagaa gaagaagatc caccgtgggt 120  
cacgacgaca acgacgacgg agagaagctg ctcggagaaa caagcaacgt tacgtcaaca 180  
agttcgtcat cgtcttctga gagaagagag attaagataa ggataacgaa aaaggaactt 240  
gaagatctca tgagaaacat tggtttgaag agtttaacgg cggaagagat tctttctaag 300  
ttaattttcg aaggtggaga ccaaatcgga ttctctgcgg tcgatgtgac gaatcaccac 360  
caaccatgga aaccggtggt gcaaagcata ccggagatgg attagtgtta ttttttttat 420  
ttttcttata aaaaaaataa taaaaaaatc tgagtgatgc gtgtgtctaa acttgaccct 480  
ctcgacaggt gatttttagct tttaaaaagt atgtacatgt ttggttttgt aattaatttt 540  
tttattgaaa tttttattga aattttt  
(2) INFORMATION FOR SEQ ID NO:295:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 72 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..72  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498245  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:  
Lys Thr Gln Gln Asn Gly Lys Leu His Met Arg Asn Gly Lys Asn Asp  
1                  5                  10                  15  
Asp Val Val Xaa Gln Glu Thr Ile Met Asp His Ile Thr Arg Glu Gly  
                  20                  25                  30  
Glu Glu Glu Asp Pro Pro Trp Phe Thr Thr Thr Thr Thr Thr Glu Arg  
                  35                  40                  45  
Ser Cys Ser Glu Lys Gln Ala Thr Leu Arg Gln Gln Val Arg His Arg  
50                  55                  60

Leu Leu Arg Glu Glu Arg Leu Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met	Arg	Asn	Gly	Lys	Asn	Asp	Asp	Val	Val	Xaa	Gln	Glu	Thr	Ile	Met
1				5				10						15	
Asp	His	Ile	Thr	Arg	Glu	Gly	Glu	Glu	Glu	Asp	Pro	Pro	Trp	Phe	Thr
			20				25						30		
Thr	Thr	Thr	Thr	Thr	Glu	Arg	Ser	Cys	Ser	Glu	Lys	Gln	Ala	Thr	Leu
		35				40						45			
Arg	Gln	Gln	Val	Arg	His	Arg	Leu	Leu	Arg	Glu	Glu	Arg	Leu	Arg	
		50				55						60			

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met	Arg	Asn	Ile	Gly	Leu	Lys	Ser	Leu	Thr	Ala	Glu	Glu	Ile	Leu	Ser
1				5				10						15	
Lys	Leu	Ile	Phe	Glu	Gly	Gly	Asp	Gln	Ile	Gly	Phe	Ser	Ala	Val	Asp
			20				25						30		
Val	Thr	Asn	His	His	Gln	Pro	Trp	Lys	Pro	Val	Leu	Gln	Ser	Ile	Pro
		35				40						45			
Glu	Met	Asp													
		50													

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

tcttctctct	acacacacac	acacacacac	acacacaaaa	tggattcttc	gaatgttgaa	60
gaaaaccta	accagaaac	aaaatccgca	gaagaacaaa	accacttgcc	cattttccat	120
tcttctctac	caatcgcatc	tctttctctg	acctgttcc	catcctcgac	tcaatttctc	180
aaattgtttg	ctcatcatcc	aaacaaggtt	aagatcccta	cgcaggcttc	ttctctcact	240
catctctctc	tttcttctgt	ctctcctttt	ccttcttcca	gaatctcttt	caaattccacc	300
atcgctgcta	accctcttca	atcccctctc	tccatcgctc	ctcgctcgcc	cgttgatcct	360
tcctccgccg	ccgctctccg	ccgtgctgct	gtcgtctggt	tccgcaatga	cctccgtgtc	420

```
cacgacaacg agtgtctcaa ctccgccaac gacgagtgcg tctccgtttt gcccgtttac 480
tgcttcgacc ctagagatta cggcaagtcc tcttccggct tcgacaaaac ggggcctttt 540
cgtgcccagt ttctgattga gtccgtttcg gagctccgga agaattctcca agccagaggg 600
tcgaatctag ttgtccgtgt cgggaaacct gaagctgttt tgggtggaatt ggctaaggag 660
attggagctg acgcggttta tgctcacaga gaagtgtctc acgacgaggt taaagcggaa 720
gggaagatag agaccgcgat gaaggaggaa ggcgttgaag tcaagtattt ctggggaagc 780
actctctatc atttgatga tttgcccttc aaaattgaag acttgccgtc aaattacgga 840
gctttcaagg ataaagtcca gaaattggag attaggaaga ctatcgcgac gcttgatcaa 900
ttgaaaagct tgccctctcg aggagacgtt gagcttggcg atattccttc tctcctggat 960
cttggcatta gccccactcc taggactagc caggagggga aaccgacaat ggttggagga 1020
gagacagagg cgttgactag actaaagagc tttgccgcgg attgtcaggc tcgggtgagc 1080
aagggaacc agaaaggagg caacaacagt gtctttggtg caaacttctc ttgcaagata 1140
tcaccttggt tagccatggg aagcatctct cctcgttcca tgttcgatga gctgaagaaa 1200
acaatctcgg catcaaccac ctccacaact ccaaggaacg gaccgggaga tacaggactc 1260
aactggttaa tgtatgagtt gctatggagg gatttcttca ggtttataac caagaaatac 1320
agctcagcga agacgcaggt cgaggctggt cgggctacag cctgtaccgg tgcctttgct 1380
taaacatttg aaaactttca ggtgaccgga aaagttagaa gcgacctgtt tctttgccct 1440
actctggtgt atggtgatta atttgctatc cggacaggac tttactgctc tcttttgaaa 1500
cttgagtgtc aggagaataa aatctaagct tctttttttg gctcaatcaa gttgtccggt 1560
ccctgttcta aacatttcgg atactcattc cataaaaagt ctctacaatt tgagacgctc 1620
tcctttgtgg tc
```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1498252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```
Ser Ser Leu Tyr Thr His Thr His Thr His Thr His Lys Met Asp Ser
1          5          10          15
Ser Asn Val Glu Glu Asn Leu Asn Pro Glu Thr Lys Ser Ala Glu Glu
20          25          30
Gln Asn Pro Leu Ala Ile Phe His Ser Ser Leu Pro Ile Ala Ser Leu
35          40          45
Ser Leu Thr Leu Phe Pro Ser Ser Thr Gln Phe Leu Lys Leu Phe Ala
50          55          60
His His Pro Asn Lys Val Lys Ile Pro Thr Gln Ala Ser Ser Leu Thr
65          70          75          80
His Leu Ser Leu Ser Ser Val Ser Pro Phe Pro Ser Ser Arg Ile Ser
85          90          95
Phe Lys Ser Thr Ile Ala Ala Asn Pro Leu Gln Ser Pro Leu Ser Ile
100          105          110
Val Pro Arg Arg Pro Val Asp Pro Ser Ser Ala Ala Ala Leu Arg Arg
115          120          125
Ala Ala Val Val Trp Phe Arg Asn Asp Leu Arg Val His Asp Asn Glu
130          135          140
Cys Leu Asn Ser Ala Asn Asp Glu Cys Val Ser Val Leu Pro Val Tyr
145          150          155          160
Cys Phe Asp Pro Arg Asp Tyr Gly Lys Ser Ser Ser Gly Phe Asp Lys
165          170          175
Thr Gly Pro Phe Arg Ala Gln Phe Leu Ile Glu Ser Val Ser Glu Leu
180          185          190
Arg Lys Asn Leu Gln Ala Arg Gly Ser Asn Leu Val Val Arg Val Gly
195          200          205
Lys Pro Glu Ala Val Leu Val Glu Leu Ala Lys Glu Ile Gly Ala Asp
210          215          220
```

```

Ala Val Tyr Ala His Arg Glu Val Ser His Asp Glu Val Lys Ala Glu
225                230                235                240
Gly Lys Ile Glu Thr Ala Met Lys Glu Glu Gly Val Glu Val Lys Tyr
                245                250                255
Phe Trp Gly Ser Thr Leu Tyr His Leu Asp Asp Leu Pro Phe Lys Ile
                260                265                270
Glu Asp Leu Pro Ser Asn Tyr Gly Ala Phe Lys Asp Lys Val Gln Lys
                275                280                285
Leu Glu Ile Arg Lys Thr Ile Ala Ala Leu Asp Gln Leu Lys Ser Leu
290                295                300
Pro Ser Arg Gly Asp Val Glu Leu Gly Asp Ile Pro Ser Leu Leu Asp
305                310                315                320
Leu Gly Ile Ser Pro Thr Pro Arg Thr Ser Gln Glu Gly Lys Pro Thr
                325                330                335
Met Val Gly Gly Glu Thr Glu Ala Leu Thr Arg Leu Lys Ser Phe Ala
                340                345                350
Ala Asp Cys Gln Ala Arg Leu Ser Lys Gly Asn Gln Lys Gly Gly Asn
                355                360                365
Asn Ser Val Phe Gly Ala Asn Phe Ser Cys Lys Ile Ser Pro Trp Leu
370                375                380
Ala Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu Leu Lys Lys
385                390                395                400
Thr Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn Gly Pro Gly
                405                410                415
Asp Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp Arg Asp Phe
                420                425                430
Phe Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr Gln Val Glu
435                440                445
Ala Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
450                455                460

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..447
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Met Asp Ser Ser Asn Val Glu Glu Asn Leu Asn Pro Glu Thr Lys Ser
1          5          10          15
Ala Glu Glu Gln Asn Pro Leu Ala Ile Phe His Ser Ser Leu Pro Ile
                20          25          30
Ala Ser Leu Ser Leu Thr Leu Phe Pro Ser Ser Thr Gln Phe Leu Lys
35          40          45
Leu Phe Ala His His Pro Asn Lys Val Lys Ile Pro Thr Gln Ala Ser
50          55          60
Ser Leu Thr His Leu Ser Leu Ser Ser Val Ser Pro Phe Pro Ser Ser
65          70          75          80
Arg Ile Ser Phe Lys Ser Thr Ile Ala Ala Asn Pro Leu Gln Ser Pro
85          90          95
Leu Ser Ile Val Pro Arg Arg Pro Val Asp Pro Ser Ser Ala Ala Ala
100         105         110
Leu Arg Arg Ala Ala Val Val Trp Phe Arg Asn Asp Leu Arg Val His
115         120         125
Asp Asn Glu Cys Leu Asn Ser Ala Asn Asp Glu Cys Val Ser Val Leu
130         135         140
Pro Val Tyr Cys Phe Asp Pro Arg Asp Tyr Gly Lys Ser Ser Ser Gly

```



145		150		155		160									
Phe	Asp	Lys	Thr	Gly	Pro	Phe	Arg	Ala	Gln	Phe	Leu	Ile	Glu	Ser	Val
				165					170					175	
Ser	Glu	Leu	Arg	Lys	Asn	Leu	Gln	Ala	Arg	Gly	Ser	Asn	Leu	Val	Val
				180				185					190		
Arg	Val	Gly	Lys	Pro	Glu	Ala	Val	Leu	Val	Glu	Leu	Ala	Lys	Glu	Ile
		195				200					205				
Gly	Ala	Asp	Ala	Val	Tyr	Ala	His	Arg	Glu	Val	Ser	His	Asp	Glu	Val
	210					215					220				
Lys	Ala	Glu	Gly	Lys	Ile	Glu	Thr	Ala	Met	Lys	Glu	Glu	Gly	Val	Glu
	225				230					235				240	
Val	Lys	Tyr	Phe	Trp	Gly	Ser	Thr	Leu	Tyr	His	Leu	Asp	Asp	Leu	Pro
			245					250						255	
Phe	Lys	Ile	Glu	Asp	Leu	Pro	Ser	Asn	Tyr	Gly	Ala	Phe	Lys	Asp	Lys
		260						265					270		
Val	Gln	Lys	Leu	Glu	Ile	Arg	Lys	Thr	Ile	Ala	Ala	Leu	Asp	Gln	Leu
		275				280						285			
Lys	Ser	Leu	Pro	Ser	Arg	Gly	Asp	Val	Glu	Leu	Gly	Asp	Ile	Pro	Ser
	290				295						300				
Leu	Leu	Asp	Leu	Gly	Ile	Ser	Pro	Thr	Pro	Arg	Thr	Ser	Gln	Glu	Gly
	305				310					315				320	
Lys	Pro	Thr	Met	Val	Gly	Gly	Glu	Thr	Glu	Ala	Leu	Thr	Arg	Leu	Lys
			325					330						335	
Ser	Phe	Ala	Ala	Asp	Cys	Gln	Ala	Arg	Leu	Ser	Lys	Gly	Asn	Gln	Lys
		340					345						350		
Gly	Gly	Asn	Asn	Ser	Val	Phe	Gly	Ala	Asn	Phe	Ser	Cys	Lys	Ile	Ser
		355				360						365			
Pro	Trp	Leu	Ala	Met	Gly	Ser	Ile	Ser	Pro	Arg	Ser	Met	Phe	Asp	Glu
	370				375						380				
Leu	Lys	Lys	Thr	Ile	Ser	Ala	Ser	Thr	Thr	Ser	Thr	Thr	Pro	Arg	Asn
	385			390				395						400	
Gly	Pro	Gly	Asp	Thr	Gly	Leu	Asn	Trp	Leu	Met	Tyr	Glu	Leu	Leu	Trp
			405					410						415	
Arg	Asp	Phe	Phe	Arg	Phe	Ile	Thr	Lys	Lys	Tyr	Ser	Ser	Ala	Lys	Thr
		420					425						430		
Gln	Val	Glu	Ala	Gly	Pro	Ala	Thr	Ala	Cys	Thr	Gly	Ala	Phe	Ala	
		435				440						445			

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..859
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

atcggattaa	aaataaaaaag	cctctctttt	tttrtctcag	tgagacaatc	gacttttctaa	60
aatcgatggc	gactgagaaa	ccgattacga	cggagactgt	tgctctcact	gagaagaaaa	120
tggacatctc	tttagatgag	attatcaaga	tggaaaaagag	caataaccaat	gtgaataagg	180
gcaagaaaca	gagagtattg	aataaaaaag	agaaatttag	tggtgctgcg	aagaatagtg	240
cgggtgaaagc	acagcgttat	atggactctc	ggtctgatgt	tagacagggt	gcttttgcta	300
agaagaggtc	taatttccaa	ggaaaccagt	ttcctgtaac	aaaacaaccg	ttgctcgtaa	360
agccgcttct	gctactccgc	gtggtagacc	ttataatggt	ggaaggatga	ctaatacgaa	420
tcaatcaagg	tttattgctc	caccagctca	gaatagagct	tcacaaagag	ggtttgctgc	480
aaagcagcag	cagcagcaaa	gggagaagat	agtgcagcag	caggcaaatg	gaggaggagg	540
agggcaaagg	caatggcctc	agacactgga	ttctcggttt	gcaaacaatg	aggaagagag	600
aatgagaatg	agaaggtttg	cagacaatag	aagcaatgta	ggcaacaatg	gagctggatc	660
gcatcagcag	cagcgttcga	tggtcccgtg	ggtgagaaga	gctacaagat	tccccaactg	720

```
atttatgacc tgcagaatag tcttgtttca agggtaggggt gaacatattt gctacttatg      780
tagtttggtt tggattcatt gtatcaagtg tagaacattc gtatgtgaag ctctaaaacc      840
ttgaatcttt ttcttggcc
```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```
Arg Ile Lys Asn Lys Lys Pro Leu Phe Phe Xaa Leu Ser Glu Thr Ile
1           5           10           15
Asp Phe Leu Lys Ser Met Ala Thr Glu Lys Pro Ile Thr Thr Glu Thr
20           25           30
Val Ala Leu Thr Glu Lys Lys Met Asp Ile Ser Leu Asp Glu Ile Ile
35           40           45
Lys Met Glu Lys Ser Asn Thr Asn Val Asn Lys Gly Lys Lys Gln Arg
50           55           60
Val Leu Asn Lys Lys Glu Lys Phe Ser Gly Ala Ala Lys Asn Ser Ala
65           70           75           80
Val Lys Ala Gln Arg Tyr Met Asp Ser Arg Ser Asp Val Arg Gln Gly
85           90           95
Ala Phe Ala Lys Lys Arg Ser Asn Phe Gln Gly Asn Gln Phe Pro Val
100          105          110
Thr Lys Gln Pro Leu Leu Val Lys Pro Leu Leu Leu Leu Arg Val Val
115          120          125
Asp Leu Ile Met Val Glu Gly
130          135
```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```
Met Ala Thr Glu Lys Pro Ile Thr Thr Glu Thr Val Ala Leu Thr Glu
1           5           10           15
Lys Lys Met Asp Ile Ser Leu Asp Glu Ile Ile Lys Met Glu Lys Ser
20           25           30
Asn Thr Asn Val Asn Lys Gly Lys Lys Gln Arg Val Leu Asn Lys Lys
35           40           45
Glu Lys Phe Ser Gly Ala Ala Lys Asn Ser Ala Val Lys Ala Gln Arg
50           55           60
Tyr Met Asp Ser Arg Ser Asp Val Arg Gln Gly Ala Phe Ala Lys Lys
65           70           75           80
Arg Ser Asn Phe Gln Gly Asn Gln Phe Pro Val Thr Lys Gln Pro Leu
85           90           95
Leu Val Lys Pro Leu Leu Leu Leu Arg Val Val Asp Leu Ile Met Val
100          105          110
Glu Gly
```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1498257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```
Met Thr Asn Thr Asn Gln Ser Arg Phe Ile Ala Pro Pro Ala Gln Asn
1           5           10           15
Arg Ala Ser Gln Arg Gly Phe Val Ala Lys Gln Gln Gln Gln Gln Arg
20           25           30
Glu Lys Ile Val Gln Gln Gln Ala Asn Gly Gly Gly Gly Gly Gln Arg
35           40           45
Gln Trp Pro Gln Thr Leu Asp Ser Arg Phe Ala Asn Met Lys Glu Glu
50           55           60
Arg Met Arg Met Arg Arg Phe Ala Asp Asn Arg Ser Asn Val Gly Asn
65           70           75           80
Asn Gly Ala Gly Ser His Gln Gln Gln Arg Ser Met Val Pro Trp Val
85           90           95
Arg Arg Ala Thr Arg Phe Pro Asn
100
```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..988

(D) OTHER INFORMATION: / Ceres Seq. ID 1498261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```
aaaagaagac ttttgtaagg aaataaacac acaactaaag agatgtcgctc aaccttgagc 60
aacgaagagt caggactcgg tgattcaaat cgttcgacgg aagtagatag cggcgacgga 120
ggaaacttca cggcttacga gtctcgattc cagtcgcagc ggtttgactc ttccttctct 180
aattttgact cccaaccgga gaaagagtca gacttaccag gcggcgattc atctcctcga 240
cccgaaactc aatctccgcc gtcgataaat agtttcgatg atacaaacgg ttcgatcttg 300
ccgccaccat cggccatgga gaaagaggaa ggtttcgctc ttagagagtg gcgaaggcta 360
aatgctctga gattggaaga gaaagaaaag gaagagaaaag aaatggttca acaaattcta 420
gaagcagcag agcaatataa ggctgagttc tatagcaagc gtaacgttac tattgaaaac 480
aacaagaaac taacccgcca gaaagagaag ttttttttgg agaatacaaga aaagttttac 540
gctgaagctg acaaaaaaaa ttggaaggcg attgcagaac tcattcctcg tgaagtgcc 600
gttatagaga atagaggga caagaagaaa acagcaacca taactgtaat ccagggacca 660
aagccaggga agcccactga tctgtgctcg tatgcgtcaa gtgctcacga aactcaagca 720
caatccgcca actcatatga agccaaaact gccctcacca tctggagctg acccgaatgt 780
gagtgtgagt gaacagggtca cagttacaga gaagttgtag ttgtgtatgt gacaagttaa 840
cttcttcttg attgatgtta aaccgtcttt actttgttag cttccctcat gttcagtcct 900
gactattgtt tgttttgatt tcgtcttttg tcttaccatt gttggtttcc cacacagttt 960
tctactttga tgtatatata atatattc
```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1498262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met	Ser	Ser	Thr	Leu	Ser	Asn	Glu	Glu	Ser	Gly	Leu	Gly	Asp	Ser	Asn	
1				5					10					15		
Arg	Ser	Thr	Glu	Val	Asp	Ser	Gly	Asp	Gly	Gly	Asn	Phe	Thr	Ala	Tyr	
			20					25					30			
Glu	Ser	Arg	Phe	Gln	Ser	Gln	Arg	Phe	Asp	Ser	Ser	Phe	Ser	Asn	Phe	
		35					40					45				
Asp	Ser	Gln	Pro	Glu	Lys	Glu	Ser	Asp	Leu	Pro	Gly	Gly	Asp	Ser	Ser	
	50					55					60					
Pro	Arg	Pro	Glu	Thr	Gln	Ser	Pro	Pro	Ser	Ile	Asn	Ser	Phe	Asp	Asp	
65					70					75					80	
Thr	Asn	Gly	Ser	Ile	Leu	Pro	Pro	Pro	Ser	Ala	Met	Glu	Lys	Glu	Glu	
				85					90					95		
Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Leu	Asn	Ala	Leu	Arg	Leu	Glu	
			100						105					110		
Glu	Lys	Glu	Lys	Glu	Glu	Lys	Glu	Met	Val	Gln	Gln	Ile	Leu	Glu	Ala	
		115					120					125				
Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe	Tyr	Ser	Lys	Arg	Asn	Val	Thr	Ile	
	130					135						140				
Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg	Glu	Lys	Glu	Lys	Phe	Phe	Leu	Glu	
145					150					155					160	
Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ala	Asp	Lys	Asn	Asn	Trp	Lys	Ala	
				165					170					175		
Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu	Val	Pro	Val	Ile	Glu	Asn	Arg	Gly	
			180					185					190			
Asn	Lys	Lys	Lys	Thr	Ala	Thr	Ile	Thr	Val	Ile	Gln	Gly	Pro	Lys	Pro	
		195					200					205				
Gly	Lys	Pro	Thr	Asp	Leu	Cys	Ser	Tyr	Ala	Ser	Ser	Ala	His	Glu	Thr	
	210					215					220					
Gln	Ala	Gln	Ser	Ala	Asn	Ser	Tyr	Glu	Ala	Lys	Thr	Ala	Leu	Thr	Ile	
225					230					235					240	
Trp	Ser															

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1498263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met	Glu	Lys	Glu	Glu	Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Leu	Asn	
1				5					10					15		
Ala	Leu	Arg	Leu	Glu	Glu	Lys	Glu	Lys	Glu	Glu	Lys	Glu	Met	Val	Gln	
			20					25					30			
Gln	Ile	Leu	Glu	Ala	Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe	Tyr	Ser	Lys	
		35					40					45				
Arg	Asn	Val	Thr	Ile	Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg	Glu	Lys	Glu	
	50					55					60					
Lys	Phe	Phe	Leu	Glu	Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ala	Asp	Lys	
65					70					75					80	
Asn	Asn	Trp	Lys	Ala	Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu	Val	Pro	Val	

85 90 95  
Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile  
100 105 110  
Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser  
115 120 125  
Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys  
130 135 140  
Thr Ala Leu Thr Ile Trp Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Val Gln Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe  
1 5 10 15  
Tyr Ser Lys Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg  
20 25 30  
Glu Lys Glu Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu  
35 40 45  
Ala Asp Lys Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu  
50 55 60  
Val Pro Val Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile  
65 70 75 80  
Thr Val Ile Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser  
85 90 95  
Tyr Ala Ser Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr  
100 105 110  
Glu Ala Lys Thr Ala Leu Thr Ile Trp Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..601
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ttccaacaaa cctcgatgaa gaaatatcgt ctcttcctgg atggaccgctc gaatcgaacc 60  
gagcagtacg gtttattgac tcagaccatt tctcggtccc cgaggggaag cgagcttttg 120  
aacctttatc gggcaaagaa ggcataatct ctcaaattgg tgagacaaag gccaacattc 180  
cgtacaagat gtctttctct ttgggacacg caggggacaa gtgtaaggaa cctttggctg 240  
taatggcttt tgctggagat caagcacaga accttcatta tatggcgcaa gcaaactcga 300  
gtttcgaaaag atcggagtgt aacttcactg cgaaagctga acgtacgagg atcgcttct 360  
acagcattta ttacaatacg aggacggacg atatgacttc attgtgtgga cctgtgattg 420  
atgacgttaa ggtttggttc tccgggtcta gtagaattgg atttagtttt ccgcttttta 480  
ttcttctttc ttgtgttttc atctagattg ttccggttca gaaattgtat tggtagaccg 540  
ggaattaaga cgggattcca cgttgtatga tgtatcgttg tatgatggat cggttcaagg 600  
t

(2) INFORMATION FOR SEQ ID NO:310:

[illegible]

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met	Ser	Phe	Ser	Leu	Gly	His	Ala	Gly	Asp	Lys	Cys	Lys	Glu	Pro	Leu
1				5					10					15	
Ala	Val	Met	Ala	Phe	Ala	Gly	Asp	Gln	Ala	Gln	Asn	Phe	His	Tyr	Met
			20					25					30		
Ala	Gln	Ala	Asn	Ser	Ser	Phe	Glu	Arg	Ser	Glu	Leu	Asn	Phe	Thr	Ala
		35					40					45			
Lys	Ala	Glu	Arg	Thr	Arg	Ile	Ala	Phe	Tyr	Ser	Ile	Tyr	Tyr	Asn	Thr
	50					55					60				
Arg	Thr	Asp	Asp	Met	Thr	Ser	Leu	Cys	Gly	Pro	Val	Ile	Asp	Asp	Val
65					70					75				80	
Lys	Val	Trp	Phe	Ser	Gly	Ser	Ser	Arg	Ile	Gly	Phe	Ser	Phe	Pro	Leu
			85						90					95	
Phe	Ile	Leu	Leu	Ser	Leu	Val	Phe	Ile							
			100					105							

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

aacccccaaaa	atagacctca	cctctctcgt	cttctcttatt	ctctccgctc	cttaatttcc	60
aattccaacc	ttctctgttt	tgccttgatg	gaaaagatag	ctccggagct	cttcctcgtc	120
gccggtaacc	cggaactctt	cgctcgtcgc	gacctcctcg	acttctctaa	cgacgacggc	180
gaagttgacg	acggcttaaa	cactcttccc	gattcttcaa	cactctccac	cggcactctc	240
accgacagtt	ccaactcctc	ctcgtttttc	accgacggca	ctggcttctc	cgacctatat	300
attccgaatg	acgatatagc	agaattagaa	tggttatcaa	attttgtgga	agaatcattc	360
gcaggagaag	accaagasaa	gkktcactta	ttttccggkt	taaaaaaccc	tcaaaccamc	420
gggtcgaccc	tgacctactt	aattaaaccc	gaasccgaac	ttgatcatca	attcatcgac	480
atcgatgaat	ccaacgtcgc	cgttcctgcc	aagsccagaa	scaagagatc	mcgttytgca	540
gcctccacgt	gggcttcccg	tytttttatcc	ttagccgatt	ccgacgaaac	caatcccaag	600
aagaaacaac	gaagagtga	agaacaagac	ttcgccggag	atatggacgt	ggattgcgga	660
gaaagcggag	gaggacgacg	ttgtttgcac	tgcgcgacgg	agaagacgcc	gcaatggagg	720
acgggaccta	tgggtccgaa	gacgctttgt	aacgcttgcg	gagtgaggta	caaatcaggg	780
aggctcgtgc	cggagtatat	accggcgctc	agtccgacgt	tcgtgatggc	gaggcactcg	840
aactctcacc	ggaaagtgat	ggagctccgg	cgacagaagg	agatgagaga	cgagcatttg	900
ctgagtcagc	ttaggtgtga	gaatctactg	atggatatca	gatccaacgg	tgaagatttc	960
ttaatgcata	ataatactaa	ccacgtggct	cctgatttta	gacacttaat	ctagttttct	1020
atttccacgt	ggataatttc	gcaataattt	gttcgtttcg	tttagcttta	tttttttttt	1080
tttccttttt	aacatttggt	tttcattttc	tgcagactac	ttctagtact	attgatatat	1140
ttg						

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..337  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498273  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Asn	Pro	Lys	Asn	Arg	Pro	His	Leu	Ser	Arg	Leu	Leu	Tyr	Ser	Leu	Arg
1			5					10						15	
Ser	Leu	Ile	Ser	Asn	Ser	Asn	Leu	Leu	Cys	Phe	Ala	Leu	Met	Glu	Lys
			20					25					30		
Ile	Ala	Pro	Glu	Leu	Phe	Leu	Val	Ala	Gly	Asn	Pro	Asp	Ser	Phe	Val
	35						40					45			
Val	Asp	Asp	Leu	Leu	Asp	Phe	Ser	Asn	Asp	Asp	Gly	Glu	Val	Asp	Asp
	50					55					60				
Gly	Leu	Asn	Thr	Leu	Pro	Asp	Ser	Ser	Thr	Leu	Ser	Thr	Gly	Thr	Leu
65					70					75					80
Thr	Asp	Ser	Ser	Asn	Ser	Ser	Ser	Leu	Phe	Thr	Asp	Gly	Thr	Gly	Phe
				85					90					95	
Ser	Asp	Leu	Tyr	Ile	Pro	Asn	Asp	Asp	Ile	Ala	Glu	Leu	Glu	Trp	Leu
			100					105					110		
Ser	Asn	Phe	Val	Glu	Glu	Ser	Phe	Ala	Gly	Glu	Asp	Gln	Xaa	Lys	Xaa
	115						120					125			
His	Leu	Phe	Ser	Xaa	Leu	Lys	Asn	Pro	Gln	Thr	Xaa	Gly	Ser	Thr	Leu
	130					135					140				
Thr	His	Leu	Ile	Lys	Pro	Glu	Xaa	Glu	Leu	Asp	His	Gln	Phe	Ile	Asp
145				150						155					160
Ile	Asp	Glu	Ser	Asn	Val	Ala	Val	Pro	Ala	Lys	Xaa	Arg	Xaa	Lys	Arg
				165					170					175	
Xaa	Arg	Xaa	Ala	Ala	Ser	Thr	Trp	Ala	Ser	Arg	Xaa	Leu	Ser	Leu	Ala
			180					185					190		
Asp	Ser	Asp	Glu	Thr	Asn	Pro	Lys	Lys	Lys	Gln	Arg	Arg	Val	Lys	Glu
	195					200						205			
Gln	Asp	Phe	Ala	Gly	Asp	Met	Asp	Val	Asp	Cys	Gly	Glu	Ser	Gly	Gly
	210					215					220				
Gly	Arg	Arg	Cys	Leu	His	Cys	Ala	Thr	Glu	Lys	Thr	Pro	Gln	Trp	Arg
225					230					235					240
Thr	Gly	Pro	Met	Gly	Pro	Lys	Thr	Leu	Cys	Asn	Ala	Cys	Gly	Val	Arg
				245					250					255	
Tyr	Lys	Ser	Gly	Arg	Leu	Val	Pro	Glu	Tyr	Arg	Pro	Ala	Ser	Ser	Pro
			260					265					270		
Thr	Phe	Val	Met	Ala	Arg	His	Ser	Asn	Ser	His	Arg	Lys	Val	Met	Glu
	275					280						285			
Leu	Arg	Arg	Gln	Lys	Glu	Met	Arg	Asp	Glu	His	Leu	Leu	Ser	Gln	Leu
	290					295					300				
Arg	Cys	Glu	Asn	Leu	Leu	Met	Asp	Ile	Arg	Ser	Asn	Gly	Glu	Asp	Phe
305					310					315					320
Leu	Met	His	Asn	Asn	Thr	Asn	His	Val	Ala	Pro	Asp	Phe	Arg	His	Leu
				325					330					335	

Ile

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 308 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:



(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```
Met Glu Lys Ile Ala Pro Glu Leu Phe Leu Val Ala Gly Asn Pro Asp
 1           5           10           15
Ser Phe Val Val Asp Asp Leu Leu Asp Phe Ser Asn Asp Asp Gly Glu
 20           25           30
Val Asp Asp Gly Leu Asn Thr Leu Pro Asp Ser Ser Thr Leu Ser Thr
 35           40           45
Gly Thr Leu Thr Asp Ser Ser Asn Ser Ser Ser Leu Phe Thr Asp Gly
 50           55           60
Thr Gly Phe Ser Asp Leu Tyr Ile Pro Asn Asp Asp Ile Ala Glu Leu
 65           70           75           80
Glu Trp Leu Ser Asn Phe Val Glu Glu Ser Phe Ala Gly Glu Asp Gln
 85           90           95
Xaa Lys Xaa His Leu Phe Ser Xaa Leu Lys Asn Pro Gln Thr Xaa Gly
 100          105          110
Ser Thr Leu Thr His Leu Ile Lys Pro Glu Xaa Glu Leu Asp His Gln
 115          120          125
Phe Ile Asp Ile Asp Glu Ser Asn Val Ala Val Pro Ala Lys Xaa Arg
 130          135          140
Xaa Lys Arg Xaa Arg Xaa Ala Ala Ser Thr Trp Ala Ser Arg Xaa Leu
 145          150          155          160
Ser Leu Ala Asp Ser Asp Glu Thr Asn Pro Lys Lys Lys Gln Arg Arg
 165          170          175
Val Lys Glu Gln Asp Phe Ala Gly Asp Met Asp Val Asp Cys Gly Glu
 180          185          190
Ser Gly Gly Arg Arg Cys Leu His Cys Ala Thr Glu Lys Thr Pro
 195          200          205
Gln Trp Arg Thr Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys
 210          215          220
Gly Val Arg Tyr Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala
 225          230          235          240
Ser Ser Pro Thr Phe Val Met Ala Arg His Ser Asn Ser His Arg Lys
 245          250          255
Val Met Glu Leu Arg Arg Gln Lys Glu Met Arg Asp Glu His Leu Leu
 260          265          270
Ser Gln Leu Arg Cys Glu Asn Leu Leu Met Asp Ile Arg Ser Asn Gly
 275          280          285
Glu Asp Phe Leu Met His Asn Asn Thr Asn His Val Ala Pro Asp Phe
 290          295          300
Arg His Leu Ile
305
```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1661

(D) OTHER INFORMATION: / Ceres Seq. ID 1498279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```
aatcaaacc aaaagcccaa aaccagaaa agaaaaatct ctcttttgaa aattctcctt      60
ttgcaaatca ttcaagttaa gcagaatcat ctctttcttc ttcttctoca gcttcatcaa      120
tctcttctaa actttttgcg tttacctgaa aaactgtttt gatcggaaga atctgattgc      180
ttcgatgtcg ctgtcgaatc agattccgt ttactctcga tgaccctctg catcttcttc      240
cacttttttt cccagtttt ctgataactt ttctcagatg agaagttcta cgttacttct      300
```

```
tctcaagttc ttcttcttct tcttcaatct gacttcgctt gagtatcaag ttgatggagc 360
atttgttgga acatatggga taaattatgg aaggtagctt gacaacatac catctccgga 420
gaaagtagtt ttacttctaa agcaagctaa aattcggaat gtgcgtatat acgatgtaga 480
tcacactggt cttgaagctt ttagtggaac tggtttagac cttgttggtg gacttcctaa 540
tggtttttta aaagagatga gttcaaatgc tgatcatgct ttcaactggg ttaaagaaaa 600
tatccagtct ttcttaccga agactcggat tcgcgggtatc gctataggta acgaagtctt 660
tgaggcggtt gattctgagc tcgcgggagc tttacttggt gctgctaaaa atgtgtacaa 720
tgcgttgaag aaaatgaatc tggaggacac tgtgcagatc actacggctc attcacagge 780
tgtgttttct gattcctacc cgccttcgtc ttgtgtgttt aaagagaatg ttgttcagtt 840
catgaagcca ttgttgaggt tttttcagca gattgggtct cctttttgtt tgaatgctta 900
cccttttttg gcgtacactt ataattccgaa ggagattgat atcaactatg ctcttttcaa 960
gccaacggaa gggatatatg acccgaaaac cgatttgcat tacgataaca tgcttgatgc 1020
tcagattgat gctgcttaca tggcggtgca agatgctggg ttttaagaaga tggaggttat 1080
gatcaactgaa actgggtggg cttctaaagg ggattcagat gaacctgcag caacaccaga 1140
gaacgcaaga acgtataact ataacctcag gaagaggctt gctaagaaga aaggacacc 1200
tcttagacca aaaacggtgc ttaaagccta tatctttgca ttgttcaatg aaaactcaaa 1260
accgggcaag agttctgaga cacacttttg actttttaaa cctgatggaa ccatatcata 1320
tgacattgga ttcaacagtc taaagtctga ttctcccaag tcactcattt catcatcaaa 1380
gtcagctcgt tactatgttg cattgggtcat ctctgtctcg gctttcctct tgatgatata 1440
aatgcggaag tgggtgtgagc tttgacgata ctcggatttg gtcgtacatt cgtagcacta 1500
taatatatat tactagggtt gggacgctaa cgaaatggta ggagcacaaa tttactgcaa 1560
ttctcatata tgtagccaag agatatccag aaaagatatc accagacact atcatatata 1620
cacatcttat gtaaaacaaa tctaatacat aaatttgggc c
```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```
Met Arg Ser Ser Thr Leu Leu Leu Leu Phe Phe Phe Phe Phe Phe
1          5          10          15
Asn Leu Thr Ser Leu Glu Tyr Gln Val Asp Gly Ala Phe Val Gly Thr
20          25          30
Tyr Gly Ile Asn Tyr Gly Arg Ile Ala Asp Asn Ile Pro Ser Pro Glu
35          40          45
Lys Val Val Leu Leu Leu Lys Gln Ala Lys Ile Arg Asn Val Arg Ile
50          55          60
Tyr Asp Val Asp His Thr Val Leu Glu Ala Phe Ser Gly Thr Gly Leu
65          70          75          80
Asp Leu Val Val Gly Leu Pro Asn Gly Phe Leu Lys Glu Met Ser Ser
85          90          95
Asn Ala Asp His Ala Phe Thr Trp Val Lys Glu Asn Ile Gln Ser Phe
100         105         110
Leu Pro Lys Thr Arg Ile Arg Gly Ile Ala Ile Gly Asn Glu Val Leu
115         120         125
Gly Gly Gly Asp Ser Glu Leu Ala Gly Ala Leu Leu Gly Ala Ala Lys
130         135         140
Asn Val Tyr Asn Ala Leu Lys Lys Met Asn Leu Glu Asp Thr Val Gln
145         150         155         160
Ile Thr Thr Ala His Ser Gln Ala Val Phe Ser Asp Ser Tyr Pro Pro
165         170         175
Ser Ser Cys Val Phe Lys Glu Asn Val Val Gln Phe Met Lys Pro Leu
180         185         190
Leu Glu Phe Phe Gln Gln Ile Gly Ser Pro Phe Cys Leu Asn Ala Tyr
195         200         205
```

```

Pro Phe Leu Ala Tyr Thr Tyr Asn Pro Lys Glu Ile Asp Ile Asn Tyr
  210                215                220
Ala Leu Phe Lys Pro Thr Glu Gly Ile Tyr Asp Pro Lys Thr Asp Leu
 225                230                235                240
His Tyr Asp Asn Met Leu Asp Ala Gln Ile Asp Ala Ala Tyr Met Ala
                245                250                255
Leu Gln Asp Ala Gly Phe Lys Lys Met Glu Val Met Ile Thr Glu Thr
                260                265                270
Gly Trp Ala Ser Lys Gly Asp Ser Asp Glu Pro Ala Ala Thr Pro Glu
 275                280                285
Asn Ala Arg Thr Tyr Asn Tyr Asn Leu Arg Lys Arg Leu Ala Lys Lys
 290                295                300
Lys Gly Thr Pro Leu Arg Pro Lys Thr Val Leu Lys Ala Tyr Ile Phe
 305                310                315                320
Ala Leu Phe Asn Glu Asn Ser Lys Pro Gly Lys Ser Ser Glu Thr His
                325                330                335
Phe Gly Leu Phe Lys Pro Asp Gly Thr Ile Ser Tyr Asp Ile Gly Phe
                340                345                350
Asn Ser Leu Lys Ser Asp Ser Pro Lys Ser Leu Ile Ser Ser Ser Lys
 355                360                365
Ser Ala Arg Tyr Tyr Val Ala Leu Val Ile Ser Val Ser Ala Phe Leu
 370                375                380
Leu Met Ile
385

```

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1498281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```

Met Ser Ser Asn Ala Asp His Ala Phe Thr Trp Val Lys Glu Asn Ile
 1                5                10                15
Gln Ser Phe Leu Pro Lys Thr Arg Ile Arg Gly Ile Ala Ile Gly Asn
                20                25                30
Glu Val Leu Gly Gly Gly Asp Ser Glu Leu Ala Gly Ala Leu Leu Gly
 35                40                45
Ala Ala Lys Asn Val Tyr Asn Ala Leu Lys Lys Met Asn Leu Glu Asp
 50                55                60
Thr Val Gln Ile Thr Thr Ala His Ser Gln Ala Val Phe Ser Asp Ser
 65                70                75                80
Tyr Pro Pro Ser Ser Cys Val Phe Lys Glu Asn Val Val Gln Phe Met
                85                90                95
Lys Pro Leu Leu Glu Phe Phe Gln Gln Ile Gly Ser Pro Phe Cys Leu
                100                105                110
Asn Ala Tyr Pro Phe Leu Ala Tyr Thr Tyr Asn Pro Lys Glu Ile Asp
 115                120                125
Ile Asn Tyr Ala Leu Phe Lys Pro Thr Glu Gly Ile Tyr Asp Pro Lys
 130                135                140
Thr Asp Leu His Tyr Asp Asn Met Leu Asp Ala Gln Ile Asp Ala Ala
 145                150                155                160
Tyr Met Ala Leu Gln Asp Ala Gly Phe Lys Lys Met Glu Val Met Ile
                165                170                175
Thr Glu Thr Gly Trp Ala Ser Lys Gly Asp Ser Asp Glu Pro Ala Ala
 180                185                190
Thr Pro Glu Asn Ala Arg Thr Tyr Asn Tyr Asn Leu Arg Lys Arg Leu

```

195	200	205
Ala Lys Lys Lys Gly Thr Pro Leu Arg Pro Lys Thr Val Leu Lys Ala		
210	215	220
Tyr Ile Phe Ala Leu Phe Asn Glu Asn Ser Lys Pro Gly Lys Ser Ser		
225	230	235
Glu Thr His Phe Gly Leu Phe Lys Pro Asp Gly Thr Ile Ser Tyr Asp		
245	250	255
Ile Gly Phe Asn Ser Leu Lys Ser Asp Ser Pro Lys Ser Leu Ile Ser		
260	265	270
Ser Ser Lys Ser Ala Arg Tyr Tyr Val Ala Leu Val Ile Ser Val Ser		
275	280	285
Ala Phe Leu Leu Met Ile		
290		

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1498282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met	Asn	Leu	Glu	Asp	Thr	Val	Gln	Ile	Thr	Thr	Ala	His	Ser	Gln	Ala
1			5						10					15	
Val	Phe	Ser	Asp	Ser	Tyr	Pro	Pro	Ser	Ser	Cys	Val	Phe	Lys	Glu	Asn
			20					25					30		
Val	Val	Gln	Phe	Met	Lys	Pro	Leu	Leu	Glu	Phe	Phe	Gln	Gln	Ile	Gly
		35					40					45			
Ser	Pro	Phe	Cys	Leu	Asn	Ala	Tyr	Pro	Phe	Leu	Ala	Tyr	Thr	Tyr	Asn
	50				55					60					
Pro	Lys	Glu	Ile	Asp	Ile	Asn	Tyr	Ala	Leu	Phe	Lys	Pro	Thr	Glu	Gly
65				70						75				80	
Ile	Tyr	Asp	Pro	Lys	Thr	Asp	Leu	His	Tyr	Asp	Asn	Met	Leu	Asp	Ala
			85						90					95	
Gln	Ile	Asp	Ala	Ala	Tyr	Met	Ala	Leu	Gln	Asp	Ala	Gly	Phe	Lys	Lys
		100					105					110			
Met	Glu	Val	Met	Ile	Thr	Glu	Thr	Gly	Trp	Ala	Ser	Lys	Gly	Asp	Ser
		115					120					125			
Asp	Glu	Pro	Ala	Ala	Thr	Pro	Glu	Asn	Ala	Arg	Thr	Tyr	Asn	Tyr	Asn
	130				135					140					
Leu	Arg	Lys	Arg	Leu	Ala	Lys	Lys	Lys	Gly	Thr	Pro	Leu	Arg	Pro	Lys
145				150						155				160	
Thr	Val	Leu	Lys	Ala	Tyr	Ile	Phe	Ala	Leu	Phe	Asn	Glu	Asn	Ser	Lys
			165						170					175	
Pro	Gly	Lys	Ser	Ser	Glu	Thr	His	Phe	Gly	Leu	Phe	Lys	Pro	Asp	Gly
		180					185					190			
Thr	Ile	Ser	Tyr	Asp	Ile	Gly	Phe	Asn	Ser	Leu	Lys	Ser	Asp	Ser	Pro
	195				200							205			
Lys	Ser	Leu	Ile	Ser	Ser	Ser	Lys	Ser	Ala	Arg	Tyr	Tyr	Val	Ala	Leu
	210				215					220					
Val	Ile	Ser	Val	Ser	Ala	Phe	Leu	Leu	Met	Ile					
225				230						235					

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..690

(D) OTHER INFORMATION: / Ceres Seq. ID 1498283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

aaaatcgctcg	ctctctgcct	ctctcgcac	tccaaatcga	aatcgctctc	cgtctccgtc	60
tccgtctccg	tctccgtctc	cgtctccgtc	tccgtctccg	tctccatctc	tctctccggt	120
aagtcaactga	aagatggggc	gtgttagaac	caagacggtg	aagaaatctt	cacgtcragt	180
cattgagaag	tactactctc	gcacgactct	tgactttcac	actaacaaga	agatccttga	240
agagggttgc	atcatcccat	caaagagact	ccgcaacaag	attgctggat	tctccaccca	300
cttgatgaaa	cgtatccaga	akkgaccagt	ccgtggmatc	tcactcaagc	ttcaagaaga	360
agagcgtgaa	cgcgctatgg	actttgttcc	cgatgagtct	gctatcaaga	ctgatgagat	420
caaggctgcac	aaagagactc	ttgagatgct	tgcttctcta	ggaatgtctg	acactctcgg	480
catctctgca	gtcgcacccac	aacaagctat	ggcaccaatc	cctgctttcg	gcggcggcag	540
ggcaccacaga	agatactaag	atggacgatt	ggctctcttt	tttcacagtt	agggacaaga	600
aagacttttg	tggttgttta	ttgtttcttt	tgattatgtc	ttaaactcaa	tgtgagactc	660
tttcgtatta	atggtttttg	agttatgtgg				

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1498284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met	Gly	Arg	Val	Arg	Thr	Lys	Thr	Val	Lys	Lys	Ser	Ser	Arg	Xaa	Val
1			5					10						15	
Ile	Glu	Lys	Tyr	Tyr	Ser	Arg	Met	Thr	Leu	Asp	Phe	His	Thr	Asn	Lys
		20						25					30		
Lys	Ile	Leu	Glu	Glu	Val	Ala	Ile	Ile	Pro	Ser	Lys	Arg	Leu	Arg	Asn
		35					40					45			
Lys	Ile	Ala	Gly	Phe	Ser	Thr	His	Leu	Met	Lys	Arg	Ile	Gln	Xaa	Xaa
	50					55				60					
Pro	Val	Arg	Xaa	Ile	Ser	Leu	Lys	Leu	Gln	Glu	Glu	Glu	Arg	Glu	Arg
65					70				75					80	
Arg	Met	Asp	Phe	Val	Pro	Asp	Glu	Ser	Ala	Ile	Lys	Thr	Asp	Glu	Ile
			85				90						95		
Lys	Val	Asp	Lys	Glu	Thr	Leu	Glu	Met	Leu	Ala	Ser	Leu	Gly	Met	Ser
		100					105						110		
Asp	Thr	Leu	Gly	Ile	Ser	Ala	Val	Asp	Pro	Gln	Gln	Ala	Met	Ala	Pro
		115					120						125		
Ile	Pro	Ala	Phe	Gly	Gly	Gly	Arg	Ala	Pro	Arg	Arg	Tyr			
	130					135						140			

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1498285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Thr Leu Asp Phe His Thr Asn Lys Lys Ile Leu Glu Glu Val Ala

1 5 10 15  
Ile Ile Pro Ser Lys Arg Leu Arg Asn Lys Ile Ala Gly Phe Ser Thr  
20 25 30  
His Leu Met Lys Arg Ile Gln Xaa Xaa Pro Val Arg Xaa Ile Ser Leu  
35 40 45  
Lys Leu Gln Glu Glu Glu Arg Glu Arg Arg Met Asp Phe Val Pro Asp  
50 55 60  
Glu Ser Ala Ile Lys Thr Asp Glu Ile Lys Val Asp Lys Glu Thr Leu  
65 70 75 80  
Glu Met Leu Ala Ser Leu Gly Met Ser Asp Thr Leu Gly Ile Ser Ala  
85 90 95  
Val Asp Pro Gln Gln Ala Met Ala Pro Ile Pro Ala Phe Gly Gly Gly  
100 105 110  
Arg Ala Pro Arg Arg Tyr  
115

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Lys Arg Ile Gln Xaa Xaa Pro Val Arg Xaa Ile Ser Leu Lys Leu  
1 5 10 15  
Gln Glu Glu Glu Arg Glu Arg Arg Met Asp Phe Val Pro Asp Glu Ser  
20 25 30  
Ala Ile Lys Thr Asp Glu Ile Lys Val Asp Lys Glu Thr Leu Glu Met  
35 40 45  
Leu Ala Ser Leu Gly Met Ser Asp Thr Leu Gly Ile Ser Ala Val Asp  
50 55 60  
Pro Gln Gln Ala Met Ala Pro Ile Pro Ala Phe Gly Gly Gly Arg Ala  
65 70 75 80  
Pro Arg Arg Tyr

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1264
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

attatgagaa agaattcac ctaatgatgt tctaggtaat ggtctcttta tgcgacagct 60  
acgagactat accacctaac atctccgaga aagaagctgc gtggctaagg tccttctacg 120  
cagcgggaga ggaggaaaaa gacgtagaa cgcattgcaat tgcggttgct gccgcgacag 180  
ctgctgcagc tgacgcagcg gttgcggcgg ctaaagcggc tgctgcgggt gttatgctcc 240  
aaggtcaagg caagagtggc ccgtaggag gtggcaaaag ccgtgagcat cgtgctgcta 300  
tgcagatcca atgtgccttt agaggctact tggcgagaaa agcgttgaga gcgttgagag 360  
gagtggtgaa gattcaagct ttagtgagag gttttttggt acggaatcaa gcggcggcga 420  
ctctccggag tatggaagca cttgttagag ctcaaaaaac tgtaaagatt caaagagctc 480  
tccgtcgtaa cggaaatgct gctccggcga gaaaatccac ggaaagattc tccggatctt 540  
tggagaatcg aaacaacggc gaagagacag ctaagatagt ggaggtagat acagggaccc 600

```
gacccgggac ttacagaatc cgagcaccgc ttttatccgc gtcggatttc ttagacaacc 660
cgtttcgacg tacgctttct tcaccgctct cgggtcgcgt cccaccgcgt ctatcaatgc 720
ctaaacctga atgggaagag tgcagtagca agttcccgac ggcgcagagc acacctcggt 780
tttctggtgg gtctccggcg aggagcgtgt gctgctctgg tggcggagta gaggcggagg 840
tggtacaga ggctgatgct aaccggttct gtttcttgtc gggggaattt aactcgggtt 900
acatggcgga tacaacgtcg tttagggcga aactgaggtc gcatagtgc cgcagacaga 960
gaccagagag taatgcttca gctggcggat ggaggaggag tatcggcggc ggtggtgtta 1020
ggatgcagag acagtcgtgt tcgggtgtca gagaagctgt ggtcgggaat atcgagaggc 1080
gtaggatgcg ttggtgattc ttatttccat aattattatc cgtttagttt tggttaatta 1140
ggggagtaat gttattaatt taatatagtt tgatattatt atagttttct aagtttact 1200
gacaaaattt aaaattggtg tttcttgtat gctacatatt ctatttctat gtaagttttt 1260
tgcc
```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```
Met Val Ser Leu Cys Asp Ser Tyr Glu Thr Ile Pro Pro Asn Ile Ser
1          5          10          15
Glu Lys Glu Ala Ala Trp Leu Arg Ser Phe Tyr Ala Ala Gly Glu Glu
20          25          30
Glu Lys Glu Arg Arg Thr His Ala Ile Ala Val Ala Ala Thr Ala
35          40          45
Ala Ala Ala Asp Ala Ala Val Ala Ala Lys Ala Ala Ala Ala Val
50          55          60
Val Met Leu Gln Gly Gln Gly Lys Ser Gly Pro Leu Gly Gly Gly Lys
65          70          75          80
Ser Arg Glu His Arg Ala Ala Met Gln Ile Gln Cys Ala Phe Arg Gly
85          90          95
Tyr Leu Ala Arg Lys Ala Leu Arg Ala Leu Arg Gly Val Val Lys Ile
100          105          110
Gln Ala Leu Val Arg Gly Phe Leu Val Arg Asn Gln Ala Ala Ala Thr
115          120          125
Leu Arg Ser Met Glu Ala Leu Val Arg Ala Gln Lys Thr Val Lys Ile
130          135          140
Gln Arg Ala Leu Arg Arg Asn Gly Asn Ala Ala Pro Ala Arg Lys Ser
145          150          155          160
Thr Glu Arg Phe Ser Gly Ser Leu Glu Asn Arg Asn Asn Gly Glu Glu
165          170          175
Thr Ala Lys Ile Val Glu Val Asp Thr Gly Thr Arg Pro Gly Thr Tyr
180          185          190
Arg Ile Arg Ala Pro Val Leu Ser Gly Ser Asp Phe Leu Asp Asn Pro
195          200          205
Phe Arg Arg Thr Leu Ser Ser Pro Leu Ser Gly Arg Val Pro Pro Arg
210          215          220
Leu Ser Met Pro Lys Pro Glu Trp Glu Glu Cys Ser Ser Lys Phe Pro
225          230          235          240
Thr Ala Gln Ser Thr Pro Arg Phe Ser Gly Gly Ser Pro Ala Arg Ser
245          250          255
Val Cys Cys Ser Gly Gly Gly Val Glu Ala Glu Val Asp Thr Glu Ala
260          265          270
Asp Ala Asn Arg Phe Cys Phe Leu Ser Gly Glu Phe Asn Ser Gly Tyr
275          280          285
Met Ala Asp Thr Thr Ser Phe Arg Ala Lys Leu Arg Ser His Ser Ala
```

290						295						300					
Pro	Arg	Gln	Arg	Pro	Glu	Ser	Asn	Ala	Ser	Ala	Gly	Gly	Trp	Arg	Arg		
305					310					315					320		
Ser	Ile	Gly	Gly	Gly	Gly	Val	Arg	Met	Gln	Arg	Gln	Ser	Cys	Ser	Gly		
				325					330					335			
Val	Arg	Glu	Ala	Val	Val	Gly	Asn	Ile	Glu	Arg	Arg	Arg	Met	Arg	Trp		
			340					345					350				

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met	Leu	Gln	Gly	Gln	Gly	Lys	Ser	Gly	Pro	Leu	Gly	Gly	Gly	Lys	Ser		
1				5					10					15			
Arg	Glu	His	Arg	Ala	Ala	Met	Gln	Ile	Gln	Cys	Ala	Phe	Arg	Gly	Tyr		
			20					25					30				
Leu	Ala	Arg	Lys	Ala	Leu	Arg	Ala	Leu	Arg	Gly	Val	Val	Lys	Ile	Gln		
			35				40					45					
Ala	Leu	Val	Arg	Gly	Phe	Leu	Val	Arg	Asn	Gln	Ala	Ala	Ala	Thr	Leu		
	50					55				60							
Arg	Ser	Met	Glu	Ala	Leu	Val	Arg	Ala	Gln	Lys	Thr	Val	Lys	Ile	Gln		
					70				75					80			
Arg	Ala	Leu	Arg	Arg	Asn	Gly	Asn	Ala	Ala	Pro	Ala	Arg	Lys	Ser	Thr		
				85				90					95				
Glu	Arg	Phe	Ser	Gly	Ser	Leu	Glu	Asn	Arg	Asn	Asn	Gly	Glu	Glu	Thr		
			100				105					110					
Ala	Lys	Ile	Val	Glu	Val	Asp	Thr	Gly	Thr	Arg	Pro	Gly	Thr	Tyr	Arg		
		115				120						125					
Ile	Arg	Ala	Pro	Val	Leu	Ser	Gly	Ser	Asp	Phe	Leu	Asp	Asn	Pro	Phe		
	130				135					140							
Arg	Arg	Thr	Leu	Ser	Ser	Pro	Leu	Ser	Gly	Arg	Val	Pro	Pro	Arg	Leu		
	145				150					155				160			
Ser	Met	Pro	Lys	Pro	Glu	Trp	Glu	Glu	Cys	Ser	Ser	Lys	Phe	Pro	Thr		
				165					170					175			
Ala	Gln	Ser	Thr	Pro	Arg	Phe	Ser	Gly	Gly	Ser	Pro	Ala	Arg	Ser	Val		
			180					185					190				
Cys	Cys	Ser	Gly	Gly	Gly	Val	Glu	Ala	Glu	Val	Asp	Thr	Glu	Ala	Asp		
		195				200					205						
Ala	Asn	Arg	Phe	Cys	Phe	Leu	Ser	Gly	Glu	Phe	Asn	Ser	Gly	Tyr	Met		
	210					215					220						
Ala	Asp	Thr	Thr	Ser	Phe	Arg	Ala	Lys	Leu	Arg	Ser	His	Ser	Ala	Pro		
	225				230					235				240			
Arg	Gln	Arg	Pro	Glu	Ser	Asn	Ala	Ser	Ala	Gly	Gly	Trp	Arg	Arg	Ser		
				245					250					255			
Ile	Gly	Gly	Gly	Gly	Val	Arg	Met	Gln	Arg	Gln	Ser	Cys	Ser	Gly	Val		
		260						265					270				
Arg	Glu	Ala	Val	Val	Gly	Asn	Ile	Glu	Arg	Arg	Arg	Met	Arg	Trp			
		275					280					285					

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid



(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..265  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498294  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Met	Gln	Ile	Gln	Cys	Ala	Phe	Arg	Gly	Tyr	Leu	Ala	Arg	Lys	Ala	Leu
1			5						10					15	
Arg	Ala	Leu	Arg	Gly	Val	Val	Lys	Ile	Gln	Ala	Leu	Val	Arg	Gly	Phe
			20					25					30		
Leu	Val	Arg	Asn	Gln	Ala	Ala	Ala	Thr	Leu	Arg	Ser	Met	Glu	Ala	Leu
			35				40					45			
Val	Arg	Ala	Gln	Lys	Thr	Val	Lys	Ile	Gln	Arg	Ala	Leu	Arg	Arg	Asn
			50				55				60				
Gly	Asn	Ala	Ala	Pro	Ala	Arg	Lys	Ser	Thr	Glu	Arg	Phe	Ser	Gly	Ser
65					70					75				80	
Leu	Glu	Asn	Arg	Asn	Gly	Glu	Glu	Thr	Ala	Lys	Ile	Val	Glu	Val	
				85				90					95		
Asp	Thr	Gly	Thr	Arg	Pro	Gly	Thr	Tyr	Arg	Ile	Arg	Ala	Pro	Val	Leu
			100					105					110		
Ser	Gly	Ser	Asp	Phe	Leu	Asp	Asn	Pro	Phe	Arg	Arg	Thr	Leu	Ser	Ser
			115				120					125			
Pro	Leu	Ser	Gly	Arg	Val	Pro	Pro	Arg	Leu	Ser	Met	Pro	Lys	Pro	Glu
			130				135				140				
Trp	Glu	Glu	Cys	Ser	Ser	Lys	Phe	Pro	Thr	Ala	Gln	Ser	Thr	Pro	Arg
145						150				155				160	
Phe	Ser	Gly	Gly	Ser	Pro	Ala	Arg	Ser	Val	Cys	Cys	Ser	Gly	Gly	Gly
				165				170						175	
Val	Glu	Ala	Glu	Val	Asp	Thr	Glu	Ala	Asp	Ala	Asn	Arg	Phe	Cys	Phe
			180					185					190		
Leu	Ser	Gly	Glu	Phe	Asn	Ser	Gly	Tyr	Met	Ala	Asp	Thr	Thr	Ser	Phe
			195				200					205			
Arg	Ala	Lys	Leu	Arg	Ser	His	Ser	Ala	Pro	Arg	Gln	Arg	Pro	Glu	Ser
			210			215					220				
Asn	Ala	Ser	Ala	Gly	Gly	Trp	Arg	Arg	Ser	Ile	Gly	Gly	Gly	Gly	Val
225					230					235				240	
Arg	Met	Gln	Arg	Gln	Ser	Cys	Ser	Gly	Val	Arg	Glu	Ala	Val	Val	Gly
				245					250					255	
Asn	Ile	Glu	Arg	Arg	Arg	Met	Arg	Trp							
			260				265								

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 727 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..727

(D) OTHER INFORMATION: / Ceres Seq. ID 1498295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

aagtaggagg	aagacgatgg	cgtagagaa	gcacatagag	aaggctactct	tcagcgatga	60
agtaattgcg	caccgggtga	atcagcttgg	aatcgatatt	acttctgatt	tctccggtga	120
ctcggaggaa	actcctat	ttgtcggcgt	agccactggg	gcttgcctct	tcttggccga	180
tctcggttagg	cgaattgact	tgccaatagc	tatagatttc	attagagctg	agtcttacgg	240
ctctggtact	gtatccagtg	gagttcccag	agtatcattt	gacttaaagc	ttgacatcac	300
gaacaagcac	gttgtcttgg	tcgaggacat	tgtggatact	ggcaatacac	ttagctgcct	360
gattgagcac	atgaaagcaa	aaaaggcgctc	atctgtttcg	gtttgcactc	tcctcgacaa	420

```
gccatcgaga agaaaggttc attataagct ggttggaag gggaaattct acagtggttt 480
tgaatgtcca gatgaatttg tcgtgggcta tggcatggat ttgcagAAC aataccgcaa 540
cctatcttac attggcgtat tgaagcctga atattacatg tgacaatatt gcatgaactg 600
gtcaatcatg acatcttttg atgacttgca cctctgttag gtgttcaaag cagtagcacc 660
aatgttatac tacaatttga cagtgtttct gatgtaaaag ctaatgcaaa ttggtgtatg 720
atatgtt
```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1498296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```
Ser Arg Arg Lys Thr Met Ala Leu Glu Lys His Ile Glu Lys Val Leu
1      5      10      15
Phe Ser Asp Glu Val Ile Ala His Arg Val Asn Gln Leu Gly Ile Asp
20     25     30
Ile Thr Ser Asp Phe Ser Gly Asp Ser Glu Glu Thr Pro Ile Phe Val
35     40     45
Gly Val Ala Thr Gly Ala Cys Leu Phe Leu Ala Asp Leu Val Arg Arg
50     55     60
Ile Asp Leu Pro Ile Ala Ile Asp Phe Ile Arg Ala Glu Ser Tyr Gly
65     70     75     80
Ser Gly Thr Val Ser Ser Gly Val Pro Arg Val Ser Phe Asp Leu Lys
85     90     95
Leu Asp Ile Thr Asn Lys His Val Val Leu Val Glu Asp Ile Val Asp
100    105    110
Thr Gly Asn Thr Leu Ser Cys Leu Ile Glu His Met Lys Ala Lys Lys
115    120    125
Ala Ser Ser Val Ser Val Cys Thr Leu Leu Asp Lys Pro Ser Arg Arg
130    135    140
Lys Val His Tyr Lys Leu Val Gly Lys Gly Lys Phe Tyr Ser Gly Phe
145    150    155    160
Glu Cys Pro Asp Glu Phe Val Val Gly Tyr Gly Met Asp Phe Ala Glu
165    170    175
Gln Tyr Arg Asn Leu Ser Tyr Ile Gly Val Leu Lys Pro Glu Tyr Tyr
180    185    190
Met
```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```
Met Ala Leu Glu Lys His Ile Glu Lys Val Leu Phe Ser Asp Glu Val
1      5      10      15
Ile Ala His Arg Val Asn Gln Leu Gly Ile Asp Ile Thr Ser Asp Phe
20     25     30
Ser Gly Asp Ser Glu Glu Thr Pro Ile Phe Val Gly Val Ala Thr Gly
```

35 40 45  
Ala Cys Leu Phe Leu Ala Asp Leu Val Arg Arg Ile Asp Leu Pro Ile  
50 55 60  
Ala Ile Asp Phe Ile Arg Ala Glu Ser Tyr Gly Ser Gly Thr Val Ser  
65 70 75 80  
Ser Gly Val Pro Arg Val Ser Phe Asp Leu Lys Leu Asp Ile Thr Asn  
85 90 95  
Lys His Val Val Leu Val Glu Asp Ile Val Asp Thr Gly Asn Thr Leu  
100 105 110  
Ser Cys Leu Ile Glu His Met Lys Ala Lys Lys Ala Ser Ser Val Ser  
115 120 125  
Val Cys Thr Leu Leu Asp Lys Pro Ser Arg Arg Lys Val His Tyr Lys  
130 135 140  
Leu Val Gly Lys Gly Lys Phe Tyr Ser Gly Phe Glu Cys Pro Asp Glu  
145 150 155 160  
Phe Val Val Gly Tyr Gly Met Asp Phe Ala Glu Gln Tyr Arg Asn Leu  
165 170 175  
Ser Tyr Ile Gly Val Leu Lys Pro Glu Tyr Tyr Met  
180 185

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1795
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

aaaataacttta	ggaaagaaaa	gagtcctcagc	agcatcagct	cgtccttaaaa	tctgatcccat	60
catcgctcact	ttctcccggc	gaattccggt	ttatcgattt	aagtaacgag	atttgtgcaa	120
agatgactca	ggacgtggag	atgaaagata	ataacacccc	ttctcaatcg	attatctctt	180
cttcgacctc	tactatgcag	aatttgaagg	agattgcagc	actcatcgat	actgggtctt	240
acacgaagga	ggttcgctgt	attgctcgtg	ctgtgcgtct	cactataggc	cttaggcaga	300
aactcaccgg	ctctgtgctc	tcttccttcc	tggattttgc	tttggttcca	ggatccgaag	360
ctcactctcg	cctctcttcc	tttgttccta	agggtgatga	acatgacatg	gaagttgata	420
ctgcctcatc	ggccacacaa	gctgctcctt	ctaagcatct	acctgcagag	ctcgagatct	480
actgctactt	cattgtttct	ctttttctga	ttgatcagaa	gaagtacaac	gaggctaaag	540
cttgtttctt	agcaagcatt	gctcgtctca	agaacgtcaa	ccgaaggacc	attgatgtga	600
tagcatcaag	actctacttt	tactattctt	tgagttatga	gcaaaccggt	gatcttgctg	660
aaattcgcgg	tactcttctt	gcgttgcatc	attctgcaac	gctaaggcac	gatgagctgg	720
gtcaggaaac	ccttctgaac	ctgttgctac	gtaactatct	gcattacaac	ctctatgatc	780
aggcagagaa	gctaagatca	aaggcacctc	gctttgaggc	tcattcaaac	caacagtttt	840
gtaggtaacct	tttctatctc	gggaagattc	gtactattca	gctcgaatat	acggacgcaa	900
aagagagcct	tcttcaggcg	gccaggaaaag	cccctatagc	agctttgggc	ttcaggatcc	960
aatgtaataa	atgggcaatt	ctggttcgtc	tactgotggg	tgagatacca	gagcgttcta	1020
tcttcactca	aaagggtagt	gagaaggccc	tcagacccta	cttcgagcta	acaaatgcgg	1080
ttaggatttg	ggacttgtag	ttgttttaga	cagtccagga	gaagttcttg	gacacatttg	1140
ctcaagacag	aacgcacaat	ctcatcgctg	gactccgcca	caatgtcatc	aggactggac	1200
tgcggaacat	aagtatctcc	tactcgagaa	tctctttacc	cgatggttgc	aaaaagctga	1260
ggctcaactc	tgaaaaccct	ggctgatgcg	gaaagcatcg	tggcaaaggc	catacgcgac	1320
ggagctatcg	atgctacaat	cgatcacaaa	aacggatgca	tggctctcaa	agaaactggg	1380
gacatctact	cgacgaatga	gccacaaact	gcgttcaact	caagaattgc	tttctgcctc	1440
aacatgcata	acgaagctgt	cagagcattg	aggtttcttc	ctaacactca	caaggagaaa	1500
gaaagcgatg	agaagaggag	agagaggaag	caacaggaag	aagagcttgc	taagcatatg	1560
gctgaggaag	acgatgatga	cttttagaca	aaggatcatc	atttcttata	agagttgact	1620
ctccatctgt	ctcacttttt	ttatgttcac	aagtttactt	ggtactcttc	tcacgtcttc	1680
taagtgtttc	tttattgagg	atttttatcc	tcaggaaacct	ttttattact	ctgggtttcac	1740
tttaggaaaa	gatattttat	ttgttggttt	cagaagatca	aattcaagtt	cgttt	

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..387

(D) OTHER INFORMATION: / Ceres Seq. ID 1498310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met	Thr	Gln	Asp	Val	Glu	Met	Lys	Asp	Asn	Asn	Thr	Pro	Ser	Gln	Ser
1				5				10						15	
Ile	Ile	Ser	Ser	Ser	Thr	Ser	Thr	Met	Gln	Asn	Leu	Lys	Glu	Ile	Ala
			20					25					30		
Ala	Leu	Ile	Asp	Thr	Gly	Ser	Tyr	Thr	Lys	Glu	Val	Arg	Arg	Ile	Ala
			35				40					45			
Arg	Ala	Val	Arg	Leu	Thr	Ile	Gly	Leu	Arg	Gln	Lys	Leu	Thr	Gly	Ser
		50					55					60			
Val	Leu	Ser	Ser	Phe	Leu	Asp	Phe	Ala	Leu	Val	Pro	Gly	Ser	Glu	Ala
65					70					75					80
His	Ser	Arg	Leu	Ser	Ser	Phe	Val	Pro	Lys	Gly	Asp	Glu	His	Asp	Met
				85					90					95	
Glu	Val	Asp	Thr	Ala	Ser	Ser	Ala	Thr	Gln	Ala	Ala	Pro	Ser	Lys	His
			100					105					110		
Leu	Pro	Ala	Glu	Leu	Glu	Ile	Tyr	Cys	Tyr	Phe	Ile	Val	Leu	Leu	Phe
			115					120					125		
Leu	Ile	Asp	Gln	Lys	Lys	Tyr	Asn	Glu	Ala	Lys	Ala	Cys	Ser	Ser	Ala
						135					140				
Ser	Ile	Ala	Arg	Leu	Lys	Asn	Val	Asn	Arg	Arg	Thr	Ile	Asp	Val	Ile
145					150					155					160
Ala	Ser	Arg	Leu	Tyr	Phe	Tyr	Tyr	Ser	Leu	Ser	Tyr	Glu	Gln	Thr	Gly
				165					170					175	
Asp	Leu	Ala	Glu	Ile	Arg	Gly	Thr	Leu	Leu	Ala	Leu	His	His	Ser	Ala
			180					185						190	
Thr	Leu	Arg	His	Asp	Glu	Leu	Gly	Gln	Glu	Thr	Leu	Leu	Asn	Leu	Leu
			195				200					205			
Leu	Arg	Asn	Tyr	Leu	His	Tyr	Asn	Leu	Tyr	Asp	Gln	Ala	Glu	Lys	Leu
						215					220				
Arg	Ser	Lys	Ala	Pro	Arg	Phe	Glu	Ala	His	Ser	Asn	Gln	Gln	Phe	Cys
225					230					235					240
Arg	Tyr	Leu	Phe	Tyr	Leu	Gly	Lys	Ile	Arg	Thr	Ile	Gln	Leu	Glu	Tyr
				245					250					255	
Thr	Asp	Ala	Lys	Glu	Ser	Leu	Leu	Gln	Ala	Ala	Arg	Lys	Ala	Pro	Ile
			260					265					270		
Ala	Ala	Leu	Gly	Phe	Arg	Ile	Gln	Cys	Asn	Lys	Trp	Ala	Ile	Leu	Val
			275				280					285			
Arg	Leu	Leu	Leu	Gly	Glu	Ile	Pro	Glu	Arg	Ser	Ile	Phe	Thr	Gln	Lys
						295					300				
Gly	Met	Glu	Lys	Ala	Leu	Arg	Pro	Tyr	Phe	Glu	Leu	Thr	Asn	Ala	Val
305					310					315					320
Arg	Ile	Gly	Asp	Leu	Glu	Leu	Phe	Arg	Thr	Val	Gln	Glu	Lys	Phe	Leu
				325					330					335	
Asp	Thr	Phe	Ala	Gln	Asp	Arg	Thr	His	Asn	Leu	Ile	Val	Arg	Leu	Arg
			340					345					350		
His	Asn	Val	Ile	Arg	Thr										

385

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1498311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met	Lys	Asp	Asn	Asn	Thr	Pro	Ser	Gln	Ser	Ile	Ile	Ser	Ser	Ser	Thr
1				5					10					15	
Ser	Thr	Met	Gln	Asn	Leu	Lys	Glu	Ile	Ala	Ala	Leu	Ile	Asp	Thr	Gly
			20					25					30		
Ser	Tyr	Thr	Lys	Glu	Val	Arg	Arg	Ile	Ala	Arg	Ala	Val	Arg	Leu	Thr
			35				40					45			
Ile	Gly	Leu	Arg	Gln	Lys	Leu	Thr	Gly	Ser	Val	Leu	Ser	Ser	Phe	Leu
	50					55					60				
Asp	Phe	Ala	Leu	Val	Pro	Gly	Ser	Glu	Ala	His	Ser	Arg	Leu	Ser	Ser
65					70					75					80
Phe	Val	Pro	Lys	Gly	Asp	Glu	His	Asp	Met	Glu	Val	Asp	Thr	Ala	Ser
			85						90					95	
Ser	Ala	Thr	Gln	Ala	Ala	Pro	Ser	Lys	His	Leu	Pro	Ala	Glu	Leu	Glu
			100					105					110		
Ile	Tyr	Cys	Tyr	Phe	Ile	Val	Leu	Leu	Phe	Leu	Ile	Asp	Gln	Lys	Lys
	115						120					125			
Tyr	Asn	Glu	Ala	Lys	Ala	Cys	Ser	Ser	Ala	Ser	Ile	Ala	Arg	Leu	Lys
	130					135					140				
Asn	Val	Asn	Arg	Arg	Thr	Ile	Asp	Val	Ile	Ala	Ser	Arg	Leu	Tyr	Phe
145					150					155					160
Tyr	Tyr	Ser	Leu	Ser	Tyr	Glu	Gln	Thr	Gly	Asp	Leu	Ala	Glu	Ile	Arg
			165						170					175	
Gly	Thr	Leu	Leu	Ala	Leu	His	His	Ser	Ala	Thr	Leu	Arg	His	Asp	Glu
			180					185					190		
Leu	Gly	Gln	Glu	Thr	Leu	Leu	Asn	Leu	Leu	Leu	Arg	Asn	Tyr	Leu	His
	195						200					205			
Tyr	Asn	Leu	Tyr	Asp	Gln	Ala	Glu	Lys	Leu	Arg	Ser	Lys	Ala	Pro	Arg
	210					215					220				
Phe	Glu	Ala	His	Ser	Asn	Gln	Gln	Phe	Cys	Arg	Tyr	Leu	Phe	Tyr	Leu
225					230				235						240
Gly	Lys	Ile	Arg	Thr	Ile	Gln	Leu	Glu	Tyr	Thr	Asp	Ala	Lys	Glu	Ser
			245						250					255	
Leu	Leu	Gln	Ala	Ala	Arg	Lys	Ala	Pro	Ile	Ala	Ala	Leu	Gly	Phe	Arg
			260					265					270		
Ile	Gln	Cys	Asn	Lys	Trp	Ala	Ile	Leu	Val	Arg	Leu	Leu	Leu	Gly	Glu
	275						280						285		
Ile	Pro	Glu	Arg	Ser	Ile	Phe	Thr	Gln	Lys	Gly	Met	Glu	Lys	Ala	Leu
	290					295					300				
Arg	Pro	Tyr	Phe	Glu	Leu	Thr	Asn	Ala	Val	Arg	Ile	Gly	Asp	Leu	Glu
305					310					315					320
Leu	Phe	Arg	Thr	Val	Gln	Glu	Lys	Phe	Leu	Asp	Thr	Phe	Ala	Gln	Asp
			325						330					335	
Arg	Thr	His	Asn	Leu	Ile	Val	Arg	Leu	Arg	His	Asn	Val	Ile	Arg	Thr
			340					345					350		
Gly	Leu	Arg	Asn	Ile	Ser	Ile	Ser	Tyr	Ser	Arg	Ile	Ser	Leu	Pro	Asp
	355						360					365			
Val	Ala	Lys	Lys	Leu	Arg	Leu	Asn	Ser	Glu	Asn	Pro	Gly			
	370					375						380			

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met	Gln	Asn	Leu	Lys	Glu	Ile	Ala	Ala	Leu	Ile	Asp	Thr	Gly	Ser	Tyr	
1				5					10					15		
Thr	Lys	Glu	Val	Arg	Arg	Ile	Ala	Arg	Ala	Val	Arg	Leu	Thr	Ile	Gly	
			20					25					30			
Leu	Arg	Gln	Lys	Leu	Thr	Gly	Ser	Val	Leu	Ser	Ser	Phe	Leu	Asp	Phe	
			35				40					45				
Ala	Leu	Val	Pro	Gly	Ser	Glu	Ala	His	Ser	Arg	Leu	Ser	Ser	Phe	Val	
	50					55					60					
Pro	Lys	Gly	Asp	Glu	His	Asp	Met	Glu	Val	Asp	Thr	Ala	Ser	Ser	Ala	
65				70						75					80	
Thr	Gln	Ala	Ala	Pro	Ser	Lys	His	Leu	Pro	Ala	Glu	Leu	Glu	Ile	Tyr	
			85						90					95		
Cys	Tyr	Phe	Ile	Val	Leu	Leu	Phe	Leu	Ile	Asp	Gln	Lys	Lys	Tyr	Asn	
			100					105					110			
Glu	Ala	Lys	Ala	Cys	Ser	Ser	Ala	Ser	Ile	Ala	Arg	Leu	Lys	Asn	Val	
		115					120					125				
Asn	Arg	Arg	Thr	Ile	Asp	Val	Ile	Ala	Ser	Arg	Leu	Tyr	Phe	Tyr	Tyr	
	130					135					140					
Ser	Leu	Ser	Tyr	Glu	Gln	Thr	Gly	Asp	Leu	Ala	Glu	Ile	Arg	Gly	Thr	
145				150						155					160	
Leu	Leu	Ala	Leu	His	His	Ser	Ala	Thr	Leu	Arg	His	Asp	Glu	Leu	Gly	
			165						170					175		
Gln	Glu	Thr	Leu	Leu	Asn	Leu	Leu	Leu	Arg	Asn	Tyr	Leu	His	Tyr	Asn	
		180						185					190			
Leu	Tyr	Asp	Gln	Ala	Glu	Lys	Leu	Arg	Ser	Lys	Ala	Pro	Arg	Phe	Glu	
		195					200					205				
Ala	His	Ser	Asn	Gln	Gln	Phe	Cys	Arg	Tyr	Leu	Phe	Tyr	Leu	Gly	Lys	
		210				215					220					
Ile	Arg	Thr	Ile	Gln	Leu	Glu	Tyr	Thr	Asp	Ala	Lys	Glu	Ser	Leu	Leu	
225				230						235					240	
Gln	Ala	Ala	Arg	Lys	Ala	Pro	Ile	Ala	Ala	Leu	Gly	Phe	Arg	Ile	Gln	
			245						250					255		
Cys	Asn	Lys	Trp	Ala	Ile	Leu	Val	Arg	Leu	Leu	Leu	Gly	Glu	Ile	Pro	
		260						265					270			
Glu	Arg	Ser	Ile	Phe	Thr	Gln	Lys	Gly	Met	Glu	Lys	Ala	Leu	Arg	Pro	
		275				280						285				
Tyr	Phe	Glu	Leu	Thr	Asn	Ala	Val	Arg	Ile	Gly	Asp	Leu	Glu	Leu	Phe	
	290					295					300					
Arg	Thr	Val	Gln	Glu	Lys	Phe	Leu	Asp	Thr	Phe	Ala	Gln	Asp	Arg	Thr	
305					310					315					320	
His	Asn	Leu	Ile	Val	Arg	Leu	Arg	His	Asn	Val	Ile	Arg	Thr	Gly	Leu	
			325						330					335		
Arg	Asn	Ile	Ser	Ile	Ser	Tyr	Ser	Arg	Ile	Ser	Leu	Pro	Asp	Val	Ala	
		340						345					350			
Lys	Lys	Leu	Arg	Leu	Asn	Ser	Glu	Asn	Pro	Gly						
		355					360									

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

(2) INFORMATION FOR SEQ ID NO:336:

(A) LENGTH: 598 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1498314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

His	Cys	Tyr	Ser	Leu	Ser	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Cys	Ile
1				5					10				15	
Ser	Ser	Thr	Ser	Ser	Phe	Pro	Met	Ala	Asp	Ala	Tyr	Glu	Pro	Tyr
			20					25					30	His
Val	Leu	Gln	Gln	Ser	Arg	Arg	Asp	Lys	Leu	Arg	Ile	Pro	Ser	Leu
		35					40					45		Asp
Ser	His	Phe	His	Phe	His	Pro	Pro	Pro	Pro	Ser	Ser	Gly	Gly	Gly
	50					55				60				

Gly Gly Val Phe Pro Leu Ala Asp Ser Asp Phe Leu Ala Ala Gly Gly  
65 70 75 80  
Phe His Ser Asn Asn Asn Asn His Ile Ser Asn Pro Ser Tyr Ser  
85 90 95  
Asn Phe Met Gly Phe Leu Gly Gly Pro Ser Ser Ser Ser Ser Thr Ala  
100 105 110  
Val Ala Val Ala Gly Asp His Ser Phe Asn Ala Gly Leu Ser Ser Gly  
115 120 125  
Asp Val Leu Val Phe Lys Pro Glu Pro Leu Ser Leu Ser Leu Ser Ser  
130 135 140  
His Pro Arg Leu Ala Tyr Asp Leu Val Val Pro Gly Val Val Asn Ser  
145 150 155 160  
Gly Phe Cys Arg Ser Ala Gly Glu Ala Asn Ala Ala Val Thr Ile  
165 170 175  
Ala Ser Arg Ser Ser Gly Pro Leu Gly Pro Phe Thr Gly Tyr Ala Ser  
180 185 190  
Ile Leu Lys Gly Ser Arg Phe Leu Lys Pro Ala Gln Met Leu Leu Asp  
195 200 205  
Glu Phe Cys Asn Val Gly Arg Gly Ile Tyr Thr Asp Lys Val Ile Asp  
210 215 220  
Asp Asp Asp Ser Ser Leu Phe Asp Pro Thr Val Glu Asn Leu Cys  
225 230 235 240  
Gly Val Ser Asp Gly Gly Gly Asp Asn Gly Lys Lys Lys Ser Lys  
245 250 255  
Leu Ile Ser Met Leu Asp Glu Val Tyr Lys Arg Tyr Lys Gln Tyr Tyr  
260 265 270  
Glu Gln Leu Gln Ala Val Met Gly Ser Phe Glu Cys Val Ala Gly Leu  
275 280 285  
Gly His Ala Ala Pro Tyr Ala Asn Leu Ala Leu Lys Ala Leu Ser Lys  
290 295 300  
His Phe Lys Cys Leu Lys Asn Ala Ile Thr Asp Gln Leu Gln Phe Ser  
305 310 315 320  
His Asn Asn Lys Ile Gln Gln Gln Gln Gln Cys Gly His Pro Met Asn  
325 330 335  
Ser Glu Asn Lys Thr Asp Ser Leu Arg Phe Gly Gly Ser Asp Ser Ser  
340 345 350  
Arg Gly Leu Cys Ser Ala Gly Gln Arg His Gly Phe Pro Asp His His  
355 360 365  
Ala Pro Val Trp Arg Pro His Arg Gly Leu Pro Glu Arg Ala Val Thr  
370 375 380  
Val Leu Arg Ala Trp Leu Phe Asp His Phe Leu His Pro Tyr Pro Thr  
385 390 395 400  
Asp Thr Asp Lys Leu Met Leu Ala Lys Gln Thr Gly Leu Ser Arg Asn  
405 410 415  
Gln Val Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Val Trp Lys Pro  
420 425 430  
Met Val Glu Glu Ile His Met Leu Glu Thr Arg Gln Ser Gln Arg Ser  
435 440 445  
Ser Ser Ser Ser Trp Arg Asp Glu Arg Thr Ser Thr Thr Val Phe Pro  
450 455 460  
Asp Asn Asn Asn Asn Asn Pro Ser Ser Ser Ser Ala Gln Gln Arg Pro  
465 470 475 480  
Asn Asn Ser Ser Pro Arg Arg Ala Arg Asn Asp Asp Val His Gly  
485 490 495  
Thr Asn Asn Asn Asn Ser Tyr Val Asn Ser Gly Ser Gly Gly Ser  
500 505 510  
Ala Val Gly Phe Ser Tyr Gly Ile Gly Ser Ser Asn Val Pro Val Met  
515 520 525  
Asn Ser Ser Thr Asn Gly Gly Val Ser Leu Thr Leu Gly Leu His His  
530 535 540  
Gln Ile Gly Leu Pro Glu Pro Phe Pro Met Thr Thr Ala Gln Arg Phe



545                      550                      555                      560  
Gly Leu Asp Gly Gly Ser Gly Asp Gly Gly Gly Tyr Glu Gly Gln  
                                 565                      570                      575  
Asn Arg Gln Phe Gly Arg Asp Phe Ile Gly Gly Ser Asn His Gln Phe  
                                 580                      585                      590  
Leu His Asp Phe Val Gly  
                                 595

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..575

(D) OTHER INFORMATION: / Ceres Seq. ID 1498315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met Ala Asp Ala Tyr Glu Pro Tyr His Val Leu Gln Gln Ser Arg Arg  
1                      5                      10                      15  
Asp Lys Leu Arg Ile Pro Ser Leu Asp Ser His Phe His Phe His Pro  
                                 20                      25                      30  
Pro Pro Pro Pro Ser Ser Gly Gly Gly Gly Gly Val Phe Pro Leu Ala  
                                 35                      40                      45  
Asp Ser Asp Phe Leu Ala Ala Gly Gly Phe His Ser Asn Asn Asn Asn  
50                      55                      60  
Asn His Ile Ser Asn Pro Ser Tyr Ser Asn Phe Met Gly Phe Leu Gly  
65                      70                      75                      80  
Gly Pro Ser Ser Ser Ser Ser Thr Ala Val Ala Val Ala Gly Asp His  
                                 85                      90                      95  
Ser Phe Asn Ala Gly Leu Ser Ser Gly Asp Val Leu Val Phe Lys Pro  
                                 100                      105                      110  
Glu Pro Leu Ser Leu Ser Leu Ser Ser His Pro Arg Leu Ala Tyr Asp  
                                 115                      120                      125  
Leu Val Val Pro Gly Val Val Asn Ser Gly Phe Cys Arg Ser Ala Gly  
130                      135                      140  
Glu Ala Asn Ala Ala Val Thr Ile Ala Ser Arg Ser Ser Gly Pro  
145                      150                      155                      160  
Leu Gly Pro Phe Thr Gly Tyr Ala Ser Ile Leu Lys Gly Ser Arg Phe  
                                 165                      170                      175  
Leu Lys Pro Ala Gln Met Leu Leu Asp Glu Phe Cys Asn Val Gly Arg  
                                 180                      185                      190  
Gly Ile Tyr Thr Asp Lys Val Ile Asp Asp Asp Asp Ser Ser Leu Leu  
                                 195                      200                      205  
Phe Asp Pro Thr Val Glu Asn Leu Cys Gly Val Ser Asp Gly Gly Gly  
210                      215                      220  
Gly Asp Asn Gly Lys Lys Ser Lys Leu Ile Ser Met Leu Asp Glu  
225                      230                      235                      240  
Val Tyr Lys Arg Tyr Lys Gln Tyr Tyr Glu Gln Leu Gln Ala Val Met  
                                 245                      250                      255  
Gly Ser Phe Glu Cys Val Ala Gly Leu Gly His Ala Ala Pro Tyr Ala  
                                 260                      265                      270  
Asn Leu Ala Leu Lys Ala Leu Ser Lys His Phe Lys Cys Leu Lys Asn  
275                      280                      285  
Ala Ile Thr Asp Gln Leu Gln Phe Ser His Asn Asn Lys Ile Gln Gln  
290                      295                      300  
Gln Gln Gln Cys Gly His Pro Met Asn Ser Glu Asn Lys Thr Asp Ser  
305                      310                      315                      320  
Leu Arg Phe Gly Gly Ser Asp Ser Ser Arg Gly Leu Cys Ser Ala Gly  
                                 325                      330                      335

```

Gln Arg His Gly Phe Pro Asp His His Ala Pro Val Trp Arg Pro His
      340      345      350
Arg Gly Leu Pro Glu Arg Ala Val Thr Val Leu Arg Ala Trp Leu Phe
      355      360      365
Asp His Phe Leu His Pro Tyr Pro Thr Asp Thr Asp Lys Leu Met Leu
      370      375      380
Ala Lys Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile
      385      390      395      400
Asn Ala Arg Val Arg Val Trp Lys Pro Met Val Glu Glu Ile His Met
      405      410      415
Leu Glu Thr Arg Gln Ser Gln Arg Ser Ser Ser Ser Trp Arg Asp
      420      425      430
Glu Arg Thr Ser Thr Thr Val Phe Pro Asp Asn Asn Asn Asn Asn Pro
      435      440      445
Ser Ser Ser Ser Ala Gln Gln Arg Pro Asn Asn Ser Ser Pro Pro Arg
      450      455      460
Arg Ala Arg Asn Asp Asp Val His Gly Thr Asn Asn Asn Asn Ser Tyr
      465      470      475      480
Val Asn Ser Gly Ser Gly Gly Gly Ser Ala Val Gly Phe Ser Tyr Gly
      485      490      495
Ile Gly Ser Ser Asn Val Pro Val Met Asn Ser Ser Thr Asn Gly Gly
      500      505      510
Val Ser Leu Thr Leu Gly Leu His His Gln Ile Gly Leu Pro Glu Pro
      515      520      525
Phe Pro Met Thr Thr Ala Gln Arg Phe Gly Leu Asp Gly Gly Ser Gly
      530      535      540
Asp Gly Gly Gly Gly Tyr Glu Gly Gln Asn Arg Gln Phe Gly Arg Asp
      545      550      555      560
Phe Ile Gly Gly Ser Asn His Gln Phe Leu His Asp Phe Val Gly
      565      570      575

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Gly Phe Leu Gly Gly Pro Ser Ser Ser Ser Thr Ala Val Ala
1      5      10      15
Val Ala Gly Asp His Ser Phe Asn Ala Gly Leu Ser Ser Gly Asp Val
      20      25      30
Leu Val Phe Lys Pro Glu Pro Leu Ser Leu Ser Ser His Pro
      35      40      45
Arg Leu Ala Tyr Asp Leu Val Val Pro Gly Val Val Asn Ser Gly Phe
      50      55      60
Cys Arg Ser Ala Gly Glu Ala Asn Ala Ala Val Thr Ile Ala Ser
      65      70      75      80
Arg Ser Ser Gly Pro Leu Gly Pro Phe Thr Gly Tyr Ala Ser Ile Leu
      85      90      95
Lys Gly Ser Arg Phe Leu Lys Pro Ala Gln Met Leu Leu Asp Glu Phe
      100      105      110
Cys Asn Val Gly Arg Gly Ile Tyr Thr Asp Lys Val Ile Asp Asp Asp
      115      120      125
Asp Ser Ser Leu Leu Phe Asp Pro Thr Val Glu Asn Leu Cys Gly Val
      130      135      140
Ser Asp Gly Gly Gly Gly Asp Asn Gly Lys Lys Lys Ser Lys Leu Ile

```

145		150		155		160
Ser Met Leu Asp	Glu Val Tyr Lys Arg	Tyr Lys Gln Tyr Tyr	Glu Gln			
	165	170	175			
Leu Gln Ala Val	Met Gly Ser Phe Glu Cys Val Ala Gly	Leu Gly His				
	180	185	190			
Ala Ala Pro Tyr	Ala Asn Leu Ala Leu Lys Ala Leu Ser Lys His Phe					
	195	200	205			
Lys Cys Leu Lys	Asn Ala Ile Thr Asp Gln Leu Gln Phe Ser His Asn					
	210	215	220			
Asn Lys Ile Gln Gln Gln Gln Gln Cys Gly His	Pro Met Asn Ser Glu					
225	230	235	240			
Asn Lys Thr Asp	Ser Leu Arg Phe Gly Gly Ser Asp Ser Ser Arg Gly					
	245	250	255			
Leu Cys Ser Ala Gly Gln Arg His Gly Phe Pro Asp His His Ala Pro						
	260	265	270			
Val Trp Arg Pro His Arg Gly Leu Pro Glu Arg Ala Val Thr Val Leu						
	275	280	285			
Arg Ala Trp Leu Phe Asp His Phe Leu His Pro Tyr Pro Thr Asp Thr						
	290	295	300			
Asp Lys Leu Met Leu Ala Lys Gln Thr Gly Leu Ser Arg Asn Gln Val						
305	310	315	320			
Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Val Trp Lys Pro Met Val						
	325	330	335			
Glu Glu Ile His Met Leu Glu Thr Arg Gln Ser Gln Arg Ser Ser Ser						
	340	345	350			
Ser Ser Trp Arg Asp Glu Arg Thr Ser Thr Thr Val Phe Pro Asp Asn						
	355	360	365			
Asn Asn Asn Asn Pro Ser Ser Ser Ala Gln Gln Arg Pro Asn Asn						
	370	375	380			
Ser Ser Pro Pro Arg Arg Ala Arg Asn Asp Asp Val His Gly Thr Asn						
385	390	395	400			
Asn Asn Asn Ser Tyr Val Asn Ser Gly Ser Gly Gly Gly Ser Ala Val						
	405	410	415			
Gly Phe Ser Tyr Gly Ile Gly Ser Ser Asn Val Pro Val Met Asn Ser						
	420	425	430			
Ser Thr Asn Gly Gly Val Ser Leu Thr Leu Gly Leu His His Gln Ile						
	435	440	445			
Gly Leu Pro Glu Pro Phe Pro Met Thr Thr Ala Gln Arg Phe Gly Leu						
	450	455	460			
Asp Gly Gly Ser Gly Asp Gly Gly Gly Gly Tyr Glu Gly Gln Asn Arg						
465	470	475	480			
Gln Phe Gly Arg Asp Phe Ile Gly Gly Ser Asn His Gln Phe Leu His						
	485	490	495			
Asp Phe Val Gly						
	500					

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

aatttcgtca agaaaaaaat tcgatttttt tgcgctcttt gtgggttggt gttgttgaaa	60
atggctggtc gtggaaaaac tcttgatcc ggtggggcga agaaagctac atctcgaggt	120
agcaaagccg gtcttcaatt cccggtgggt cgtatcgctc gtttcttaaa agccggtaaa	180
tacgccgaac gtgttggtgc cgggtgctccg gtttatytgc ccgccgttct cgaatatattg	240

```
gccgccgagg ttcttgaatt agctggaaac gcagcaagag acaacaagaa gacacgtatt 300
gttgtctctt gctgcgtttc cagctaattc aagaacctcg gcagcmttct atttcttcac 360
aaagctccag atcactaagc tcgtctcagc tatgctctac ttgggataca tgctcatcgc 420
ctcttacgcg tttttcgtgc tgaccggaac aatcggggtc tacgcttgtc tctggttcac 480
aagactcatc tattcctcgg taaagatcga ttgattcaga aaaacattca agagaagaac 540
gaaagaaaga aggaaggtaa tatagttaat gattttcaca agtttgtttt tgctcaatag 600
gggtctcttc ttgtttcgtc ctggttttgg tttacaagta acaaaagaaa aggttttata 660
tgtaaaccctt ttcttttttt agagtgtatt ctgtttgatt tccccaaatg tcactttgga 720
ttatcttcct taattgmcaa ttatgtgatt ctttc
```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1498318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```
Asn Phe Val Lys Lys Lys Ile Arg Phe Cys Ala Leu Cys Gly Leu
1           5           10           15
Leu Leu Leu Lys Met Ala Gly Arg Gly Lys Thr Leu Gly Ser Gly Gly
20           25           30
Ala Lys Lys Ala Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro
35           40           45
Val Gly Arg Ile Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu Arg
50           55           60
Val Gly Ala Gly Ala Pro Val Tyr Xaa Ala Ala Val Leu Glu Tyr Leu
65           70           75           80
Ala Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys
85           90           95
Lys Thr Arg Ile Val Val Ser Cys Cys Val Ser Ser
100          105
```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1498319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```
Met Ala Gly Arg Gly Lys Thr Leu Gly Ser Gly Gly Ala Lys Lys Ala
1           5           10           15
Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile
20           25           30
Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly Ala Gly
35           40           45
Ala Pro Val Tyr Xaa Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val
50           55           60
Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile
65           70           75           80
Val Val Ser Cys Cys Val Ser Ser
85
```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1233  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

atccagaaaa	aacaaaaaaa	acaaaaaaat	aataaaacaa	aaaaatatct	tttttttttc	60
taataaaaaa	aaaaaaaata	aataaatatg	gaatacacaa	atgtgtccat	tttattaggc	120
atgttggtga	tccttggttc	accaatggtg	ttcgcagatg	atttgacacc	aatcccagag	180
ggcaaaccoc	aagtgggtgca	gtggttcaat	accacagttg	gtccattggt	tcaacgtaaa	240
ggcttagatc	ctgctctcgt	agctgctgag	gctgctccac	gtatcatcaa	cgtgaatcca	300
aagggaggtg	aattcaaaac	actaacagac	gcaataaaga	gcgttcctgc	agggaaacaca	360
aagcgggtga	tcataaagat	ggctcctggt	gagtacagag	agaaggtcac	tatcgacagg	420
aacaaaccct	tcattacatt	gatgggacaa	cccaatgcca	tgctgttat	cacctacgac	480
ggtaccgccg	ccaagtatgg	aaccgttgat	agtgcctctc	tcattatctt	atccgactat	540
ttcatggccg	ttaacatcgt	cgtaaagaac	actgcaccgg	caccagatgg	taaaactaag	600
ggagcacaag	ccttatccat	gagaatctcc	ggaaactttg	ctgctttcta	caactgcaaa	660
ttctacgggt	tccaagatata	aatctgtgat	gataccggaa	accattttct	caaggattgt	720
tacgtcgaag	gaacattcga	tttcatcttc	ggaagtggaa	cctctatgta	cttgggaaca	780
caattgcacg	tgggtggaga	cggtattaga	gtgatcgag	cgcatgcagg	aaagagcgca	840
gaagaaaata	gtggatactc	tttctgtcac	tgcaagggtga	ctggaaactgg	aggagtaatc	900
tatttgggaa	gagcatggat	gagccaccct	aagggtgtct	atgcctacac	cgagatgacc	960
agcgttgtca	acccaccggg	atggcaagaa	aacaagactc	ccgcacatga	caagaccgtg	1020
ttctacggag	agtacaagtg	ttcaggacca	gggtcacaca	aagccaagag	agtgccattc	1080
acacaagaca	tcgacgacaa	agaagctaac	cgtttcctat	ccctcggcta	catccaagga	1140
tccaagtggc	ttctcccacc	acccgctttg	ttaattcttt	aatatcaacc	tattaaaatt	1200
aaaattaaaa	cgtaaaacta	aaattaaac	ttc			

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..361  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Met	Glu	Tyr	Thr	Asn	Val	Ser	Ile	Leu	Leu	Gly	Met	Leu	Val	Ile	Phe	
1				5				10						15		
Val	Ser	Pro	Met	Val	Phe	Ala	Asp	Asp	Leu	Thr	Pro	Ile	Pro	Glu	Gly	
		20						25				30				
Lys	Pro	Gln	Val	Val	Gln	Trp	Phe	Asn	Thr	His	Val	Gly	Pro	Leu	Val	
		35					40					45				
Gln	Arg	Lys	Gly	Leu	Asp	Pro	Ala	Leu	Val	Ala	Ala	Glu	Ala	Ala	Pro	
	50					55				60						
Arg	Ile	Ile	Asn	Val	Asn	Pro	Lys	Gly	Gly	Glu	Phe	Lys	Thr	Leu	Thr	
65			70					75						80		
Asp	Ala	Ile	Lys	Ser	Val	Pro	Ala	Gly	Asn	Thr	Lys	Arg	Val	Ile	Ile	
		85						90						95		
Lys	Met	Ala	Pro	Gly	Glu	Tyr	Arg	Glu	Lys	Val	Thr	Ile	Asp	Arg	Asn	
	100							105					110			
Lys	Pro	Phe	Ile	Thr	Leu	Met	Gly	Gln	Pro	Asn	Ala	Met	Pro	Val	Ile	
	115						120					125				
Thr	Tyr	Asp	Gly	Thr	Ala	Ala	Lys	Tyr	Gly	Thr	Val	Asp	Ser	Ala	Ser	
	130						135					140				

Leu Ile Ile Leu Ser Asp Tyr Phe Met Ala Val Asn Ile Val Val Lys  
145 150 155 160  
Asn Thr Ala Pro Ala Pro Asp Gly Lys Thr Lys Gly Ala Gln Ala Leu  
165 170 175  
Ser Met Arg Ile Ser Gly Asn Phe Ala Ala Phe Tyr Asn Cys Lys Phe  
180 185 190  
Tyr Gly Phe Gln Asp Thr Ile Cys Asp Asp Thr Gly Asn His Phe Phe  
195 200 205  
Lys Asp Cys Tyr Val Glu Gly Thr Phe Asp Phe Ile Phe Gly Ser Gly  
210 215 220  
Thr Ser Met Tyr Leu Gly Thr Gln Leu His Val Val Gly Asp Gly Ile  
225 230 235 240  
Arg Val Ile Ala Ala His Ala Gly Lys Ser Ala Glu Glu Asn Ser Gly  
245 250 255  
Tyr Ser Phe Val His Cys Lys Val Thr Gly Thr Gly Gly Val Ile Tyr  
260 265 270  
Leu Gly Arg Ala Trp Met Ser His Pro Lys Val Val Tyr Ala Tyr Thr  
275 280 285  
Glu Met Thr Ser Val Val Asn Pro Thr Gly Trp Gln Glu Asn Lys Thr  
290 295 300  
Pro Ala His Asp Lys Thr Val Phe Tyr Gly Glu Tyr Lys Cys Ser Gly  
305 310 315 320  
Pro Gly Ser His Lys Ala Lys Arg Val Pro Phe Thr Gln Asp Ile Asp  
325 330 335  
Asp Lys Glu Ala Asn Arg Phe Leu Ser Leu Gly Tyr Ile Gln Gly Ser  
340 345 350  
Lys Trp Leu Leu Pro Pro Pro Ala Leu  
355 360

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met Leu Val Ile Phe Val Ser Pro Met Val Phe Ala Asp Asp Leu Thr  
1 5 10 15  
Pro Ile Pro Glu Gly Lys Pro Gln Val Val Gln Trp Phe Asn Thr His  
20 25 30  
Val Gly Pro Leu Val Gln Arg Lys Gly Leu Asp Pro Ala Leu Val Ala  
35 40 45  
Ala Glu Ala Ala Pro Arg Ile Ile Asn Val Asn Pro Lys Gly Gly Glu  
50 55 60  
Phe Lys Thr Leu Thr Asp Ala Ile Lys Ser Val Pro Ala Gly Asn Thr  
65 70 75 80  
Lys Arg Val Ile Ile Lys Met Ala Pro Gly Glu Tyr Arg Glu Lys Val  
85 90 95  
Thr Ile Asp Arg Asn Lys Pro Phe Ile Thr Leu Met Gly Gln Pro Asn  
100 105 110  
Ala Met Pro Val Ile Thr Tyr Asp Gly Thr Ala Ala Lys Tyr Gly Thr  
115 120 125  
Val Asp Ser Ala Ser Leu Ile Ile Leu Ser Asp Tyr Phe Met Ala Val  
130 135 140  
Asn Ile Val Val Lys Asn Thr Ala Pro Ala Pro Asp Gly Lys Thr Lys  
145 150 155 160  
Gly Ala Gln Ala Leu Ser Met Arg Ile Ser Gly Asn Phe Ala Ala Phe

Met	Val	Phe	Ala	Asp	Asp	Leu	Thr	Pro	Ile	Pro	Glu	Gly	Lys	Pro	Gln
1				5					10					15	
Val	Val	Gln	Trp	Phe	Asn	Thr	His	Val	Gly	Pro	Leu	Val	Gln	Arg	Lys
			20					25					30		
Gly	Leu	Asp	Pro	Ala	Leu	Val	Ala	Ala	Glu	Ala	Ala	Pro	Arg	Ile	Ile
			35				40					45			
Asn	Val	Asn	Pro	Lys	Gly	Gly	Glu	Phe	Lys	Thr	Leu	Thr	Asp	Ala	Ile
	50					55					60				
Lys	Ser	Val	Pro	Ala	Gly	Asn	Thr	Lys	Arg	Val	Ile	Ile	Lys	Met	Ala
65					70				75					80	
Pro	Gly	Glu	Tyr	Arg	Glu	Lys	Val	Thr	Ile	Asp	Arg	Asn	Lys	Pro	Phe
				85					90					95	
Ile	Thr	Leu	Met	Gly	Gln	Pro	Asn	Ala	Met	Pro	Val	Ile	Thr	Tyr	Asp
			100					105					110		
Gly	Thr	Ala	Ala	Lys	Tyr	Gly	Thr	Val	Asp	Ser	Ala	Ser	Leu	Ile	Ile
			115					120				125			
Leu	Ser	Asp	Tyr	Phe	Met	Ala	Val	Asn	Ile	Val	Val	Lys	Asn	Thr	Ala
			130			135						140			
Pro	Ala	Pro	Asp	Gly	Lys	Thr	Lys	Gly	Ala	Gln	Ala	Leu	Ser	Met	Arg
145					150					155					160
Ile	Ser	Gly	Asn	Phe	Ala	Ala	Phe	Tyr	Asn	Cys	Lys	Phe	Tyr	Gly	Phe
				165					170					175	
Gln	Asp	Thr	Ile	Cys	Asp	Asp	Thr	Gly	Asn	His	Phe	Phe	Lys	Asp	Cys
			180					185					190		
Tyr	Val	Glu	Gly	Thr	Phe	Asp	Phe	Ile	Phe	Gly	Ser	Gly	Thr	Ser	Met
		195					200					205			

Tyr Leu Gly Thr Gln Leu His Val Val Gly Asp Gly Ile Arg Val Ile  
210 215 220  
Ala Ala His Ala Gly Lys Ser Ala Glu Glu Asn Ser Gly Tyr Ser Phe  
225 230 235 240  
Val His Cys Lys Val Thr Gly Thr Gly Gly Val Ile Tyr Leu Gly Arg  
245 250 255  
Ala Trp Met Ser His Pro Lys Val Val Tyr Ala Tyr Thr Glu Met Thr  
260 265 270  
Ser Val Val Asn Pro Thr Gly Trp Gln Glu Asn Lys Thr Pro Ala His  
275 280 285  
Asp Lys Thr Val Phe Tyr Gly Glu Tyr Lys Cys Ser Gly Pro Gly Ser  
290 295 300  
His Lys Ala Lys Arg Val Pro Phe Thr Gln Asp Ile Asp Asp Lys Glu  
305 310 315 320  
Ala Asn Arg Phe Leu Ser Leu Gly Tyr Ile Gln Gly Ser Lys Trp Leu  
325 330 335  
Leu Pro Pro Pro Ala Leu  
340

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1415
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

cctttctacc catttcgtct ccttcatttt gacgttttct ttagatctgt taataatcca	60
tccatggctt ggtctagtca ctagtggtgt tatctctctg tgtggaagaa aaagcaaggt	120
tttttgatca cttggattgt tttaagatat ggcaactttg aacccttttg atttggtgga	180
tgatgatgct gaggatccaa gccagctcgc tgtttccatc gagaagattg ataagtccaa	240
gaaatctgga ccggttttga gcttgccctgc taagtcagct cctaagcttc cctctaagcc	300
acttcctcct gctcaagccg tgagagaggc caggagtgt gctccacgtg gtgggtggagg	360
ccgtggagga tttaatcgtg gtcgtggtgg ttacaaccgt gatgatggt acaatggata	420
tttaggggga tacactaagc cctcagatga aggagatgt tcaaagtctt cttacgagag	480
gcgtggcggg ggtgaagggg agcgtcctcg aagggccttt gagcgtcgta gtggaactgg	540
cagagggaat gacttcaagc gtgacggatc tggctcgtggg aattggggaa ctccagggga	600
agagatagct gctgagactg aagcagtagc tgggtgttgag actgagaagg atgttgagga	660
gaagccagct gttgatgatg tagctgctga tgctaacaag gagaatactg ttgttgagga	720
gaaagagcct gaggataagg aaatgactct tgatgagtat gagaaaatac ttgaggagaa	780
gaaaaaggca cttcaatcat taaccacctc tgagaggaaa gttgatacga aagtgtttga	840
atcaatgcaa caactgtcaa acaagaagtc taatgatgaa atcttcatca agctgggttc	900
tgataaggac aaacgcaaag atgacaaaga agagaaggct aagaaggctg tgagcatcaa	960
tgagtttctg aagccagcag aggggtgggaa ctactaccga ggaggccgtg gtggccgtgg	1020
acgtggtggt cgtggccgtg gaggtgttct tagtggcgaa tctggtggtt accgtaatga	1080
agctgcacca gctattggag atgctgctca gttcccatct cttgggggca agtaagatac	1140
atccatgata acgtccatac tcgtgcatcc tccttttagga ttttggtgga ggatttactg	1200
tttactggtc tctcgttgtc agatgtaaat aattaggtgt cgctcgtcagt ttttagattt	1260
tatgctaaac tttacacttg ttggtgttct ttacttttga aacactacac tcttcttagt	1320
tttaccattt tactcgtttt gtgtttgttg ttttcttatt gggatatgaa acatgttttg	1380
agacggacat atctaattgt atcggggttg agtct	

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1498325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```
Met Ala Thr Leu Asn Pro Phe Asp Leu Leu Asp Asp Asp Ala Glu Asp
1          5          10          15
Pro Ser Gln Leu Ala Val Ser Ile Glu Lys Ile Asp Lys Ser Lys Lys
20          25          30
Ser Gly Pro Val Ser Ser Leu Pro Ala Lys Ser Ala Pro Lys Leu Pro
35          40          45
Ser Lys Pro Leu Pro Pro Ala Gln Ala Val Arg Glu Ala Arg Ser Asp
50          55          60
Ala Pro Arg Gly Gly Gly Gly Arg Gly Gly Phe Asn Arg Gly Arg Gly
65          70          75          80
Gly Tyr Asn Arg Asp Asp Gly Asn Asn Gly Tyr Leu Gly Gly Tyr Thr
85          90          95
Lys Pro Ser Asp Glu Gly Asp Val Ser Lys Ser Ser Tyr Glu Arg Arg
100         105         110
Gly Gly Gly Glu Gly Glu Arg Pro Arg Arg Ala Phe Glu Arg Arg Ser
115         120         125
Gly Thr Gly Arg Gly Ser Asp Phe Lys Arg Asp Gly Ser Gly Arg Gly
130         135         140
Asn Trp Gly Thr Pro Gly Glu Glu Ile Ala Ala Glu Thr Glu Ala Val
145         150         155         160
Ala Gly Val Glu Thr Glu Lys Asp Val Gly Glu Lys Pro Ala Val Asp
165         170         175
Asp Val Ala Ala Asp Ala Asn Lys Glu Asn Thr Val Val Glu Glu Lys
180         185         190
Glu Pro Glu Asp Lys Glu Met Thr Leu Asp Glu Tyr Glu Lys Ile Leu
195         200         205
Glu Glu Lys Lys Lys Ala Leu Gln Ser Leu Thr Thr Ser Glu Arg Lys
210         215         220
Val Asp Thr Lys Val Phe Glu Ser Met Gln Gln Leu Ser Asn Lys Lys
225         230         235         240
Ser Asn Asp Glu Ile Phe Ile Lys Leu Gly Ser Asp Lys Asp Lys Arg
245         250         255
Lys Asp Asp Lys Glu Glu Lys Ala Lys Lys Ala Val Ser Ile Asn Glu
260         265         270
Phe Leu Lys Pro Ala Glu Gly Gly Asn Tyr Tyr Arg Gly Gly Arg Gly
275         280         285
Gly Arg Gly Arg Gly Gly Arg Gly Arg Gly Gly Val Ser Ser Gly Glu
290         295         300
Ser Gly Gly Tyr Arg Asn Glu Ala Ala Pro Ala Ile Gly Asp Ala Ala
305         310         315         320
Gln Phe Pro Ser Leu Gly Gly Lys
325
```

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1498326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```
acaaacatta ctcattcaca aaaccatctt aaagcaacta cacaaatctt gaaattttct
catattttct atttactata taaactttta atcaaataca gattaactat ggctgaggag
```

60  
120

tacaagaaca acgttccccga gcacgagaca ccaacgggtcg caacagagga atcaccagcg 180  
acgacaacag aggttacgga tcgtcgattg tttgatttct tggggaagaa ggaagaggaa 240  
gtgaaacctc aagagacaac gacgctcgag tctgagttcg atcataaggc tcagatctct 300  
gaaccggagt tagctgcgga sacgaggaag tgaaggagaa caagattact ctgctagagg 360  
agcttcaaga aaagaccgag gaagatgagg agaacaagcc tagtgtcatc gaaaagcttc 420  
accgatccaa cagctcttct tcctcttcga gcgatgaaga aggtgaggaa aagaaggaga 480  
agaagaagaa gatcgttgaa ggagaggaag ataagaaagg actag

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1498327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Thr	Asn	Ile	Thr	His	Ser	Gln	Asn	His	Leu	Lys	Ala	Thr	Thr	Gln	Ile
1			5						10					15	
Leu	Lys	Phe	Ser	His	Ile	Phe	Tyr	Leu	Leu	Tyr	Lys	Leu	Leu	Ile	Lys
			20					25						30	
Ser	Arg	Leu	Thr	Met	Ala	Glu	Glu	Tyr	Lys	Asn	Asn	Val	Pro	Glu	His
			35					40				45			
Glu	Thr	Pro	Thr	Val	Ala	Thr	Glu	Glu	Ser	Pro	Ala	Thr	Thr	Thr	Glu
			50				55				60				
Val	Thr	Asp	Arg	Arg	Leu	Phe	Asp	Phe	Leu	Gly	Lys	Lys	Glu	Glu	Glu
65					70					75				80	
Val	Lys	Pro	Gln	Glu	Thr	Thr	Thr	Leu	Glu	Ser	Glu	Phe	Asp	His	Lys
			85					90						95	
Ala	Gln	Ile	Ser	Glu	Pro	Glu	Leu	Ala	Ala	Xaa	Thr	Arg	Lys		
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1498328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met	Ala	Glu	Glu	Tyr	Lys	Asn	Asn	Val	Pro	Glu	His	Glu	Thr	Pro	Thr
1				5				10						15	
Val	Ala	Thr	Glu	Glu	Ser	Pro	Ala	Thr	Thr	Thr	Glu	Val	Thr	Asp	Arg
			20					25						30	
Arg	Leu	Phe	Asp	Phe	Leu	Gly	Lys	Lys	Glu	Glu	Glu	Val	Lys	Pro	Gln
			35				40					45			
Glu	Thr	Thr	Thr	Leu	Glu	Ser	Glu	Phe	Asp	His	Lys	Ala	Gln	Ile	Ser
			50			55					60				
Glu	Pro	Glu	Leu	Ala	Ala	Xaa	Thr	Arg	Lys						
65					70										

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1354

(D) OTHER INFORMATION: / Ceres Seq. ID 1498329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

atctctttct	cacaattaga	ttctgtgctt	cttctgcat	caactaagat	ccgatccgcg	60
agcgtttcag	acttcgatca	gatccgatta	agagaagcaa	atcgggtcgg	gtatgactcg	120
tcgatgttct	cactgcaatc	acaatggcca	caactctcgg	acttgctcca	atcgcgccgt	180
gaagctcttt	ggtgttcggc	tcaccgaagg	ttcgatccgg	aaaagtgcaa	gtatgggtaa	240
tcttagccat	tacacgggtt	ctggatcggg	tgggcatgga	accgggtcca	acactccggg	300
ttctccgggt	gatgtccctg	accatgtcgc	tggatggtg	tacgcttctg	aggatttcgt	360
tgctggctct	tcctctagcc	gcgagagaaa	gaaaggaact	ccatggacag	aggaagaaca	420
caggatgttc	ttattaggtt	tacagaagct	gggtaaagg	gattggagag	gtatctcaag	480
aaactatgtg	accactmnga	cacctacaca	agttgctagc	catgctcaga	agtatttcat	540
cagacaatcc	aatgtctctc	gtcgcaaaag	acgttctagt	ctctttgata	tggttcctga	600
tgaggttgga	gatattccca	tggatttgca	agaaccagag	gaagataata	ttcctgtgga	660
aactgaaatg	caagggtcgt	actctattca	tcagacactt	gctcctagct	cacttcacgc	720
accgtcaatc	ttggaaatcg	aagaatgtga	atcaatggac	tccacaaact	ctaccaccgg	780
ggaaccaacc	gcaactgccg	ctgctgcttc	ttcttcttcc	agactagaag	aaaccacaca	840
actgcaatca	caactgcaac	cgcagccgca	actacctggc	tcattcccca	tactatatcc	900
gacctacttt	tcaccatatt	accggtttcc	attcccaata	tggcctgctg	gttatgttcc	960
tgaaccaccc	aagaaagagg	aaactcatga	aattctcaga	ccaactgctg	tgcactcgaa	1020
agctcctatc	aatgttgacg	agcttcttgg	tatgtctaag	ctcagccttg	cagagtccaa	1080
caaacatgga	gaatccgatc	agtctctttc	attgaagcta	ggtggcgggt	catcttcaag	1140
acaatcagca	tttcacccga	atcctagctc	tgatagttca	gacatcaaaa	gcgtgataca	1200
cgctttataa	aagacctgag	gaagtgatgg	tctaaaatgg	gatctgggtt	gggggtttaca	1260
ggttagttgt	tggtcacagt	aacttaaata	agtttttctt	tgttaggttg	tttaacttgg	1320
gtaggatgtt ttagttcagc tttgatcatt aggg						

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1498330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met	Thr	Arg	Arg	Cys	Ser	His	Cys	Asn	His	Asn	Gly	His	Asn	Ser	Arg	
1				5				10						15		
Thr	Cys	Pro	Asn	Arg	Gly	Val	Lys	Leu	Phe	Gly	Val	Arg	Leu	Thr	Glu	
			20					25						30		
Gly	Ser	Ile	Arg	Lys	Ser	Ala	Ser	Met	Gly	Asn	Leu	Ser	His	Tyr	Thr	
			35					40						45		
Gly	Ser	Gly	Ser	Gly	Gly	His	Gly	Thr	Gly	Ser	Asn	Thr	Pro	Gly	Ser	
			50					55						60		
Pro	Gly	Asp	Val	Pro	Asp	His	Val	Ala	Gly	Asp	Gly	Tyr	Ala	Ser	Glu	
			65					70						75		80
Asp	Phe	Val	Ala	Gly	Ser	Ser	Ser	Ser	Arg	Glu	Arg	Lys	Lys	Gly	Thr	
			85						90					95		
Pro	Trp	Thr	Glu	Glu	Glu	His	Arg	Met	Phe	Leu	Leu	Gly	Leu	Gln	Lys	
			100					105						110		
Leu	Gly	Lys	Gly	Asp	Trp	Arg	Gly	Ile	Ser	Arg	Asn	Tyr	Val	Thr	Thr	
			115					120						125		
Xaa	Thr	Pro	Thr	Gln	Val	Ala	Ser	His	Ala	Gln	Lys	Tyr	Phe	Ile	Arg	
			130					135						140		
Gln	Ser	Asn	Val	Ser	Arg	Arg	Lys	Arg	Arg	Ser	Ser	Leu	Phe	Asp	Met	
			145					150						155		160

(2) INFORMATION FOR SEQ ID NO:353:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1498331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met	Gly	Asn	Leu		Ser	His	Tyr	Thr	Gly		Ser	Gly	Ser	Gly	Gly	His	Gly
1				5						10						15	
Thr	Gly	Ser	Asn	Thr	Pro	Gly	Ser	Pro	Gly	Asp	Val	Pro	Asp	His	Val		
			20					25						30			
Ala	Gly	Asp	Gly	Tyr	Ala	Ser	Glu	Asp	Phe	Val	Ala	Gly	Ser	Ser	Ser		
		35					40					45					
Ser	Arg	Glu	Arg	Lys	Lys	Gly	Thr	Pro	Trp	Thr	Glu	Glu	Glu	His	Arg		
	50					55					60						
Met	Phe	Leu	Leu	Gly	Leu	Gln	Lys	Leu	Gly	Lys	Gly	Asp	Trp	Arg	Gly		
65				70						75					80		
Ile	Ser	Arg	Asn	Tyr	Val	Thr	Thr	Xaa	Thr	Pro	Thr	Gln	Val	Ala	Ser		
			85						90					95			
His	Ala	Gln	Lys	Tyr	Phe	Ile	Arg	Gln	Ser	Asn	Val	Ser	Arg	Arg	Lys		
			100					105					110				
Arg	Arg	Ser	Ser	Leu	Phe	Asp	Met	Val	Pro	Asp	Glu	Val	Gly	Asp	Ile		
		115					120					125					
Pro	Met	Asp	Leu	Gln	Glu	Pro	Glu	Glu	Asp	Asn	Ile	Pro	Val	Glu	Thr		
	130					135					140						
Glu	Met	Gln	Gly	Ala	Asp	Ser	Ile	His	Gln	Thr	Leu	Ala	Pro	Ser	Ser		
145				150						155					160		
Leu	His	Ala	Pro	Ser	Ile	Leu	Glu	Ile	Glu	Glu	Cys	Glu	Ser	Met	Asp		
			165						170					175			
Ser	Thr	Asn	Ser	Thr	Thr	Gly	Glu	Pro	Thr	Ala	Thr	Ala	Ala	Ala	Ala		

Met	Phe	Leu	Leu	Gly	Leu	Gln	Lys	Leu	Gly	Lys	Gly	Asp	Trp	Arg	Gly
1				5					10					15	
Ile	Ser	Arg	Asn	Tyr	Val	Thr	Thr	Xaa	Thr	Pro	Thr	Gln	Val	Ala	Ser
			20					25					30		
His	Ala	Gln	Lys	Tyr	Phe	Ile	Arg	Gln	Ser	Asn	Val	Ser	Arg	Arg	Lys
			35				40					45			
Arg	Arg	Ser	Ser	Leu	Phe	Asp	Met	Val	Pro	Asp	Glu	Val	Gly	Asp	Ile
			50			55					60				
Pro	Met	Asp	Leu	Gln	Glu	Pro	Glu	Glu	Asp	Asn	Ile	Pro	Val	Glu	Thr
65					70					75					80
Glu	Met	Gln	Gly	Ala	Asp	Ser	Ile	His	Gln	Thr	Leu	Ala	Pro	Ser	Ser
				85					90					95	
Leu	His	Ala	Pro	Ser	Ile	Leu	Glu	Ile	Glu	Glu	Cys	Glu	Ser	Met	Asp
			100					105					110		
Ser	Thr	Asn	Ser	Thr	Thr	Gly	Glu	Pro	Thr	Ala	Thr	Ala	Ala	Ala	Ala
			115				120					125			
Ser	Ser	Ser	Ser	Arg	Leu	Glu	Glu	Thr	Thr	Gln	Leu	Gln	Ser	Gln	Leu
			130			135					140				
Gln	Pro	Gln	Pro	Gln	Leu	Pro	Gly	Ser	Phe	Pro	Ile	Leu	Tyr	Pro	Thr
145					150					155					160
Tyr	Phe	Ser	Pro	Tyr	Tyr	Pro	Phe	Pro	Phe	Pro	Ile	Trp	Pro	Ala	Gly
				165					170					175	
Tyr	Val	Pro	Glu	Pro	Pro	Lys	Lys	Glu	Glu	Thr	His	Glu	Ile	Leu	Arg
			180					185					190		
Pro	Thr	Ala	Val	His	Ser	Lys	Ala	Pro	Ile	Asn	Val	Asp	Glu	Leu	Leu
			195				200					205			
Gly	Met	Ser	Lys	Leu	Ser	Leu	Ala	Glu	Ser	Asn	Lys	His	Gly	Glu	Ser
			210			215					220				
Asp	Gln	Ser	Leu	Ser	Leu	Lys	Leu	Gly	Gly	Gly	Ser	Ser	Ser	Arg	Gln
225					230					235					240

Ser Ala Phe His Pro Asn Pro Ser Ser Asp Ser Ser Asp Ile Lys Ser  
245 250 255  
Val Ile His Ala Leu  
260

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..553
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

actttagttt	ttttcacagt	tgagaaatct	cgccgccgtt	tgaagaaaga	agaagagatg	60
ggagttttct	cattcgtgtg	caaaagcaaa	ggcggagaat	ggaccgcaaa	gcaacacgaa	120
ggagatcttg	aagcttcagc	ttcttccacc	tacgatctcc	agcgcaagct	tgttcagact	180
gctctctccg	ccgattcatc	tgccggcggt	cagtcttctt	tctctcttgt	ctctcctacc	240
tccgccgtct	tcgtgggtgt	cattgggtgt	ggtgggtgtg	gaggatttgc	tgccggagga	300
ggtgcagctg	ctggaggtgg	tggtgggtgt	gaggctgccg	cagccacaaa	ggaggaagag	360
aagaagaagg	aagaatctga	agaggaagag	ggagactttg	gatttgatct	ctttgggttaa	420
gagacctaaa	acaactttgt	tagtggttct	aggtttttct	atctcaatth	tctctcttta	480
tgaaatatcg	tgtttctttt	tcggagaaag	agtaagatac	atgatgaaaa	tctgtttttg	540
gggcgttttt	gct					

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Thr	Leu	Val	Phe	Phe	Thr	Val	Glu	Lys	Ser	Arg	Arg	Arg	Leu	Lys	Lys
1			5					10					15		
Glu	Glu	Glu	Met	Gly	Val	Phe	Ser	Phe	Val	Cys	Lys	Ser	Lys	Gly	Gly
			20					25					30		
Glu	Trp	Thr	Ala	Lys	Gln	His	Glu	Gly	Asp	Leu	Glu	Ala	Ser	Ala	Ser
			35				40					45			
Ser	Thr	Tyr	Asp	Leu	Gln	Arg	Lys	Leu	Val	Gln	Thr	Ala	Leu	Ser	Ala
			50			55				60					
Asp	Ser	Ser	Gly	Gly	Val	Gln	Ser	Ser	Phe	Ser	Leu	Val	Ser	Pro	Thr
65					70				75					80	
Ser	Ala	Val	Phe	Val	Val	Val	Ile	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Phe
			85					90						95	
Ala	Ala	Gly	Gly	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala
			100					105						110	
Ala	Ala	Ala	Thr	Lys	Glu	Glu	Glu	Lys	Lys	Lys	Glu	Glu	Ser	Glu	Glu
			115				120					125			
Glu	Glu	Gly	Asp	Phe	Gly	Phe	Asp	Leu	Phe	Gly					
			130				135								

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498335  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:  
Met Gly Val Phe Ser Phe Val Cys Lys Ser Lys Gly Gly Glu Trp Thr  
1                  5                  10                  15  
Ala Lys Gln His Glu Gly Asp Leu Glu Ala Ser Ala Ser Ser Thr Tyr  
                  20                  25                  30  
Asp Leu Gln Arg Lys Leu Val Gln Thr Ala Leu Ser Ala Asp Ser Ser  
                  35                  40                  45  
Gly Gly Val Gln Ser Ser Phe Ser Leu Val Ser Pro Thr Ser Ala Val  
                  50                  55                  60  
Phe Val Val Val Ile Gly Gly Gly Gly Gly Gly Gly Phe Ala Ala Gly  
65                  70                  75                  80  
Gly Gly Ala Ala Ala Gly Gly Gly Gly Gly Gly Glu Ala Ala Ala Ala  
                  85                  90                  95  
Thr Lys Glu Glu Lys Lys Lys Glu Glu Ser Glu Glu Glu Glu Gly  
                  100                  105                  110  
Asp Phe Gly Phe Asp Leu Phe Gly  
                  115                  120

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..623  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
aatctctctc aacacaaaaga agaacaaaaga agttatgagc tcaatgatgg agactctcca      60
gattcgtaaa cccacttccc tcccogtttc tcaacgccct aatgcagcag ccamcgccga      120
cgatgagcct ggtctcatcc gccgtcgtct ctcttctcta tcaactcaasc tctcaaacca      180
accagyagcg atmgmagcta gattcscgag atccaaatct gtttccgccca tgggagaaca      240
agcaggaagc tctgtgaaag aatggtggga atgggggttg tcatggatcc tttcaagaaa      300
acctatatcc atcagagatc ttgagcttaa caaagacgaa gctaaatcga ttgggttcaca      360
aaacagagga agtataatgc acgttttctt caaactccgr tctcagatcc gtaatttcat      420
gggaccttct tcagaagatt ctcttcctct ttcttgcaaa tacaagcgtc aacgataaaa      480
tgattcatat aaggttgaga ttttgatgatt tgtctgttct ttttttactt ttgtgcaatg      540
gagtataatg aatgtataat tcgtcttttt tttttaaaact tgatgttgta ttttgctata      600
attaatttgc ctagattatt att
```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..158  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Ile Ser Leu Asn Thr Lys Lys Asn Lys Glu Val Met Ser Ser Met Met  
1                  5                  10                  15  
Glu Thr Leu Gln Ile Arg Lys Pro Thr Ser Leu Pro Val Ser Gln Arg

	20		25		30										
Pro	Asn	Ala	Ala	Xaa	Ala	Asp	Glu	Pro	Gly	Leu	Ile	Arg	Arg		
	35		40		45										
Arg	Leu	Ser	Ser	Leu	Ser	Leu	Xaa	Leu	Ser	Asn	Gln	Pro	Xaa	Ala	Xaa
	50				55					60					
Xaa	Ala	Arg	Phe	Xaa	Arg	Ser	Lys	Ser	Val	Ser	Ala	Met	Gly	Glu	Gln
	65				70					75					80
Ala	Gly	Ser	Ser	Val	Lys	Glu	Trp	Trp	Glu	Trp	Gly	Trp	Ser	Trp	Ile
				85					90					95	
Leu	Ser	Arg	Lys	Pro	Ile	Phe	Ile	Arg	Asp	Leu	Glu	Leu	Asn	Lys	Asp
			100						105					110	
Glu	Ala	Lys	Ser	Ile	Gly	Ser	Gln	Asn	Arg	Gly	Ser	Ile	Met	His	Val
		115					120					125			
Phe	Phe	Lys	Leu	Xaa	Ser	Gln	Ile	Arg	Asn	Phe	Met	Gly	Pro	Ser	Ser
	130					135					140				
Glu	Asp	Ser	Leu	Pro	Leu	Ser	Cys	Lys	Tyr	Lys	Arg	Gln	Arg		
	145				150					155					

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1498338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Met	Ser	Ser	Met	Glu	Thr	Leu	Gln	Ile	Arg	Lys	Pro	Thr	Ser	Leu	
1			5				10						15		
Pro	Val	Ser	Gln	Arg	Pro	Asn	Ala	Ala	Xaa	Ala	Asp	Asp	Glu	Pro	
			20				25				30				
Gly	Leu	Ile	Arg	Arg	Arg	Leu	Ser	Ser	Leu	Ser	Leu	Xaa	Leu	Ser	Asn
		35				40					45				
Gln	Pro	Xaa	Ala	Xaa	Xaa	Ala	Arg	Phe	Xaa	Arg	Ser	Lys	Ser	Val	Ser
	50					55					60				
Ala	Met	Gly	Glu	Gln	Ala	Gly	Ser	Ser	Val	Lys	Glu	Trp	Trp	Glu	Trp
	65			70						75					80
Gly	Trp	Ser	Trp	Ile	Leu	Ser	Arg	Lys	Pro	Ile	Phe	Ile	Arg	Asp	Leu
			85						90					95	
Glu	Leu	Asn	Lys	Asp	Glu	Ala	Lys	Ser	Ile	Gly	Ser	Gln	Asn	Arg	Gly
		100					105					110			
Ser	Ile	Met	His	Val	Phe	Phe	Lys	Leu	Xaa	Ser	Gln	Ile	Arg	Asn	Phe
		115					120					125			
Met	Gly	Pro	Ser	Ser	Glu	Asp	Ser	Leu	Pro	Leu	Ser	Cys	Lys	Tyr	Lys
	130					135					140				
Arg	Gln	Arg													
	145														

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1498339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:



Met	Met	Glu	Thr	Leu	Gln	Ile	Arg	Lys	Pro	Thr	Ser	Leu	Pro	Val	Ser
1				5					10					15	
Gln	Arg	Pro	Asn	Ala	Ala	Ala	Xaa	Ala	Asp	Asp	Glu	Pro	Gly	Leu	Ile
			20					25					30		
Arg	Arg	Arg	Leu	Ser	Ser	Leu	Ser	Leu	Xaa	Leu	Ser	Asn	Gln	Pro	Xaa
			35					40					45		
Ala	Xaa	Xaa	Ala	Arg	Phe	Xaa	Arg	Ser	Lys	Ser	Val	Ser	Ala	Met	Gly
			50				55				60				
Glu	Gln	Ala	Gly	Ser	Ser	Val	Lys	Glu	Trp	Trp	Glu	Trp	Gly	Trp	Ser
65					70					75					80
Trp	Ile	Leu	Ser	Arg	Lys	Pro	Ile	Phe	Ile	Arg	Asp	Leu	Glu	Leu	Asn
				85					90					95	
Lys	Asp	Glu	Ala	Lys	Ser	Ile	Gly	Ser	Gln	Asn	Arg	Gly	Ser	Ile	Met
			100					105					110		
His	Val	Phe	Phe	Lys	Leu	Xaa	Ser	Gln	Ile	Arg	Asn	Phe	Met	Gly	Pro
			115					120					125		
Ser	Ser	Glu	Asp	Ser	Leu	Pro	Leu	Ser	Cys	Lys	Tyr	Lys	Arg	Gln	Arg
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

accactatga	gaggatccta	gggttactac	taatctcgaa	atcaatcaaa	tcaaagcatc	60
catttttgat	tcagacttca	gagagacaaa	gaaggaagaa	gaagaagaag	aagaagaaaa	120
aactatggag	aatgagaggg	aaaagcaggt	ttacttggct	aagctctccg	agcaaaccga	180
aagatacgat	gaaatggttg	aggcgatgaa	gaaagttgct	cagcttgatg	tggagctaac	240
tgtggaagag	aggaatcttg	tatctgtagg	gtacaagaat	gtgattggtg	caaggagagc	300
atcatggaga	atactatctt	ccattgagca	gaaggaagag	tccaagggaa	atgatgaaaa	360
tgtcaagagg	cttaagaatt	atcgtaagag	agttgaagat	gagcttgcta	aagtttgtaa	420
tgacatcttg	tctgtcattg	ataagcatct	cattccatcg	tctaacgctg	tggagtcac	480
tgtctttttc	tacaaaatga	aaggagatta	ctatcgctat	cttgccggagt	tcagttctgg	540
tgctgaacgc	aaggaagctg	cagatcagtc	tcttgaagca	tataaggctg	ctggttgctgc	600
tgcagagaat	ggtttggcac	ccacacatcc	agtttagactt	ggcttggcgt	tgaacttttc	660
agttttctac	tatgagatct	tgaactctcc	cgaaagcgca	tgccaatttg	ctaagcaagc	720
attcgatgat	gcaattgctg	aacttgacag	cctcaacgag	gaatcataca	aagacagcac	780
tcttattatg	cagctactta	gagacaatct	caccttggtg	acttcagacc	ttaatgagga	840
aggagatgag	agaaccaaag	gtgctgatga	gcctcaagat	gagaactaaa	tcctctgtga	900
gaagagaaac	gactcttgct	gcatacctgaa	tcttgaagtg	aagacagcaa	gtgtcgttgt	960
ttgttactcg	aatgtgtaat	ttttaatcta	tgtctttctt	gatgatgttt	tccagattct	1020
tgaacttttc	acaacacaac	actgcgttgc	gtatcttcaa	ccctcttatg	atgtggttga	1080
attctgtttt	acgcttagtt	tgcttctttt	gttggttgaat	tgagccagca	ggcatgattt	1140
gggtttttgt	tt					

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met	Glu	Asn	Glu	Arg	Glu	Lys	Gln	Val	Tyr	Leu	Ala	Lys	Leu	Ser	Glu
1				5					10					15	
Gln	Thr	Glu	Arg	Tyr	Asp	Glu	Met	Val	Glu	Ala	Met	Lys	Lys	Val	Ala
		20						25					30		
Gln	Leu	Asp	Val	Glu	Leu	Thr	Val	Glu	Glu	Arg	Asn	Leu	Val	Ser	Val
		35					40					45			
Gly	Tyr	Lys	Asn	Val	Ile	Gly	Ala	Arg	Arg	Ala	Ser	Trp	Arg	Ile	Leu
	50					55					60				
Ser	Ser	Ile	Glu	Gln	Lys	Glu	Glu	Ser	Lys	Gly	Asn	Asp	Glu	Asn	Val
65					70					75				80	
Lys	Arg	Leu	Lys	Asn	Tyr	Arg	Lys	Arg	Val	Glu	Asp	Glu	Leu	Ala	Lys
				85					90					95	
Val	Cys	Asn	Asp	Ile	Leu	Ser	Val	Ile	Asp	Lys	His	Leu	Ile	Pro	Ser
		100						105					110		
Ser	Asn	Ala	Val	Glu	Ser	Thr	Val	Phe	Phe	Tyr	Lys	Met	Lys	Gly	Asp
		115					120						125		
Tyr	Tyr	Arg	Tyr	Leu	Ala	Glu	Phe	Ser	Ser	Gly	Ala	Glu	Arg	Lys	Glu
	130					135					140				
Ala	Ala	Asp	Gln	Ser	Leu	Glu	Ala	Tyr	Lys	Ala	Ala	Val	Ala	Ala	Ala
145					150					155				160	
Glu	Asn	Gly	Leu	Ala	Pro	Thr	His	Pro	Val	Arg	Leu	Gly	Leu	Ala	Leu
				165					170					175	
Asn	Phe	Ser	Val	Phe	Tyr	Tyr	Glu	Ile	Leu	Asn	Ser	Pro	Glu	Ser	Ala
		180					185						190		
Cys	Gln	Leu	Ala	Lys	Gln	Ala	Phe	Asp	Asp	Ala	Ile	Ala	Glu	Leu	Asp
	195					200						205			
Ser	Leu	Asn	Glu	Glu	Ser	Tyr	Lys	Asp	Ser	Thr	Leu	Ile	Met	Gln	Leu
	210					215					220				
Leu	Arg	Asp	Asn	Leu	Thr	Leu	Trp	Thr	Ser	Asp	Leu	Asn	Glu	Glu	Gly
225				230						235				240	
Asp	Glu	Arg	Thr	Lys	Gly	Ala	Asp	Glu	Pro	Gln	Asp	Glu	Asn		
				245				250							

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met	Val	Glu	Ala	Met	Lys	Lys	Val	Ala	Gln	Leu	Asp	Val	Glu	Leu	Thr
1				5					10					15	
Val	Glu	Glu	Arg	Asn	Leu	Val	Ser	Val	Gly	Tyr	Lys	Asn	Val	Ile	Gly
		20						25					30		
Ala	Arg	Arg	Ala	Ser	Trp	Arg	Ile	Leu	Ser	Ser	Ile	Glu	Gln	Lys	Glu
		35				40						45			
Glu	Ser	Lys	Gly	Asn	Asp	Glu	Asn	Val	Lys	Arg	Leu	Lys	Asn	Tyr	Arg
	50					55				60					
Lys	Arg	Val	Glu	Asp	Glu	Leu	Ala	Lys	Val	Cys	Asn	Asp	Ile	Leu	Ser
65				70						75				80	
Val	Ile	Asp	Lys	His	Leu	Ile	Pro	Ser	Ser	Asn	Ala	Val	Glu	Ser	Thr
			85					90					95		
Val	Phe	Phe	Tyr	Lys	Met	Lys	Gly	Asp	Tyr	Tyr	Arg	Tyr	Leu	Ala	Glu
			100					105					110		

Phe Ser Ser Gly Ala Glu Arg Lys Glu Ala Ala Asp Gln Ser Leu Glu  
115 120 125  
Ala Tyr Lys Ala Ala Val Ala Ala Glu Asn Gly Leu Ala Pro Thr  
130 135 140  
His Pro Val Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr  
145 150 155 160  
Glu Ile Leu Asn Ser Pro Glu Ser Ala Cys Gln Leu Ala Lys Gln Ala  
165 170 175  
Phe Asp Asp Ala Ile Ala Glu Leu Asp Ser Leu Asn Glu Glu Ser Tyr  
180 185 190  
Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu  
195 200 205  
Trp Thr Ser Asp Leu Asn Glu Glu Gly Asp Glu Arg Thr Lys Gly Ala  
210 215 220  
Asp Glu Pro Gln Asp Glu Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1498351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Lys Lys Val Ala Gln Leu Asp Val Glu Leu Thr Val Glu Glu Arg  
1 5 10 15  
Asn Leu Val Ser Val Gly Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala  
20 25 30  
Ser Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu Glu Ser Lys Gly  
35 40 45  
Asn Asp Glu Asn Val Lys Arg Leu Lys Asn Tyr Arg Lys Arg Val Glu  
50 55 60  
Asp Glu Leu Ala Lys Val Cys Asn Asp Ile Leu Ser Val Ile Asp Lys  
65 70 75 80  
His Leu Ile Pro Ser Ser Asn Ala Val Glu Ser Thr Val Phe Phe Tyr  
85 90 95  
Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Ala Glu Phe Ser Ser Gly  
100 105 110  
Ala Glu Arg Lys Glu Ala Ala Asp Gln Ser Leu Glu Ala Tyr Lys Ala  
115 120 125  
Ala Val Ala Ala Ala Glu Asn Gly Leu Ala Pro Thr His Pro Val Arg  
130 135 140  
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Glu Ile Leu Asn  
145 150 155 160  
Ser Pro Glu Ser Ala Cys Gln Leu Ala Lys Gln Ala Phe Asp Asp Ala  
165 170 175  
Ile Ala Glu Leu Asp Ser Leu Asn Glu Glu Ser Tyr Lys Asp Ser Thr  
180 185 190  
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp  
195 200 205  
Leu Asn Glu Glu Gly Asp Glu Arg Thr Lys Gly Ala Asp Glu Pro Gln  
210 215 220  
Asp Glu Asn  
225

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1396
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```
aaagatgaaa agtaataccc ttctctctctt gccctttttg ctggtctggg tgaaacatag      60
aaaagtttct cttgctcaag ttaatgataa aaggttggtg taggatttgt tgctctggct      120
ctggtggtag gtctatgaaa tcaaccata tcgtgaatgg actgcaacat ggtatcttgc      180
tcccagtggg attgggagca tttgatcatg tccaatccgt caaggactga agatgacagc      240
aaacagctac ctactgagtg ggaaattgaa aaaggtgaag gaattgaatc tatagttcca      300
catttctcag gccttgagag agtcagtagg tggctctgcc accagcttct ggcacactgc      360
tgtatcgaaa agctcacagt cgacctctat caactcatca tctcccgaag ccaaacgatg      420
caagcttgca tcagaaagtt cccctggaga ttcttgacgc aacatagact ttgtccagggt      480
gaaggctccc acagctctcg aggtatccgt tgcctcagct gaatcagatc tttgtttaaa      540
actaggaaa ggcacatact ctgaagaata ctggggtaga aacaataatg aaatttcagc      600
ggtttctatg aagttgttaa tcccatctgt tgtcgtctgg aaatccaaat tgtgtggtca      660
gagcatgcca gtcccgcgtt gccaaattga tggctgtgaa ctggatctct catctgctaa      720
gggttatcat gctaagcaca aagtctgcga aaagcattca aagtgcccaa aagttagcgt      780
gagtggcctg gaacgtcggg tctgccaaca gtgtagcagg ttccatgctg tctctgaatt      840
tgatgagaag aaacgaagct gccgaaaacg tctttctcat cataatgcga ggcgctgtaa      900
gccacaagga gtattttcaa tgaatcccga gaggggtgat gatcgaagac agcatacaaa      960
tatgttgttg aatggggtgt cccttaacgc gagatctgaa gaaatgtatg aatggggtaa     1020
taacacttat gatacaaacg ctagacaaac ggaaaaaagc tttactctga gcttccagag     1080
aggtaatggc tctgaggacc agctgggtgc tagtagcagc cgtatgttcc tctacatctc     1140
aaacctcagg tgggttccca gcaggaaagt ccaagtttca acttcatggc gaagatgtgg     1200
gagaataact aggaagtcctc catgaatctc aagatatcca ccgtgctctc tctcttctgt     1260
caacctcttc ggatcccctg gcccaaccac atgtgcagcc attttctcta ctctgttcat     1320
atgatgttgt accaaaatag atgagtaagt aatgtgtaat ttgtaaacct gttactcagt     1380
aggtggatac ttttcc
```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```
Met Asp Cys Asn Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu
1           5           10           15
Ile Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro
          20          25          30
Thr Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro
          35          40          45
His Phe Ser Gly Leu Glu Arg Val Ser Arg Trp Leu Cys His Gln Leu
          50          55          60
Leu Ala His Cys Cys Ile Glu Lys Leu Thr Val Asp Leu Tyr Gln Leu
          65          70          75          80
Ile Ile Ser Arg Ser Gln Thr Met Gln Ala Cys Ile Arg Lys Phe Pro
          85          90          95
Trp Arg Phe Leu Gln Gln His Arg Leu Cys Pro Gly Glu Gly Ser His
          100         105         110
Ser Ser Arg Gly Ile Arg Cys Leu Ser
          115         120
```

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met	Lys	Leu	Leu	Pro	Ser	Val	Val	Ala	Gly	Lys	Ser	Lys	Leu	Cys
1				5				10					15	
Gly	Gln	Ser	Met	Pro	Val	Pro	Arg	Cys	Gln	Ile	Asp	Gly	Cys	Glu
			20					25					30	Leu
Asp	Leu	Ser	Ser	Ala	Lys	Gly	Tyr	His	Arg	Lys	His	Lys	Val	Cys
			35				40						45	Glu
Lys	His	Ser	Lys	Cys	Pro	Lys	Val	Ser	Val	Ser	Gly	Leu	Glu	Arg
			50			55					60			Arg
Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Ala	Val	Ser	Glu	Phe	Asp
65					70					75				80
Lys	Lys	Arg	Ser	Cys	Arg	Lys	Arg	Leu	Ser	His	His	Asn	Ala	Arg
				85				90						95
Arg	Lys	Pro	Gln	Gly	Val	Phe	Ser	Met	Asn	Pro	Glu	Arg	Val	Tyr
			100					105					110	Asp
Arg	Arg	Gln	His	Thr	Asn	Met	Leu	Trp	Asn	Gly	Val	Ser	Leu	Asn
			115				120						125	Ala
Arg	Ser	Glu	Glu	Met	Tyr	Glu	Trp	Gly	Asn	Asn	Thr	Tyr	Asp	Thr
			130			135					140			Lys
Pro	Arg	Gln	Thr	Glu	Lys	Ser	Phe	Thr	Leu	Ser	Phe	Gln	Arg	Gly
145					150					155				160
Gly	Ser	Glu	Asp	Gln	Leu	Val	Ala	Ser	Ser	Ser	Arg	Met	Phe	Leu
				165					170					175
Ile	Ser	Asn	Leu	Arg	Trp	Val	Pro	Ser	Arg	Lys	Val	Gln	Val	Ser
			180				185						190	Thr
Ser	Trp	Arg	Arg	Cys	Gly	Arg	Ile	Leu	Arg	Ser	Pro	Pro		
			195			200					205			

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met	Pro	Val	Pro	Arg	Cys	Gln	Ile	Asp	Gly	Cys	Glu	Leu	Asp	Leu	Ser
1					5				10					15	
Ser	Ala	Lys	Gly	Tyr	His	Arg	Lys	His	Lys	Val	Cys	Glu	Lys	His	Ser
			20					25					30		
Lys	Cys	Pro	Lys	Val	Ser	Val	Ser	Gly	Leu	Glu	Arg	Arg	Phe	Cys	Gln
			35				40						45		
Gln	Cys	Ser	Arg	Phe	His	Ala	Val	Ser	Glu	Phe	Asp	Glu	Lys	Lys	Arg
			50			55					60				
Ser	Cys	Arg	Lys	Arg	Leu	Ser	His	His	Asn	Ala	Arg	Arg	Arg	Lys	Pro
65					70					75				80	
Gln	Gly	Val	Phe	Ser	Met	Asn	Pro	Glu	Arg	Val	Tyr	Asp	Arg	Arg	Gln

				85					90					95			
His	Thr	Asn	Met	Leu	Trp	Asn	Gly	Val	Ser	Leu	Asn	Ala	Arg	Ser	Glu		
			100					105					110				
Glu	Met	Tyr	Glu	Trp	Gly	Asn	Asn	Thr	Tyr	Asp	Thr	Lys	Pro	Arg	Gln		
		115					120					125					
Thr	Glu	Lys	Ser	Phe	Thr	Leu	Ser	Phe	Gln	Arg	Gly	Asn	Gly	Ser	Glu		
	130					135					140						
Asp	Gln	Leu	Val	Ala	Ser	Ser	Ser	Arg	Met	Phe	Leu	Tyr	Ile	Ser	Asn		
145					150					155					160		
Leu	Arg	Trp	Val	Pro	Ser	Arg	Lys	Val	Gln	Val	Ser	Thr	Ser	Trp	Arg		
			165						170					175			
Arg	Cys	Gly	Arg	Ile	Leu	Arg	Ser	Pro	Pro								
			180					185									

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1021
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

aataaaaaatt	tgtttctttc	ttctctgttt	ttttttgctt	tcgtcttcaa	gagagagaga	60
gagagagata	caaagagaga	aatttggttg	tttgttgacg	gaagcttctt	cggtctctct	120
tctccgtctt	acgattgtca	acgcgtggtt	ccatcttcaa	ttttgtttct	atttttagcag	180
aagttttctg	agcttcaa	actgtttcag	atcaatcaat	cagtcaatca	tggctagctc	240
tggaacaag	aacatcaacg	ccaaattggt	attactagga	gatgttgagg	ctggaaaatc	300
aagtcttggtg	ctacggtttg	tgaaagatca	gtttgttgaa	tttcaggaat	caaccattgg	360
tgcagctttt	ttctctcaaa	cattggctgt	gaatgatgcg	actgtgaagt	ttgagatatg	420
ggatacagct	ggtcaggaac	gataccacag	tttggtcca	atgtactaca	ggggtgcagc	480
tgctgctatt	attgtctttg	acattactaa	tcaagcctca	tttgagaggg	cgaaraaatg	540
ggttcaggaa	ctgcaggcac	aaggtaaccc	taatatggtg	atggctcttg	ctggaaacaa	600
agctgattta	ttagacgcaa	ggaagggtgc	tgcagaggag	gcagagatat	atgctcaaga	660
gaacagcctt	ttctttatgg	aaacctcagc	gaagaccgca	acaaatgtca	aagacatatt	720
ctacgaaata	gcgaaaaggc	taccacgtat	acagccagct	gaaaaccgca	caggaatggt	780
tctcccaaac	gggccagggg	ctacggcagt	gagttcatcg	tggttgctt	agattcgtac	840
ctgaagagag	atctcatttg	gttagtcaca	tagtagagaa	catctggact	ttcatgtgtt	900
tgcttcttct	tcgtctttgt	tactttactt	tgcttgcat	gacaacaaca	acagtgtata	960
tcatgatgat	acttattctg	cctttgtgaa	aatctgaaga	tatttgtatt	tgagagagatt	1020

t

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Ile	Lys	Ile	Cys	Phe	Phe	Leu	Leu	Cys	Phe	Phe	Leu	Leu	Ser	Ser	Ser		
1			5					10					15				
Arg	Glu	Arg	Glu	Arg	Glu	Ile	Gln	Arg	Glu	Lys	Phe	Gly	Cys	Leu	Leu		
		20					25					30					
Thr	Glu	Ala	Ser	Ser	Val	Ser	Leu	Arg	Leu	Thr	Ile	Val	Asn	Ala			
		35					40					45					

Trp Phe His Leu Gln Phe Cys Phe Tyr Phe Ser Arg Ser Phe Ser Ser  
50 55 60  
Phe Lys Tyr Cys Phe Arg Ser Ile Asn Gln Ser Ile Met Ala Ser Ser  
65 70 75 80  
Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu Gly Asp Val Gly  
85 90 95  
Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys Asp Gln Phe Val  
100 105 110  
Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe Ser Gln Thr Leu  
115 120 125  
Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp Asp Thr Ala Gly  
130 135 140  
Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr Tyr Arg Gly Ala Ala  
145 150 155 160  
Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala Ser Phe Glu Arg  
165 170 175  
Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly Asn Pro Asn Met  
180 185 190  
Val Met Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu Asp Ala Arg Lys  
195 200 205  
Val Ser Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu Asn Ser Leu Phe  
210 215 220  
Phe Met Glu Thr Ser Ala Lys Thr Ala Thr Asn Val Lys Asp Ile Phe  
225 230 235 240  
Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro Ala Glu Asn Pro  
245 250 255  
Thr Gly Met Val Leu Pro Asn Gly Pro Gly Ala Thr Ala Val Ser Ser  
260 265 270  
Ser Cys Cys Ala  
275

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Met Ala Ser Ser Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu  
1 5 10 15  
Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys  
20 25 30  
Asp Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe  
35 40 45  
Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp  
50 55 60  
Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr Tyr  
65 70 75 80  
Arg Gly Ala Ala Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala  
85 90 95  
Ser Phe Glu Arg Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly  
100 105 110  
Asn Pro Asn Met Val Met Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu  
115 120 125  
Asp Ala Arg Lys Val Ser Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu  
130 135 140  
Asn Ser Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala Thr Asn Val

145 150 155 160  
Lys Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro  
165 170 175  
Ala Glu Asn Pro Thr Gly Met Val Leu Pro Asn Gly Pro Gly Ala Thr  
180 185 190  
Ala Val Ser Ser Ser Cys Cys Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..644
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

aaaaaagagt	cgcccat	tttctcatt	ttttttgctc	ttgacgaaga	aaccaaaaaa	60
aaaaaaaatg	agagagatcc	ttcatatcca	aggcggtcaa	tgtggaaacc	agatcggagc	120
aaagtctctg	gaagtgatct	gcgacgaaca	cggcattgat	cacaccggtc	aatacgtcgg	180
cgattctccg	ttacagcttg	aacgtatcga	tgtctatttc	aacgaagcta	gcggtggaaa	240
gtacgttcct	cgcgctgttc	ttatggatct	ggagcctggg	accatggatt	ctctcagatc	300
tggtcctgtc	ggtcagattt	tccgtcctga	taacttcgtc	tttgggtcaat	ctggtgcccg	360
aaataactgg	gcgaaagggtc	attacaccga	agtcntngag	ttgattgatt	ctgttctcga	420
tgtgtgaggg	aaggaagctg	agaacagcga	ttgtcttcaa	ggtttccaag	tgtgtcattc	480
attgggagga	ggaactggat	ctggaatggg	aactctattg	atttctaaga	taagagaaga	540
gtatccagat	cgtatgatga	tgactttctc	agtgtttctt	ctcctaaggt	ctctgacact	600
gttgttgagc	atacantgca	ctctctctgt	gcatacagctt	gtcg		

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Lys	Lys	Ser	Arg	Pro	Phe	Ser	Ser	His	Phe	Phe	Leu	Leu	Leu	Thr	Lys
1				5					10					15	
Lys	Pro	Lys	Lys	Lys	Lys	Met	Arg	Glu	Ile	Leu	His	Ile	Gln	Gly	Gly
			20					25					30		
Gln	Cys	Gly	Asn	Gln	Ile	Gly	Ala	Lys	Phe	Trp	Glu	Val	Ile	Cys	Asp
		35				40					45				
Glu	His	Gly	Ile	Asp	His	Thr	Gly	Gln	Tyr	Val	Gly	Asp	Ser	Pro	Leu
	50				55				60						
Gln	Leu	Glu	Arg	Ile	Asp	Val	Tyr	Phe	Asn	Glu	Ala	Ser	Gly	Gly	Lys
65				70					75					80	
Tyr	Val	Pro	Arg	Ala	Val	Leu	Met	Asp	Leu	Glu	Pro	Gly	Thr	Met	Asp
			85					90					95		
Ser	Leu	Arg	Ser	Gly	Pro	Phe	Gly	Gln	Ile	Phe	Arg	Pro	Asp	Asn	Phe
		100					105					110			
Val	Phe	Gly	Gln	Ser	Gly	Ala	Gly	Asn	Asn	Trp	Ala	Lys	Gly	His	Tyr
	115					120					125				
Thr	Glu	Val	Xaa	Glu	Leu	Ile	Asp	Ser	Val	Leu	Asp	Val	Val	Arg	Lys
	130				135					140					
Glu	Ala	Glu	Asn	Ser	Asp	Cys	Leu	Gln	Gly	Phe	Gln	Val	Cys	His	Ser



145					150					155					160
Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gly	Met	Gly	Thr	Leu	Leu	Ile	Ser	Lys
				165					170					175	
Ile	Arg	Glu	Glu	Tyr	Pro	Asp	Arg	Met	Met	Met	Thr	Phe	Ser	Val	Phe
			180					185					190		
Leu	Leu	Leu	Arg	Ser	Leu	Thr	Leu	Leu	Leu	Ser	Ile	Xaa	Cys	Thr	Leu
		195					200					205			
Ser	Val	His	Gln	Leu	Val										
	210														

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1498364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met	Arg	Glu	Ile	Leu	His	Ile	Gln	Gly	Gly	Gln	Cys	Gly	Asn	Gln	Ile
1				5				10						15	
Gly	Ala	Lys	Phe	Trp	Glu	Val	Ile	Cys	Asp	Glu	His	Gly	Ile	Asp	His
			20					25					30		
Thr	Gly	Gln	Tyr	Val	Gly	Asp	Ser	Pro	Leu	Gln	Leu	Glu	Arg	Ile	Asp
		35				40						45			
Val	Tyr	Phe	Asn	Glu	Ala	Ser	Gly	Gly	Lys	Tyr	Val	Pro	Arg	Ala	Val
	50					55					60				
Leu	Met	Asp	Leu	Glu	Pro	Gly	Thr	Met	Asp	Ser	Leu	Arg	Ser	Gly	Pro
65				70					75					80	
Phe	Gly	Gln	Ile	Phe	Arg	Pro	Asp	Asn	Phe	Val	Phe	Gly	Gln	Ser	Gly
			85					90					95		
Ala	Gly	Asn	Asn	Trp	Ala	Lys	Gly	His	Tyr	Thr	Glu	Val	Xaa	Glu	Leu
		100					105						110		
Ile	Asp	Ser	Val	Leu	Asp	Val	Val	Arg	Lys	Glu	Ala	Glu	Asn	Ser	Asp
	115					120						125			
Cys	Leu	Gln	Gly	Phe	Gln	Val	Cys	His	Ser	Leu	Gly	Gly	Gly	Thr	Gly
	130					135					140				
Ser	Gly	Met	Gly	Thr	Leu	Leu	Ile	Ser	Lys	Ile	Arg	Glu	Glu	Tyr	Pro
145					150				155					160	
Asp	Arg	Met	Met	Met	Thr	Phe	Ser	Val	Phe	Leu	Leu	Leu	Arg	Ser	Leu
			165					170						175	
Thr	Leu	Leu	Leu	Ser	Ile	Xaa	Cys	Thr	Leu	Ser	Val	His	Gln	Leu	Val
		180					185						190		

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1498365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Met	Asp	Leu	Glu	Pro	Gly	Thr	Met	Asp	Ser	Leu	Arg	Ser	Gly	Pro	Phe
1				5				10						15	

Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly Ala  
20 25 30  
Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Val Xaa Glu Leu Ile  
35 40 45  
Asp Ser Val Leu Asp Val Val Arg Lys Glu Ala Glu Asn Ser Asp Cys  
50 55 60  
Leu Gln Gly Phe Gln Val Cys His Ser Leu Gly Gly Gly Thr Gly Ser  
65 70 75 80  
Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp  
85 90 95  
Arg Met Met Met Thr Phe Ser Val Phe Leu Leu Leu Arg Ser Leu Thr  
100 105 110  
Leu Leu Leu Ser Ile Xaa Cys Thr Leu Ser Val His Gln Leu Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

ctgaaagacc	ctaggctcaa	ctgggctcag	gctggggctg	gagagaaacg	attccagact	60
gaagggcctg	accataccat	tttcgtaggt	gacttggcac	ctgaggtgac	tgactatatg	120
ctctcggaca	cattcaagaa	tgtgtatggg	tctgtcaaag	gggctaaagt	tgtgcttgac	180
aggaccactg	gaaggtccaa	ggggatggg	tttgttaggt	ttgcggatga	aaatgagcag	240
atgctgtgcca	tgactgaaat	gaatggtcaa	tactgctcga	caaggcctat	gcgtattggt	300
ccggctgcca	ataagaatgc	tcttcgatg	caaccagcta	tgtatcaaaa	cactcaagga	360
gcaaatgctg	gagataatga	tcctaataac	acaacaattt	ttgttgagg	tctggatgct	420
aatgttacag	acgatgaatt	aaagtcaatt	tttgggtcaat	ttgggtgaact	tcttcatgtg	480
aaaatacctc	caggaaaacg	ttgtggattc	gttcaatatg	ccaacaaggc	gtctgcagag	540
catgcacttt	cgggtgctgaa	tggaacacaa	ttaggtggac	aaagcatccg	tctttcgtgg	600
ggacgtagtc	caaacaagca	gtctgatcaa	gcgcaatgga	acggtggtgg	atactatgga	660
taccctc						

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Leu Lys Asp Pro Arg Leu Asn Trp Ala Gln Ala Gly Ala Gly Glu Lys  
1 5 10 15  
Arg Phe Gln Thr Glu Gly Pro Asp His Thr Ile Phe Val Gly Asp Leu  
20 25 30  
Ala Pro Glu Val Thr Asp Tyr Met Leu Ser Asp Thr Phe Lys Asn Val  
35 40 45  
Tyr Gly Ser Val Lys Gly Ala Lys Val Val Leu Asp Arg Thr Thr Gly  
50 55 60  
Arg Ser Lys Gly Tyr Gly Phe Val Arg Phe Ala Asp Glu Asn Glu Gln  
65 70 75 80  
Met Arg Ala Met Thr Glu Met Asn Gly Gln Tyr Cys Ser Thr Arg Pro

				85						90						95
Met	Arg	Ile	Gly	Pro	Ala	Ala	Asn	Lys	Asn	Ala	Leu	Pro	Met	Gln	Pro	
			100					105					110			
Ala	Met	Tyr	Gln	Asn	Thr	Gln	Gly	Ala	Asn	Ala	Gly	Asp	Asn	Asp	Pro	
		115					120					125				
Asn	Asn	Thr	Thr	Ile	Phe	Val	Gly	Gly	Leu	Asp	Ala	Asn	Val	Thr	Asp	
		130				135					140					
Asp	Glu	Leu	Lys	Ser	Ile	Phe	Gly	Gln	Phe	Gly	Glu	Leu	Leu	His	Val	
145					150					155					160	
Lys	Ile	Pro	Pro	Gly	Lys	Arg	Cys	Gly	Phe	Val	Gln	Tyr	Ala	Asn	Lys	
				165					170					175		
Ala	Ser	Ala	Glu	His	Ala	Leu	Ser	Val	Leu	Asn	Gly	Thr	Gln	Leu	Gly	
			180					185					190			
Gly	Gln	Ser	Ile	Arg	Leu	Ser	Trp	Gly	Arg	Ser	Pro	Asn	Lys	Gln	Ser	
		195					200					205				
Asp	Gln	Ala	Gln	Trp	Asn	Gly	Gly	Gly	Tyr	Tyr	Gly	Tyr	Pro			
210						215					220					

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Met	Leu	Ser	Asp	Thr	Phe	Lys	Asn	Val	Tyr	Gly	Ser	Val	Lys	Gly	Ala	
1			5					10						15		
Lys	Val	Val	Leu	Asp	Arg	Thr	Thr	Gly	Arg	Ser	Lys	Gly	Tyr	Gly	Phe	
			20					25				30				
Val	Arg	Phe	Ala	Asp	Glu	Asn	Glu	Gln	Met	Arg	Ala	Met	Thr	Glu	Met	
		35				40					45					
Asn	Gly	Gln	Tyr	Cys	Ser	Thr	Arg	Pro	Met	Arg	Ile	Gly	Pro	Ala	Ala	
50					55					60						
Asn	Lys	Asn	Ala	Leu	Pro	Met	Gln	Pro	Ala	Met	Tyr	Gln	Asn	Thr	Gln	
65				70					75					80		
Gly	Ala	Asn	Ala	Gly	Asp	Asn	Asp	Pro	Asn	Asn	Thr	Thr	Ile	Phe	Val	
			85						90				95			
Gly	Gly	Leu	Asp	Ala	Asn	Val	Thr	Asp	Asp	Glu	Leu	Lys	Ser	Ile	Phe	
		100					105					110				
Gly	Gln	Phe	Gly	Glu	Leu	Leu	His	Val	Lys	Ile	Pro	Pro	Gly	Lys	Arg	
		115				120					125					
Cys	Gly	Phe	Val	Gln	Tyr	Ala	Asn	Lys	Ala	Ser	Ala	Glu	His	Ala	Leu	
	130					135					140					
Ser	Val	Leu	Asn	Gly	Thr	Gln	Leu	Gly	Gly	Gln	Ser	Ile	Arg	Leu	Ser	
145				150					155					160		
Trp	Gly	Arg	Ser	Pro	Asn	Lys	Gln	Ser	Asp	Gln	Ala	Gln	Trp	Asn	Gly	
			165					170					175			
Gly	Gly	Tyr	Tyr	Gly	Tyr	Pro										
			180													

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Met	Arg	Ala	Met	Thr	Glu	Met	Asn	Gly	Gln	Tyr	Cys	Ser	Thr	Arg	Pro
1			5					10						15	
Met	Arg	Ile	Gly	Pro	Ala	Ala	Asn	Lys	Asn	Ala	Leu	Pro	Met	Gln	Pro
			20					25						30	
Ala	Met	Tyr	Gln	Asn	Thr	Gln	Gly	Ala	Asn	Ala	Gly	Asp	Asn	Asp	Pro
			35				40					45			
Asn	Asn	Thr	Thr	Ile	Phe	Val	Gly	Gly	Leu	Asp	Ala	Asn	Val	Thr	Asp
			50				55					60			
Asp	Glu	Leu	Lys	Ser	Ile	Phe	Gly	Gln	Phe	Gly	Glu	Leu	Leu	His	Val
65					70					75				80	
Lys	Ile	Pro	Pro	Gly	Lys	Arg	Cys	Gly	Phe	Val	Gln	Tyr	Ala	Asn	Lys
				85						90				95	
Ala	Ser	Ala	Glu	His	Ala	Leu	Ser	Val	Leu	Asn	Gly	Thr	Gln	Leu	Gly
			100							105				110	
Gly	Gln	Ser	Ile	Arg	Leu	Ser	Trp	Gly	Arg	Ser	Pro	Asn	Lys	Gln	Ser
			115				120						125		
Asp	Gln	Ala	Gln	Trp	Asn	Gly	Gly	Gly	Tyr	Tyr	Gly	Tyr	Pro		
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

agttgaaatt	ccacaagcaa	ccagtcaccg	cgctccatct	cacaagcgac	ctgaagcagt	60
tactaagcgg	tgattcagct	ggacagttac	tttcatggac	agtaccagat	gagacattaa	120
gagcttcaat	gaaacaagct	tcattaaaac	aggcttcatt	aaaacaggct	tcactgaaac	180
aggcttcac	ggttttagaat	ccaaagcaga	gaccagtaaa	tccccttttg	gtttctctga	240
ctagaatcga	aagagctggc	cagggaaactt	aaggacagga	ccacgtagga	ggaagcgagac	300
caaagtctga	acatagtgtt	gtctccgaaa	gagagtata	cgagccactc	tcaactctgc	360
tttggttggtg	agtttttcagg	tttgagaagg	agaaggagaa	gagggttggt	ttgagaattt	420
gtgtaaatag	atgaaaagat	tacaagcttt	ttacagggaa	gtgtgtgtac	tgtgtacagt	480
attgtatttt	tgcggcctct	ttttttgtat	tctttacgta	aaattatttc	ctacacaaaa	540
ttcccactca	ccacacacaa	caaaagaata	gtgatcgaag	ctcatggcgt	ctcttgcaac	600
cgtcgccgct	gtgaaaccat	ccgccgccat	aaaaggactc	ggcggcgagct	cactcgccgg	660
agctaagctc	tccatcaagc	cttcccgcct	gagcttttaa	cccaaatcca	tccgggctaa	720
tggtgtggtg	gctaagtatg	gagacaaaag	tgtctacttt	gacttagaag	atttgggtaa	780
cacaacaggt	caatgggacg	tatacggtc	tgatgtcct	tctccttaca	atcctcttca	840
gagcaagttc	tttgagacat	tcgctgcccc	attcacaaag	agaggattgc	tcctcaagtt	900
cttgatcctt	ggaggaggct	ctttgcttac	ttatgtcagc	gctacctcta	ccggcgaagt	960
tcttcccac	aagagaggtc	ctcaggagcc	gcctaagctc	ggctcctcgcg	gcaagctctg	1020
atctatat	atgttacctt	tctcttcttc	cttctaaaa	tcatacaat	ttctcaatac	1080
tgcaaacctt	tttaagtaat	tttatgtata	ttatgtttat	ctgtt		

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Ala Ser Leu Ala Thr Val Ala Ala Val Lys Pro Ser Ala Ala Ile  
1 5 10 15  
Lys Gly Leu Gly Gly Ser Ser Leu Ala Gly Ala Lys Leu Ser Ile Lys  
20 25 30  
Pro Ser Arg Leu Ser Phe Lys Pro Lys Ser Ile Arg Ala Asn Gly Val  
35 40 45  
Val Ala Lys Tyr Gly Asp Lys Ser Val Tyr Phe Asp Leu Glu Asp Leu  
50 55 60  
Gly Asn Thr Thr Gly Gln Trp Asp Val Tyr Gly Ser Asp Ala Pro Ser  
65 70 75 80  
Pro Tyr Asn Pro Leu Gln Ser Lys Phe Phe Glu Thr Phe Ala Ala Pro  
85 90 95  
Phe Thr Lys Arg Gly Leu Leu Leu Lys Phe Leu Ile Leu Gly Gly Gly  
100 105 110  
Ser Leu Leu Thr Tyr Val Ser Ala Thr Ser Thr Gly Glu Val Leu Pro  
115 120 125  
Ile Lys Arg Gly Pro Gln Glu Pro Pro Lys Leu Gly Pro Arg Gly Lys  
130 135 140  
Leu  
145

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1112  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

aaggtatgac tcaatcttca cttagttggt gaatttagtt ctgatcttta ttagattgta 60  
gttctggcct ttgtagatat gctatagtta ctggaggga tagaggaatt ggatttgaga 120  
tatgcagaca attagcaaac aaagggatta gggttatttt gacatctaga gatgagaaac 180  
aagggcctga agctgttgag acattgaaga aagagcctga gatttctgat caaagcattg 240  
tctttcatca gcttgatgtc tctgatcctt ctagtgtcac ttctcttgct aagtttgtga 300  
aaaccattt cggaaaactc gatattctga tcaataatgc tgggggttgg ggtgtaatca 360  
ctgatgttga tgctcttaga gctgggacag ggaaagaagg tttcaagtgg gaggaacta 420  
tcactgagac ttatgagtta gctgaagaat gcataaagat taactattat ggaccaaaga 480  
gaatgtgtga ggcttttatt catcttctgc agttatctaa ttctccaaga atcgtaatg 540  
tatcatcctt catgggtcaa gtaagaat tactaaacga atgggcaaaa gggatcctga 600  
gtgacgcaga gaatctaacg gagtaagaa ttgaccaagt gatcaaccaa cttctcaatg 660  
atctgaaaga agatacggct aagacaaaag attgggctaa agtcatgtcg gcttacgttg 720  
tttcgaaagc cggtttgaat gcttacacga ggatcttagc gaagaaacat cccgagattc 780  
gcgttaactc ggtttgtcct ggatttgtga agactgatat gaatyttaaa actggaattt 840  
tatctgtgga agaaggagca tcaagtcctg tgagggttagc ttgcttoca catcaagaat 900  
ctccttctgg ttgtttcttt gatcgcaaac aagtttcaga gttctgaaat ctttgtgtgg 960  
agatagataa gccaaagttt tattcatgta atgagaatta ttgtttgaaa gctaaacaga 1020  
aagtatcgac tattcaataa acagaaacat tattaagcct taaaaaaaa aaaaaaaaaa 1080  
aaaaaaaaaa aaaaaaaaaa attkttcccc cc

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Cys Glu Ala Phe Ile His Leu Leu Gln Leu Ser Asn Ser Pro Arg  
1 5 10 15  
Ile Val Asn Val Ser Ser Phe Met Gly Gln Val Lys Asn Leu Leu Asn  
20 25 30  
Glu Trp Ala Lys Gly Ile Leu Ser Asp Ala Glu Asn Leu Thr Glu Val  
35 40 45  
Arg Ile Asp Gln Val Ile Asn Gln Leu Leu Asn Asp Leu Lys Glu Asp  
50 55 60  
Thr Ala Lys Thr Lys Asp Trp Ala Lys Val Met Ser Ala Tyr Val Val  
65 70 75 80  
Ser Lys Ala Gly Leu Asn Ala Tyr Thr Arg Ile Leu Ala Lys Lys His  
85 90 95  
Pro Glu Ile Arg Val Asn Ser Val Cys Pro Gly Phe Val Lys Thr Asp  
100 105 110  
Met Asn Xaa Lys Thr Gly Ile Leu Ser Val Glu Glu Gly Ala Ser Ser  
115 120 125  
Pro Val Arg Leu Ala Leu Leu Pro His Gln Glu Ser Pro Ser Gly Cys  
130 135 140  
Phe Phe Asp Arg Lys Gln Val Ser Glu Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1498381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Gly Gln Val Lys Asn Leu Leu Asn Glu Trp Ala Lys Gly Ile Leu  
1 5 10 15  
Ser Asp Ala Glu Asn Leu Thr Glu Val Arg Ile Asp Gln Val Ile Asn  
20 25 30  
Gln Leu Leu Asn Asp Leu Lys Glu Asp Thr Ala Lys Thr Lys Asp Trp  
35 40 45  
Ala Lys Val Met Ser Ala Tyr Val Val Ser Lys Ala Gly Leu Asn Ala  
50 55 60  
Tyr Thr Arg Ile Leu Ala Lys Lys His Pro Glu Ile Arg Val Asn Ser  
65 70 75 80  
Val Cys Pro Gly Phe Val Lys Thr Asp Met Asn Xaa Lys Thr Gly Ile  
85 90 95  
Leu Ser Val Glu Gly Ala Ser Ser Pro Val Arg Leu Ala Leu Leu  
100 105 110  
Pro His Gln Glu Ser Pro Ser Gly Cys Phe Phe Asp Arg Lys Gln Val  
115 120 125  
Ser Glu Phe  
130

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..80  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498382  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:  
Met Ser Ala Tyr Val Val Ser Lys Ala Gly Leu Asn Ala Tyr Thr Arg  
1                    5                    10                    15  
Ile Leu Ala Lys Lys His Pro Glu Ile Arg Val Asn Ser Val Cys Pro  
                    20                    25                    30  
Gly Phe Val Lys Thr Asp Met Asn Xaa Lys Thr Gly Ile Leu Ser Val  
                    35                    40                    45  
Glu Glu Gly Ala Ser Ser Pro Val Arg Leu Ala Leu Leu Pro His Gln  
                    50                    55                    60  
Glu Ser Pro Ser Gly Cys Phe Phe Asp Arg Lys Gln Val Ser Glu Phe  
65                    70                    75                    80

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```
cttttgccct cactcacttg tcttcttcaa ttctgccgac gacgaatccg acgtcagtaa      60
cttccgaccg cagtttccga aactcgtgat cgctttctct ttcgaaaatg ttggcgctcg      120
tacgggtgaa tcagctgcaa agacttcttc tctctgctcg tcgattatct tcttcaccaa      180
taatacctcc gtcgcgttta cttcaccagc ggctattctc gacctcagac actgatgctt      240
cggctgcata ttttcttctc tcgcatccga aaatacaaac gcttgaaggc aaagctttcta      300
ataaaagccg aagcacatcg tcaacaacat ctttgaatga agatgaactt gccaaattct      360
ctgccattgc tcatacctgg tggcattctg aaggaccctt taaaccgttg catcaaatga      420
atccaactcg gttggctttc atccgctcga ccttatgcag gcacttcagt aaggatccga      480
gttctgctaa gccttttygam ggactgaaat ttatcgatat aggttgcggt ggcggactac      540
tttctgagcc tctagcacgg atgggagcaa ctgtcacagg agttgatgct gttgataaga      600
atgtcaaaat tgctcgtctt cacgctgata tggatccagt gacttcaacg attgaatact      660
tatgtactac agcagaaaag ctagcggatg aaggcaggaa gtttgatgct gttctttctt      720
tagaggatcat cgagcatgta gcaaaccctg cagagttctg taagtcgttg tcagcattga      780
ctatcccca cggggctaca gtactttcta caatcaatcg cactatgcga gcatatgcat      840
caaccattgt tggagcagag tacattctac gttggcttcc taaaggcaca caccagtgg      900
caagttttgt aactcctgaa gaaatgagta tgatattaca acgtgcttca gtcgatgtga      960
aagagatagc tggatttggt tacaacccaa taacaggaag atggttattg tcagatgata      1020
ttagtgtcaa ctatattgct tatgggacga aaaggaagga tcttggagac atataatcaa      1080
tcgttccaag tcgtgtttct ctgcatactt gcttctgagt tataactcta gttcatgctt      1140
taaaaactag gtactctgga agttgcttag gacgaggaca gtagttgttt tgcaataagt      1200
gagaaacatt c
```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1498384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```
Met Leu Ala Ser Val Arg Val Asn Gln Leu Gln Arg Leu Leu Leu Ser
1      5      10      15
Ala Arg Arg Leu Ser Ser Ser Pro Ile Ile Pro Pro Ser Arg Leu Leu
20      25      30
His Gln Arg Leu Phe Ser Thr Ser Asp Thr Asp Ala Ser Ala Ala Ser
35      40      45
Phe Ser Ser Ser His Pro Lys Ile Gln Thr Leu Glu Gly Lys Ala Ser
50      55      60
Asn Lys Ser Arg Ser Thr Ser Ser Thr Thr Ser Leu Asn Glu Asp Glu
65      70      75      80
Leu Ala Lys Phe Ser Ala Ile Ala His Thr Trp Trp His Ser Glu Gly
85      90      95
Pro Phe Lys Pro Leu His Gln Met Asn Pro Thr Arg Leu Ala Phe Ile
100     105     110
Arg Ser Thr Leu Cys Arg His Phe Ser Lys Asp Pro Ser Ser Ala Lys
115     120     125
Pro Xaa Xaa Gly Leu Lys Phe Ile Asp Ile Gly Cys Gly Gly Gly Leu
130     135     140
Leu Ser Glu Pro Leu Ala Arg Met Gly Ala Thr Val Thr Gly Val Asp
145     150     155     160
Ala Val Asp Lys Asn Val Lys Ile Ala Arg Leu His Ala Asp Met Asp
165     170     175
Pro Val Thr Ser Thr Ile Glu Tyr Leu Cys Thr Thr Ala Glu Lys Leu
180     185     190
Ala Asp Glu Gly Arg Lys Phe Asp Ala Val Leu Ser Leu Glu Val Ile
195     200     205
Glu His Val Ala Asn Pro Ala Glu Phe Cys Lys Ser Leu Ser Ala Leu
210     215     220
Thr Ile Pro Asn Gly Ala Thr Val Leu Ser Thr Ile Asn Arg Thr Met
225     230     235     240
Arg Ala Tyr Ala Ser Thr Ile Val Gly Ala Glu Tyr Ile Leu Arg Trp
245     250     255
Leu Pro Lys Gly Thr His Gln Trp Ser Ser Phe Val Thr Pro Glu Glu
260     265     270
Met Ser Met Ile Leu Gln Arg Ala Ser Val Asp Val Lys Glu Ile Ala
275     280     285
Gly Phe Val Tyr Asn Pro Ile Thr Gly Arg Trp Leu Leu Ser Asp Asp
290     295     300
Ile Ser Val Asn Tyr Ile Ala Tyr Gly Thr Lys Arg Lys Asp Leu Gly
305     310     315     320
Asp Ile
```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1498385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```
Met Asn Pro Thr Arg Leu Ala Phe Ile Arg Ser Thr Leu Cys Arg His
1      5      10      15
Phe Ser Lys Asp Pro Ser Ser Ala Lys Pro Xaa Xaa Gly Leu Lys Phe
20      25      30
```



Ile Asp Ile Gly Cys Gly Gly Gly Leu Leu Ser Glu Pro Leu Ala Arg  
35 40 45  
Met Gly Ala Thr Val Thr Gly Val Asp Ala Val Asp Lys Asn Val Lys  
50 55 60  
Ile Ala Arg Leu His Ala Asp Met Asp Pro Val Thr Ser Thr Ile Glu  
65 70 75 80  
Tyr Leu Cys Thr Thr Ala Glu Lys Leu Ala Asp Glu Gly Arg Lys Phe  
85 90 95  
Asp Ala Val Leu Ser Leu Glu Val Ile Glu His Val Ala Asn Pro Ala  
100 105 110  
Glu Phe Cys Lys Ser Leu Ser Ala Leu Thr Ile Pro Asn Gly Ala Thr  
115 120 125  
Val Leu Ser Thr Ile Asn Arg Thr Met Arg Ala Tyr Ala Ser Thr Ile  
130 135 140  
Val Gly Ala Glu Tyr Ile Leu Arg Trp Leu Pro Lys Gly Thr His Gln  
145 150 155 160  
Trp Ser Ser Phe Val Thr Pro Glu Glu Met Ser Met Ile Leu Gln Arg  
165 170 175  
Ala Ser Val Asp Val Lys Glu Ile Ala Gly Phe Val Tyr Asn Pro Ile  
180 185 190  
Thr Gly Arg Trp Leu Leu Ser Asp Asp Ile Ser Val Asn Tyr Ile Ala  
195 200 205  
Tyr Gly Thr Lys Arg Lys Asp Leu Gly Asp Ile  
210 215

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met Gly Ala Thr Val Thr Gly Val Asp Ala Val Asp Lys Asn Val Lys  
1 5 10 15  
Ile Ala Arg Leu His Ala Asp Met Asp Pro Val Thr Ser Thr Ile Glu  
20 25 30  
Tyr Leu Cys Thr Thr Ala Glu Lys Leu Ala Asp Glu Gly Arg Lys Phe  
35 40 45  
Asp Ala Val Leu Ser Leu Glu Val Ile Glu His Val Ala Asn Pro Ala  
50 55 60  
Glu Phe Cys Lys Ser Leu Ser Ala Leu Thr Ile Pro Asn Gly Ala Thr  
65 70 75 80  
Val Leu Ser Thr Ile Asn Arg Thr Met Arg Ala Tyr Ala Ser Thr Ile  
85 90 95  
Val Gly Ala Glu Tyr Ile Leu Arg Trp Leu Pro Lys Gly Thr His Gln  
100 105 110  
Trp Ser Ser Phe Val Thr Pro Glu Glu Met Ser Met Ile Leu Gln Arg  
115 120 125  
Ala Ser Val Asp Val Lys Glu Ile Ala Gly Phe Val Tyr Asn Pro Ile  
130 135 140  
Thr Gly Arg Trp Leu Leu Ser Asp Asp Ile Ser Val Asn Tyr Ile Ala  
145 150 155 160  
Tyr Gly Thr Lys Arg Lys Asp Leu Gly Asp Ile  
165 170

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1397  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

aaaaaatatt	tatgttgggt	caggcttaaa	ccagagagag	actgtgtgtg	gtcgagccat	60
ttgacaaaaa	gcaaaaactt	aaaactgggt	tcagatctga	agtaaaaggg	ttttgottcg	120
gattctccgg	cgtcgtttaa	atgatctctg	acccatcttc	cttggcttaa	taattctggt	180
ccctcctttt	atctcttttt	actgttgatt	tatctgaata	tgccacgctc	tttcttccac	240
atgtttattc	tctcttcctt	tcttcaacac	aagcgtctgg	actaaggaaa	gccaacaaca	300
aaatctgggt	tcaagacggt	tggcaggagt	ttgtcaaccg	tttctccatt	cggattgggt	360
tcagatacaa	agttacagtc	tacattttca	atztatcttc	cacactctga	gatcaaccac	420
cattctagta	gtgaagctct	tatgcaaagt	gattccgcac	agaatcagtt	caacaaacgt	480
gctcgattgt	ttgaagatcc	tgaactcaaa	gatgctaagg	tcatttatcc	atcgaaccct	540
gaatctactg	aaccagtgaa	taaaggttat	ggcggttcta	cagccatcca	aagctttttc	600
aaagaatcta	aagctgaaga	aacgccccag	gtacttaaga	agagaggaag	gaagaagaag	660
aatcctaata	ccgaggaagt	aaactcttca	actcccgggt	gagatgactc	agagaaccgc	720
tcaaagttct	acgagagtgc	ttctgtcaga	aagagaactg	taactgcaga	ggaaagagag	780
agagccgtca	atgcagccaa	aacattcgaa	ccaacaaatc	ctttacttta	gagttgttct	840
gcgaccatca	tatctataca	gaggttgcac	catgtacttg	ccatctgggt	ttgctgagaa	900
atacctaagt	gggatatctg	gtttcatcaa	gctccagctc	ggtgagaaac	aatggccagt	960
gaggtgcctc	tacaaagcag	ggagagctaa	gtttagccaa	ggatggtagt	agttcacact	1020
cgagaacaat	ataggcgaa	gagatgtatg	tgtgtttgag	ctactcagaa	ctcgggattt	1080
cgttctcgaa	gtcaccgcct	ttcgtgtcaa	tgagtatgtg	tgacaaaaaa	agattttccct	1140
ttcatcagcg	atcttgacag	tagctttcca	aagttaaaat	tttatgtagg	ggctctctaa	1200
ccattctctc	tcttgacatt	gttgctctct	ttctagtagt	gttttgagtg	aaatttcagg	1260
ttcctatgtt	tggatgtgga	taagtatttg	acgattataa	taacctctga	gtgaaaactc	1320
tttgtttgag	tggtagctag	gttcaaaaag	agagttgtat	atacttttat	cttcatcagg	1380
ataattatgt	ttattttg					

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Met	Gln	Met	Asp	Ser	Ala	Gln	Asn	Gln	Phe	Asn	Lys	Arg	Ala	Arg	Leu
1			5					10					15		
Phe	Glu	Asp	Pro	Glu	Leu	Lys	Asp	Ala	Lys	Val	Ile	Tyr	Pro	Ser	Asn
			20					25					30		
Pro	Glu	Ser	Thr	Glu	Pro	Val	Asn	Lys	Gly	Tyr	Gly	Gly	Ser	Thr	Ala
			35				40						45		
Ile	Gln	Ser	Phe	Phe	Lys	Glu	Ser	Lys	Ala	Glu	Glu	Thr	Pro	Lys	Val
			50			55					60				
Leu	Lys	Lys	Arg	Gly	Arg	Lys	Lys	Lys	Asn	Pro	Asn	Pro	Glu	Glu	Val
65				70				75					80		
Asn	Ser	Ser	Thr	Pro	Gly	Gly	Asp	Asp	Ser	Glu	Asn	Arg	Ser	Lys	Phe
			85					90					95		
Tyr	Glu	Ser	Ala	Ser	Ala	Arg	Lys	Arg	Thr	Val	Thr	Ala	Glu	Glu	Arg
			100					105					110		
Glu	Arg	Ala	Val	Asn	Ala	Ala	Lys	Thr	Phe	Glu	Pro	Thr	Asn	Pro	Leu
			115				120						125		

Leu

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

```
Met Asp Ser Ala Gln Asn Gln Phe Asn Lys Arg Ala Arg Leu Phe Glu
1          5          10          15
Asp Pro Glu Leu Lys Asp Ala Lys Val Ile Tyr Pro Ser Asn Pro Glu
          20          25          30
Ser Thr Glu Pro Val Asn Lys Gly Tyr Gly Gly Ser Thr Ala Ile Gln
          35          40          45
Ser Phe Phe Lys Glu Ser Lys Ala Glu Glu Thr Pro Lys Val Leu Lys
          50          55          60
Lys Arg Gly Arg Lys Lys Lys Asn Pro Asn Pro Glu Glu Val Asn Ser
65          70          75          80
Ser Thr Pro Gly Gly Asp Asp Ser Glu Asn Arg Ser Lys Phe Tyr Glu
          85          90          95
Ser Ala Ser Ala Arg Lys Arg Thr Val Thr Ala Glu Glu Arg Glu Arg
          100          105          110
Ala Val Asn Ala Ala Lys Thr Phe Glu Pro Thr Asn Pro Leu Leu
          115          120          125
```

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```
Met Gln Pro Lys His Ser Asn Gln Gln Ile Leu Tyr Phe Arg Val Val
1          5          10          15
Leu Arg Pro Ser Tyr Leu Tyr Arg Gly Cys Ile Met Tyr Leu Pro Ser
          20          25          30
Gly Phe Ala Glu Lys Tyr Leu Ser Gly Ile Ser Gly Phe Ile Lys Leu
          35          40          45
Gln Leu Gly Glu Lys Gln Trp Pro Val Arg Cys Leu Tyr Lys Ala Gly
          50          55          60
Arg Ala Lys Phe Ser Gln Gly Trp Tyr Glu Phe Thr Leu Glu Asn Asn
65          70          75          80
Ile Gly Glu Gly Asp Val Cys Val Phe Glu Leu Leu Arg Thr Arg Asp
          85          90          95
Phe Val Leu Glu Val Thr Ala Phe Arg Val Asn Glu Tyr Val
          100          105          110
```

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1267  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

atctatcttt	aaaaacatac	ttgaaaatgc	aaggaacgat	ttcttgtgca	agaaattata	60
acatgacgac	aaccgtcggg	gaatctctgc	ggccgctatc	gcttaaaacg	cagggaaacg	120
gcgagagagt	tcggatggtg	gtggaggaga	acgcggtgat	tgtgattgga	cggagaggat	180
gttgcatgtg	tcatgtggtg	aggaggctgc	ttcttggact	tggagtgaat	ccggcgggcc	240
ttgagattga	tgaggagagg	gaagatgaag	ttttgagtga	gttggagaat	attggagttc	300
aaggcggcgg	aggtacggtg	aagttaccgg	cggtttatgt	aggagggagg	aaaaaaaaaa	360
actcagagag	acaaatctaa	atggcgatga	ttacgcgcaa	caccgccacg	cgctccctc	420
tcctcctcca	atctcaacgc	gccgtcgccg	ctgcctcggt	ctctcacctc	cacacatccc	480
ttcccgtctc	ctctccctcc	acatcaccga	cttccctacac	cagacctggt	cctccttcga	540
cctcccctcc	tcctcctggt	ctctctaaag	cggccgaatt	tgtgatctcc	aaggatatgat	600
ctcatgaact	gggctcgta	cggatcgatc	tggcctatga	cctttggtct	cgcttgctgc	660
gccgtcgaaa	tgatgcatac	cgggtgctgt	cgctacgatc	tccatcgatt	cggatatcatc	720
ttcaggccta	gtcctcgcca	gtctgattgt	atgattgtcg	cgggtactct	taccaataag	780
atggctccgg	ctcttcgcaa	ggtttatgac	cagatgcctg	agccaagggtg	ggtgatttca	840
atgggaagtt	gtgccaatgg	atgtggatac	tatcactact	cctactcggt	ggttcgagga	900
tgtgacagaa	ttgtcccagt	cgacatatac	gtcccggggg	gcccaccaac	cgctgaggct	960
ttgctctatg	gactactcca	gcttcagaag	aaaatcaaca	ggcgcaagga	tttcttgcac	1020
tgggtgaaca	agtgaagctc	gaacccgtcc	tccaatcggt	aaagggactt	ttttcagaca	1080
gttttaccaa	agttttgggg	ataataaatc	gtggacgttt	cattgcatat	ttctttgtgg	1140
tggagatgcc	atgtaaagga	gtgtgtttct	aagtttggtg	tggaaactta	ataaacttaa	1200
gatgtttggt	gtctgagttc	ttttatgggc	tcttttatta	tatatctctc	tctaccagtt	1260
ttcagcc						

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 125 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Leu	Ser	Leu	Lys	Thr	Tyr	Leu	Lys	Met	Gln	Gly	Thr	Ile	Ser	Cys	Ala
1			5					10						15	
Arg	Asn	Tyr	Asn	Met	Thr	Thr	Thr	Val	Gly	Glu	Ser	Leu	Arg	Pro	Leu
		20						25					30		
Ser	Leu	Lys	Thr	Gln	Gly	Asn	Gly	Glu	Arg	Val	Arg	Met	Val	Val	Glu
		35					40					45			
Glu	Asn	Ala	Val	Ile	Val	Ile	Gly	Arg	Arg	Gly	Cys	Cys	Met	Cys	His
	50					55					60				
Val	Val	Arg	Arg	Leu	Leu	Leu	Gly	Leu	Gly	Val	Asn	Pro	Ala	Val	Leu
	65					70				75				80	
Glu	Ile	Asp	Glu	Glu	Arg	Glu	Asp	Glu	Val	Leu	Ser	Glu	Leu	Glu	Asn
			85					90					95		
Ile	Gly	Val	Gln	Gly	Gly	Gly	Gly	Thr	Val	Lys	Leu	Pro	Ala	Val	Tyr
		100						105					110		
Val	Gly	Gly	Arg	Lys	Lys	Lys	Asn	Ser	Glu	Arg	Gln	Ile			
	115					120					125				

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 143 amino acids  
    (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..143  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498393  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:  
Met Asn Trp Ala Arg Thr Gly Ser Ile Trp Pro Met Thr Phe Gly Leu  
1 5 10 15  
Ala Cys Cys Ala Val Glu Met Met His Thr Gly Ala Ala Arg Tyr Asp  
20 25 30  
Leu Asp Arg Phe Gly Ile Ile Phe Arg Pro Ser Pro Arg Gln Ser Asp  
35 40 45  
Cys Met Ile Val Ala Gly Thr Leu Thr Asn Lys Met Ala Pro Ala Leu  
50 55 60  
Arg Lys Val Tyr Asp Gln Met Pro Glu Pro Arg Trp Val Ile Ser Met  
65 70 75 80  
Gly Ser Cys Ala Asn Gly Cys Gly Tyr Tyr His Tyr Ser Tyr Ser Val  
85 90 95  
Val Arg Gly Cys Asp Arg Ile Val Pro Val Asp Ile Tyr Val Pro Gly  
100 105 110  
Cys Pro Pro Thr Ala Glu Ala Leu Leu Tyr Gly Leu Leu Gln Leu Gln  
115 120 125  
Lys Lys Ile Asn Arg Arg Lys Asp Phe Leu His Trp Trp Asn Lys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1498394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met Thr Phe Gly Leu Ala Cys Cys Ala Val Glu Met Met His Thr Gly  
1 5 10 15  
Ala Ala Arg Tyr Asp Leu Asp Arg Phe Gly Ile Ile Phe Arg Pro Ser  
20 25 30  
Pro Arg Gln Ser Asp Cys Met Ile Val Ala Gly Thr Leu Thr Asn Lys  
35 40 45  
Met Ala Pro Ala Leu Arg Lys Val Tyr Asp Gln Met Pro Glu Pro Arg  
50 55 60  
Trp Val Ile Ser Met Gly Ser Cys Ala Asn Gly Cys Gly Tyr Tyr His  
65 70 75 80  
Tyr Ser Tyr Ser Val Val Arg Gly Cys Asp Arg Ile Val Pro Val Asp  
85 90 95  
Ile Tyr Val Pro Gly Cys Pro Pro Thr Ala Glu Ala Leu Leu Tyr Gly  
100 105 110  
Leu Leu Gln Leu Gln Lys Lys Ile Asn Arg Arg Lys Asp Phe Leu His  
115 120 125  
Trp Trp Asn Lys  
130

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2084 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..2084  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```
aagcacttct tctccgcctt cgtaagttcc gccgaaaaga accaaatcct tcactactct      60
gtctcagctt tcgacctctc tcttctcatt cctttgcaac ttctcacttc tcgaattcct      120
tctcttcaaa atcagaaatg gctcaagtgg ttgctaccag gtcaattcaa ggctcgatgt      180
tatctcccaa cgggtggatct gtgtctacaa gatccgagaa gctattgaaa ccagcgagtt      240
ttgcagtgaa ggttctttgga aacgaagcaa agagaagtgg aagagtctct ggtaagaagc      300
agaagaggtg gttgatacta ctgtgagatc cgctcgagtt gagactgaag tcattcctgt      360
ttctcctgaa gatgtgccta acagagagga gcagcntgag aggttggttg aaatgcagca      420
gtttggtgat acatcggtag ggatgtggtc gaagccgaca gtgaggagga agacaaagat      480
tgtttgccacc gttggtccgt cgaccaacac acgagaaatg atatggaaat tggctgaagc      540
tgggatgaat gttgctagga tgaatatgtc tcatggagat catgcttcac ataagaaggt      600
tattgatttg gttaaagaat acaatgcaca aactaaagac aacactattg ctatcatgct      660
tgacaccaag ggtccggaag ttaggagtg agatttacct cagccaatta tgtagatcc      720
tggtcaagag tttaccttta caattgagag aggagtcagc acaccaagtt gtgtcagtgt      780
taactatgat gatttcgtta atgacgtgga agcgggtgac atgcttcttg ttgatggttg      840
tatgatgtcg tttatggtga agtcaaagac caaagactct gtcaaagtgt aagttggtga      900
tggtggagaa cttaagtcaa ggagacacct gaatgtccga ggaaagagt caactttacc      960
ttcaatcact gagaaggatt gggaggatat taaatttgga gtggagaaca aagttgactt     1020
ttatgcagtt tcctttgtca aagatgctca agttgtacac gagttgaaga aataccttca     1080
aaatagtggg gctgatatac acgtgatagt gaaaattgag agtgcagact ccatacctaa     1140
cttgcactcc attatcacag catcagatgg ggcaatggtt gcaagaggtg atcttggtgc     1200
agagcttcca attgaagaag tccccattct tcaggaggag atcattaacc tgtgccgtag     1260
tatgggaaaa gctgttattg ttgcgactaa catgcttgag agtatgatag ttcatccaac     1320
tccaaccogg gcagaggtct cagacattgc tatcgctgtt agagaaggtg ctgatgcggt     1380
aatgctttca ggagaaactg ctcaocgaaa gttcccattg aaagctgctg gagtgatgca     1440
cactgttgca ttgcgaacag aagcaacctat tactagcggg gaaatgccac ctaatcttgg     1500
tcaagccttc aagaaccata tgagtgaagt gtttgcatac catgcaacca tgatgtcaaa     1560
cacacttgga acttcaactg ttgtcttcac cagaaccggg ttcatggcca tattgttaag     1620
tcactatcgt ccttccggca caatctatgc cttcacaaat gagaaaaaaa tacaacaaag     1680
attagctttg tatcaagggt tatgccccat atatatggag ttcacagatg atgcagaaga     1740
aacttttgct aatgcttttg ctacattact gaaacaagga atggtgaaga agggagagga     1800
aatagcaatc gtacagagcg gtacacagcc aatctggcga tctcaatcga cacataacat     1860
ccaagtccgc aaggttttaa gcttctttta agatgggatg tctttaatat gtagaacctc     1920
gtttttggtt ataattttcg ttgcatgtct ctcttctctt gtactattca cacttggtgt     1980
ttgctgtatc ttcttcttca gtttgctttg ctacgattgt ggtttttgga gacattatag     2040
ctcattaact gtttgtgaga ccaaatgtgt cagaatccgc tatt
```

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 488 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..488  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```
Met Gln Gln Phe Gly Asp Thr Ser Val Met Trp Ser Lys Pro Thr
1           5           10           15
Val Arg Arg Lys Thr Lys Ile Val Cys Thr Val Gly Pro Ser Thr Asn
20           25           30
Thr Arg Glu Met Ile Trp Lys Leu Ala Glu Ala Gly Met Asn Val Ala
35           40           45
Arg Met Asn Met Ser His Gly Asp His Ala Ser His Lys Lys Val Ile
```

50	55	60
Asp Leu Val Lys Glu Tyr Asn Ala Gln Thr Lys Asp Asn Thr Ile Ala		
65	70	75
Ile Met Leu Asp Thr Lys Gly Pro Glu Val Arg Ser Gly Asp Leu Pro		80
	85	90
Gln Pro Ile Met Leu Asp Pro Gly Gln Glu Phe Thr Phe Thr Ile Glu		95
	100	105
Arg Gly Val Ser Thr Pro Ser Cys Val Ser Val Asn Tyr Asp Asp Phe		110
	115	120
Val Asn Asp Val Glu Ala Gly Asp Met Leu Leu Val Asp Gly Gly Met		125
	130	135
Met Ser Phe Met Val Lys Ser Lys Thr Lys Asp Ser Val Lys Cys Glu		140
145	150	155
Val Val Asp Gly Gly Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg		160
	165	170
Gly Lys Ser Ala Thr Leu Pro Ser Ile Thr Glu Lys Asp Trp Glu Asp		175
	180	185
Ile Lys Phe Gly Val Glu Asn Lys Val Asp Phe Tyr Ala Val Ser Phe		190
	195	200
Val Lys Asp Ala Gln Val Val His Glu Leu Lys Lys Tyr Leu Gln Asn		205
	210	215
Ser Gly Ala Asp Ile His Val Ile Val Lys Ile Glu Ser Ala Asp Ser		220
225	230	235
Ile Pro Asn Leu His Ser Ile Ile Thr Ala Ser Asp Gly Ala Met Val		240
	245	250
Ala Arg Gly Asp Leu Gly Ala Glu Leu Pro Ile Glu Glu Val Pro Ile		255
	260	265
Leu Gln Glu Glu Ile Ile Asn Leu Cys Arg Ser Met Gly Lys Ala Val		270
	275	280
Ile Val Ala Thr Asn Met Leu Glu Ser Met Ile Val His Pro Thr Pro		285
	290	295
Thr Arg Ala Glu Val Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala		300
305	310	315
Asp Ala Val Met Leu Ser Gly Glu Thr Ala His Gly Lys Phe Pro Leu		320
	325	330
Lys Ala Ala Gly Val Met His Thr Val Ala Leu Arg Thr Glu Ala Thr		335
	340	345
Ile Thr Ser Gly Glu Met Pro Pro Asn Leu Gly Gln Ala Phe Lys Asn		350
	355	360
His Met Ser Glu Met Phe Ala Tyr His Ala Thr Met Met Ser Asn Thr		365
	370	375
Leu Gly Thr Ser Thr Val Val Phe Thr Arg Thr Gly Phe Met Ala Ile		380
385	390	395
Leu Leu Ser His Tyr Arg Pro Ser Gly Thr Ile Tyr Ala Phe Thr Asn		400
	405	410
Glu Lys Lys Ile Gln Gln Arg Leu Ala Leu Tyr Gln Gly Val Cys Pro		415
	420	425
Ile Tyr Met Glu Phe Thr Asp Asp Ala Glu Glu Thr Phe Ala Asn Ala		430
	435	440
Leu Ala Thr Leu Leu Lys Gln Gly Met Val Lys Lys Gly Glu Glu Ile		445
	450	455
Ala Ile Val Gln Ser Gly Thr Gln Pro Ile Trp Arg Ser Gln Ser Thr		460
465	470	475
His Asn Ile Gln Val Arg Lys Val		480
	485	

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1498397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met	Trp	Ser	Lys	Pro	Thr	Val	Arg	Arg	Lys	Thr	Lys	Ile	Val	Cys	Thr
1				5					10					15	
Val	Gly	Pro	Ser	Thr	Asn	Thr	Arg	Glu	Met	Ile	Trp	Lys	Leu	Ala	Glu
			20					25					30		
Ala	Gly	Met	Asn	Val	Ala	Arg	Met	Asn	Met	Ser	His	Gly	Asp	His	Ala
		35					40					45			
Ser	His	Lys	Lys	Val	Ile	Asp	Leu	Val	Lys	Glu	Tyr	Asn	Ala	Gln	Thr
	50					55					60				
Lys	Asp	Asn	Thr	Ile	Ala	Ile	Met	Leu	Asp	Thr	Lys	Gly	Pro	Glu	Val
65					70					75				80	
Arg	Ser	Gly	Asp	Leu	Pro	Gln	Pro	Ile	Met	Leu	Asp	Pro	Gly	Gln	Glu
			85						90					95	
Phe	Thr	Phe	Thr	Ile	Glu	Arg	Gly	Val	Ser	Thr	Pro	Ser	Cys	Val	Ser
			100					105						110	
Val	Asn	Tyr	Asp	Asp	Phe	Val	Asn	Asp	Val	Glu	Ala	Gly	Asp	Met	Leu
		115					120					125			
Leu	Val	Asp	Gly	Gly	Met	Met	Ser	Phe	Met	Val	Lys	Ser	Lys	Thr	Lys
	130					135					140				
Asp	Ser	Val	Lys	Cys	Glu	Val	Val	Asp	Gly	Gly	Glu	Leu	Lys	Ser	Arg
145					150					155				160	
Arg	His	Leu	Asn	Val	Arg	Gly	Lys	Ser	Ala	Thr	Leu	Pro	Ser	Ile	Thr
			165					170						175	
Glu	Lys	Asp	Trp	Glu	Asp	Ile	Lys	Phe	Gly	Val	Glu	Asn	Lys	Val	Asp
		180						185					190		
Phe	Tyr	Ala	Val	Ser	Phe	Val	Lys	Asp	Ala	Gln	Val	Val	His	Glu	Leu
	195						200					205			
Lys	Lys	Tyr	Leu	Gln	Asn	Ser	Gly	Ala	Asp	Ile	His	Val	Ile	Val	Lys
	210					215					220				
Ile	Glu	Ser	Ala	Asp	Ser	Ile	Pro	Asn	Leu	His	Ser	Ile	Ile	Thr	Ala
225					230					235				240	
Ser	Asp	Gly	Ala	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Ala	Glu	Leu	Pro
			245						250					255	
Ile	Glu	Glu	Val	Pro	Ile	Leu	Gln	Glu	Glu	Ile	Ile	Asn	Leu	Cys	Arg
		260						265					270		
Ser	Met	Gly	Lys	Ala	Val	Ile	Val	Ala	Thr	Asn	Met	Leu	Glu	Ser	Met
	275							280				285			
Ile	Val	His	Pro	Thr	Pro	Thr	Arg	Ala	Glu	Val	Ser	Asp	Ile	Ala	Ile
	290					295					300				
Ala	Val	Arg	Glu	Gly	Ala	Asp	Ala	Val	Met	Leu	Ser	Gly	Glu	Thr	Ala
305					310					315				320	
His	Gly	Lys	Phe	Pro	Leu	Lys	Ala	Ala	Gly	Val	Met	His	Thr	Val	Ala
			325						330					335	
Leu	Arg	Thr	Glu	Ala	Thr	Ile	Thr	Ser	Gly	Glu	Met	Pro	Pro	Asn	Leu
		340						345					350		
Gly	Gln	Ala	Phe	Lys	Asn	His	Met	Ser	Glu	Met	Phe	Ala	Tyr	His	Ala
		355					360					365			
Thr	Met	Met	Ser	Asn	Thr	Leu	Gly	Thr	Ser	Thr	Val	Val	Phe	Thr	Arg
	370					375					380				
Thr	Gly	Phe	Met	Ala	Ile	Leu	Leu	Ser	His	Tyr	Arg	Pro	Ser	Gly	Thr
385					390					395				400	
Ile	Tyr	Ala	Phe	Thr	Asn	Glu	Lys	Lys	Ile	Gln	Gln	Arg	Leu	Ala	Leu
			405						410					415	
Tyr	Gln	Gly	Val	Cys	Pro	Ile	Tyr	Met	Glu	Phe	Thr	Asp	Asp	Ala	Glu
		420						425				430			
Glu	Thr	Phe	Ala	Asn	Ala	Leu	Ala	Thr	Leu	Leu	Lys	Gln	Gly	Met	Val



	435		440		445	
Lys	Lys Gly Glu Glu Ile	Ala Ile Val	Gln Ser Gly	Thr Gln Pro	Ile	
450		455		460		
Trp	Arg Ser Gln Ser Thr	His Asn Ile	Gln Val Arg	Lys Val		
465		470		475		

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1498398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met	Ile	Trp	Lys	Leu	Ala	Glu	Ala	Gly	Met	Asn	Val	Ala	Arg	Met	Asn
1			5					10						15	
Met	Ser	His	Gly	Asp	His	Ala	Ser	His	Lys	Lys	Val	Ile	Asp	Leu	Val
			20					25					30		
Lys	Glu	Tyr	Asn	Ala	Gln	Thr	Lys	Asp	Asn	Thr	Ile	Ala	Ile	Met	Leu
			35				40					45			
Asp	Thr	Lys	Gly	Pro	Glu	Val	Arg	Ser	Gly	Asp	Leu	Pro	Gln	Pro	Ile
			50			55					60				
Met	Leu	Asp	Pro	Gly	Gln	Glu	Phe	Thr	Phe	Thr	Ile	Glu	Arg	Gly	Val
65					70				75					80	
Ser	Thr	Pro	Ser	Cys	Val	Ser	Val	Asn	Tyr	Asp	Asp	Phe	Val	Asn	Asp
			85					90					95		
Val	Glu	Ala	Gly	Asp	Met	Leu	Leu	Val	Asp	Gly	Gly	Met	Met	Ser	Phe
			100					105					110		
Met	Val	Lys	Ser	Lys	Thr	Lys	Asp	Ser	Val	Lys	Cys	Glu	Val	Val	Asp
			115				120					125			
Gly	Gly	Glu	Leu	Lys	Ser	Arg	Arg	His	Leu	Asn	Val	Arg	Gly	Lys	Ser
			130				135				140				
Ala	Thr	Leu	Pro	Ser	Ile	Thr	Glu	Lys	Asp	Trp	Glu	Asp	Ile	Lys	Phe
145					150				155					160	
Gly	Val	Glu	Asn	Lys	Val	Asp	Phe	Tyr	Ala	Val	Ser	Phe	Val	Lys	Asp
			165					170						175	
Ala	Gln	Val	Val	His	Glu	Leu	Lys	Lys	Tyr	Leu	Gln	Asn	Ser	Gly	Ala
			180					185					190		
Asp	Ile	His	Val	Ile	Val	Lys	Ile	Glu	Ser	Ala	Asp	Ser	Ile	Pro	Asn
			195				200					205			
Leu	His	Ser	Ile	Ile	Thr	Ala	Ser	Asp	Gly	Ala	Met	Val	Ala	Arg	Gly
			210				215				220				
Asp	Leu	Gly	Ala	Glu	Leu	Pro	Ile	Glu	Glu	Val	Pro	Ile	Leu	Gln	Glu
225				230					235					240	
Glu	Ile	Ile	Asn	Leu	Cys	Arg	Ser	Met	Gly	Lys	Ala	Val	Ile	Val	Ala
			245						250					255	
Thr	Asn	Met	Leu	Glu	Ser	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Arg	Ala
			260					265					270		
Glu	Val	Ser	Asp	Ile	Ala	Ile	Ala	Val	Arg	Glu	Gly	Ala	Asp	Ala	Val
			275				280					285			
Met	Leu	Ser	Gly	Glu	Thr	Ala	His	Gly	Lys	Phe	Pro	Leu	Lys	Ala	Ala
			290				295				300				
Gly	Val	Met	His	Thr	Val	Ala	Leu	Arg	Thr	Glu	Ala	Thr	Ile	Thr	Ser
305				310						315				320	
Gly	Glu	Met	Pro	Pro	Asn	Leu	Gly	Gln	Ala	Phe	Lys	Asn	His	Met	Ser
			325						330					335	
Glu	Met	Phe	Ala	Tyr	His	Ala	Thr	Met	Met	Ser	Asn	Thr	Leu	Gly	Thr
			340					345					350		

Ser Thr Val Val Phe Thr Arg Thr Gly Phe Met Ala Ile Leu Leu Ser  
355 360 365  
His Tyr Arg Pro Ser Gly Thr Ile Tyr Ala Phe Thr Asn Glu Lys Lys  
370 375 380  
Ile Gln Gln Arg Leu Ala Leu Tyr Gln Gly Val Cys Pro Ile Tyr Met  
385 390 395 400  
Glu Phe Thr Asp Asp Ala Glu Glu Thr Phe Ala Asn Ala Leu Ala Thr  
405 410 415  
Leu Leu Lys Gln Gly Met Val Lys Lys Gly Glu Glu Ile Ala Ile Val  
420 425 430  
Gln Ser Gly Thr Gln Pro Ile Trp Arg Ser Gln Ser Thr His Asn Ile  
435 440 445  
Gln Val Arg Lys Val  
450

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..692
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

atcacttact	taacatacta	agagagttat	tagatcttga	aaaacatggc	ttccaaggct	60
ttgattctgt	tgggtctctt	cgcaattctt	ctggtggtct	ccgaagtttc	tgccgcaagg	120
atncgggcat	ggtgaagcca	gagagtgagg	aaactgtgca	acctgaaggt	tatcacggag	180
gacatggtgg	tcacggaggg	ggaggccact	acggaggagg	aggccacggg	catggaggac	240
acaacggagg	agggggccac	ggacttgacg	gatacggagg	aggacatgga	ggacactacg	300
gaggaggagg	ccacggactt	gacggatacg	gaggagggtg	aggacactat	ggaggagggtg	360
gaggacacta	cggaggaggt	ggaggacact	acggaggagg	tggaggacac	tacggaggag	420
gtggtggagg	acacggaggt	ggaggacact	acggagggtg	tggaggagga	tacggagggtg	480
gaggaggaca	ccacggagga	ggaggccacg	ggctaaacga	acctgttcag	actaagccgg	540
gtgtttaaaa	ctatataata	tcttcactac	catgcatgat	tgcatatata	tatatacgct	600
tatgtattat	ctatatgcct	ataaataaac	catggtgagt	ttgtaacgca	gtgccttcag	660
aaatgttcgg	aataaatttc	cataatatta	gt			

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

His	Leu	Leu	Asn	Ile	Leu	Arg	Glu	Leu	Leu	Asp	Leu	Glu	Lys	His	Gly
1			5					10					15		
Phe	Gln	Gly	Phe	Asp	Ser	Val	Gly	Ser	Leu	Arg	Asn	Ser	Ser	Gly	Gly
			20					25					30		
Leu	Arg	Ser	Phe	Cys	Arg	Lys	Asp	Xaa	Gly	Met	Val	Lys	Pro	Glu	Ser
			35				40					45			
Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	His	Gly	Gly	His	Gly	Gly	His
			50			55				60					
Gly	Gly	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	His
65				70				75						80	
Asn	Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly	Gly	Gly	His	Gly

85 90 95  
Gly His Tyr Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly  
100 105 110  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly  
115 120 125  
His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Gly His  
130 135 140  
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Gly Tyr Gly Gly Gly  
145 150 155 160  
Gly Gly His His Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln  
165 170 175  
Thr Lys Pro Gly Val  
180

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly  
20 25 30  
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly  
35 40 45  
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly His Gly Leu  
50 55 60  
Asp Gly Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His  
65 70 75 80  
Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly  
85 90 95  
Gly Gly Gly Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
100 105 110  
Gly Gly Tyr Gly Gly Gly Gly Gly Gly His His Gly Gly Gly Gly His Gly  
115 120 125  
Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val  
130 135

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly  
1 5 10 15  
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu  
20 25 30  
Glu Asp Met Glu Asp Thr Thr Glu Glu Ala Thr Asp Leu Thr Asp  
35 40 45

Thr Glu Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu  
50 55 60  
Glu Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val  
65 70 75 80  
Val Glu Asp Thr Glu Val Glu Asp Thr Thr Glu Val Val Glu Glu Asp  
85 90 95  
Thr Glu Val Glu Glu Asp Thr Thr Glu Glu Glu Ala Thr Gly  
100 105 110

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

accagaagaa	gagccacaca	ctcacaaatt	aaaaagagag	agagagagag	agagacagag	60
agagagagag	attctgcgga	ggagcttctt	cttcgtaggg	tgttcatcgt	tattaacgtt	120
atcgcccccta	cgtcagctcc	atctccagaa	acatgggtgc	aggtggaaga	atgccgggtc	180
ctacttcttc	caagaaatcg	gaaaccgaca	ccacaaagcg	tgtgccgtgc	gagaaaccgc	240
ctttctcggg	gggagatctg	aagaaagcaa	tcccgccgca	ttgtttcaaa	cgctcaatcc	300
ctcgtctctt	ctcctacctt	atcagtgcga	tcattatagc	ctcatgcttc	tactacgtcg	360
ccaccaatta	cttctctctc	ctccctcagc	ctctctctta	cttggcttgg	ccactctatt	420
gggcctgtca	aggtctgtgc	ctaactggta	tctgggtcat	agcccacgaa	tgcggtcacc	480
acgcattcag	cgactaccaa	tggctgggat	acacagttgg	tcttatcttc	cattccttcc	540
tcctcgtccc	ttaattctcc	tgggaagtata	gtcatcgccg	tcaccattcc	aacactggat	600
ccctcgaaaag	agatgaagta	tttgtcccaa	agcagaaatc	agcaatcaag	tggtagcgga	660
aataacctcaa	caacctctct	ggacgcata	tgatgttaac	cgtccagttt	gtcctcgggt	720
ggcccttgta	cttagccttt	aacgtctctg	gcagaccgta	tgacgggttc	gcttgccatt	780
tcttcccaa	cgctcccatc	tacaatgacc	gagaacgcct	ccagatatac	ctctctgatg	840
cgggtattct	agccgtctgt	tttgggtctt	accgttacgc	tgctgcacaa	gggatggcct	900
cgatgatctg	cctctacgga	gtaccgcttc	tgatagtga	tgcgttcctc	gtcttgatca	960
cttacttgca	gcacactcat	ccctcggttg	ctcactacga	ttcatcagag	tgggactggc	1020
tcaggggagc	tttggctacc	gtagacagag	actacnga	attgaacaag	gtgttccaca	1080
acattacaga	cacacacgtg	gtcatcacc	tggtctcgac	aatgccgc	tataacgcaa	1140
tgggaagctac	aaaggcgata	aagccaattc	tgggagacta	ttaccagttc	gatggaacac	1200
cgtgggatgt	ggcgatgtat	agggaggcaa	aggagtgtat	ctatgtagaa	ccggacaggg	1260
aaggtgacaa	gaaaggtgtg	tactggtaca	acaataagtt	atgaggatga	tggatgaagaa	1320
attgtcgact	tttctcttgt	ctgtttgtct	tttgttaaag	aagctatgct	tcgtttta	1380
aatcttattg	tccattttgt	tgtgttatga	cattttggct	gctcattatg	ttatgtggga	1440
agttagtgtc	c					

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser	
1 5 10 15	
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser	
20 25 30	

```

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
    35                                40                                45
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
    50                                55                                60
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
    65                                70                                75                                80
Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
    85                                90                                95
Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
    100                                105                                110
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
    115                                120                                125
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
    130                                135                                140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
    145                                150                                155                                160
Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
    165                                170                                175
Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
    180                                185                                190
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
    195                                200                                205
His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
    210                                215                                220
Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
    225                                230                                235                                240
Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
    245                                250                                255
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
    260                                265                                270
Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
    275                                280                                285
Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Xaa Ile Leu
    290                                295                                300
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
    305                                310                                315                                320
Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
    325                                330                                335
Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
    340                                345                                350
Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
    355                                360                                365
Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
    370                                375                                380

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(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1498409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```

Met Pro Val Pro Thr Ser Ser Lys Lys Ser Glu Thr Asp Thr Thr Lys
 1              5              10              15
Arg Val Pro Cys Glu Lys Pro Pro Phe Ser Val Gly Asp Leu Lys Lys
    20              25              30
Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser

```

35 40 45  
Tyr Leu Ile Ser Asp Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala  
50 55 60  
Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro Leu Ser Tyr Leu Ala Trp  
65 70 75 80  
Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val  
85 90 95  
Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu  
100 105 110  
Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr  
115 120 125  
Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser  
130 135 140  
Leu Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys  
145 150 155 160  
Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met Met Leu  
165 170 175  
Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val  
180 185 190  
Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala  
195 200 205  
Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala  
210 215 220  
Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala Ala Ala Gln  
225 230 235 240  
Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val  
245 250 255  
Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser  
260 265 270  
Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu  
275 280 285  
Ala Thr Val Asp Arg Asp Tyr Xaa Ile Leu Asn Lys Val Phe His Asn  
290 295 300  
Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His  
305 310 315 320  
Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp  
325 330 335  
Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu  
340 345 350  
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys  
355 360 365  
Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1498410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala  
1 5 10 15  
Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe  
20 25 30  
Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu  
35 40 45

Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala  
50 55 60  
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu  
65 70 75 80  
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr  
85 90 95  
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg  
100 105 110  
Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Xaa Ile Leu Asn Lys Val  
115 120 125  
Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr  
130 135 140  
Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  
145 150 155 160  
Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met  
165 170 175  
Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly  
180 185 190  
Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

aaaccaa	amcaattaag	ctaaaaaaa	aaccaaagga	tgtctcagaa	actcatgttc	60
ttgttcacc	ttgcctgcct	ctcctcgta	ccatctcctt	ttatctccgc	ccaaataccg	120
gccattggaa	atgccacttc	accgtcaaat	atatgtagat	tcgcgccgga	tccatcttat	180
tgtagatcgg	ttcttccaaa	ccagcccggga	gatatatatt	cctacggacg	tttgtctcta	240
cgaagatccc	tctccagccc	gccggttcat	ttcgatgatc	gacgctgaac	ttgaccggaa	300
aggcaaatg	gctgctaaat	ccacagtagg	ggctctcgaa	gactgcaaat	tcctagccag	360
cctgactatg	gactacctcc	ttagtagctc	acagacggct	gattccacca	aaacactgtc	420
gttatctagg	gccgaggatg	ttcatacatt	tctgagtgtc	gccatcacca	atgagcagac	480
ttgtcttgaa	ggacttaaat	caacggcgct	cgaaaatggg	ctttccgggt	atcttttcaa	540
cgatacaaaa	ctctatgggg	tgtctcttgc	cctttttctc	aaaggttggg	tgccaagaag	600
gcaaagatcg	agaccgattt	ggcaaccaca	agccagggtc	aaaaagtttt	ttggtttccg	660
taacggtaaa	ttaccgttaa	agatgacgga	aagggcacgt	gccgtttaca	acaccgtgac	720
tagaagaaa	cttctccaat	cggatgcaga	cgccgttcag	gtgagcgaca	ttgtgacggt	780
gatccagaac	gggacgggaa	acttcacgac	cataaacgcc	gccattgcag	ctgcacaaaa	840
taaaactgac	ggtagtaacg	gttacttctt	gatctacgta	acggcgggat	tgtacgagga	900
atacgtggaa	gttcccaaga	acaagagata	tgtgatgatg	atcggtgacg	gcatcaacca	960
gaccgttatc	accggaacaa	ggagtgtcgt	tgatggatgg	acaactttca	attcagccac	1020
atttattcta	tcagggtcca	actttattgg	tgtaaacata	acaatccgca	atacggcagg	1080
accaaccaaa	ggccaagctg	tggcattgag	gagtgggtgg	gacttgtctg	ttttctacag	1140
ttgtagtttt	gaagcctatc	aagacacgtt	atacacacat	tctctcagac	agttttatcg	1200
tgaatgtgat	gtctatggta	ctgttgattt	tatatattgg	aacgctgcag	tggatttaca	1260
aaactgtaat	ttgtatccac	gtcaacctcg	caaagggtcaa	tcgaacgagg	ttacgggtca	1320
aggctgtact	gatccgaacc	aaaacactgg	gacggcaatt	catggttgta	ctataagacc	1380
ggcagatgat	ttggctacga	gcaactatac	agtgaagact	tatcttggtc	gaccatggaa	1440
ggaatattct	agaaccgttg	tcatgcaaac	ttacatagac	gggtttctag	aaccgagtgg	1500
ttggaatgca	tgggtctggtg	attttgcat	gagcacactt	tactacgcgg	aatataataa	1560
taccggacct	ggttctgaca	cgacaaaaccg	agtcacttgg	cctgggttatc	acgtcatcaa	1620
cgcaactgat	gcttccaatt	tcacggtcac	caatttcctt	gttggtgaag	gttggtattgg	1680
acaaaccgga	gtgccttttcg	tgggtggact	gatcgcataa	tcaaccaacc	ttatactata	1740

tatgatatgt taattagttta aattatttttaa tcattcatgt gttgtttttt taatcaaata 1800  
attatttagt ggtgcctgat tcaatagcat ttgtaataac tttaacttac tattgtacaa 1860  
ccgaatgggt ttcttcg

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met	Pro	Leu	His	Arg	Gln	Ile	Tyr	Val	Asp	Ser	Arg	Arg	Ile	His	Leu
1				5				10						15	
Ile	Val	Asp	Arg	Phe	Phe	Gln	Thr	Ser	Pro	Glu	Ile	Tyr	Ile	Pro	Thr
			20					25					30		
Asp	Val	Cys	Leu	Tyr	Glu	Asp	Pro	Ser	Pro	Ala	Arg	Arg	Phe	Ile	Ser
		35					40					45			
Met	Ile	Asp	Ala	Glu	Leu	Asp	Arg	Lys	Gly	Lys	Val	Ala	Ala	Lys	Ser
		50				55					60				
Thr	Val	Gly	Ala	Leu	Glu	Asp	Cys	Lys	Phe	Leu	Ala	Ser	Leu	Thr	Met
65					70					75					80
Asp	Tyr	Leu	Leu	Ser	Ser	Ser	Gln	Thr	Ala	Asp	Ser	Thr	Lys	Thr	Leu
				85					90					95	
Ser	Leu	Ser	Arg	Ala	Glu	Asp	Val	His	Thr	Phe	Leu	Ser	Ala	Ala	Ile
			100					105					110		
Thr	Asn	Glu	Gln	Thr	Cys	Leu	Glu	Gly	Leu	Lys	Ser	Thr	Ala	Ser	Glu
		115					120						125		
Asn	Gly	Leu	Ser	Gly	Asp	Leu	Phe	Asn	Asp	Thr	Lys	Leu	Tyr	Gly	Val
		130				135					140				
Ser	Leu	Ala	Leu	Phe	Ser	Lys	Gly	Trp	Val	Pro	Arg	Arg	Gln	Arg	Ser
145					150					155					160
Arg	Pro	Ile	Trp	Gln	Pro	Gln	Ala	Arg	Phe	Lys	Lys	Phe	Phe	Gly	Phe
				165					170					175	
Arg	Asn	Gly	Lys	Leu	Pro	Leu	Lys	Met	Thr	Glu	Arg	Ala	Arg	Ala	Val
			180					185					190		
Tyr	Asn	Thr	Val	Thr	Arg	Arg	Lys	Leu	Leu	Gln	Ser	Asp	Ala	Asp	Ala
		195					200					205			
Val	Gln	Val	Ser	Asp	Ile	Val	Thr	Val	Ile	Gln	Asn	Gly	Thr	Gly	Asn
		210				215					220				
Phe	Thr	Thr	Ile	Asn	Ala	Ala	Ile	Ala	Ala	Ala	Pro	Asn	Lys	Thr	Asp
225					230					235					240
Gly	Ser	Asn	Gly	Tyr	Phe	Leu	Ile	Tyr	Val	Thr	Ala	Gly	Leu	Tyr	Glu
			245						250					255	
Glu	Tyr	Val	Glu	Val	Pro	Lys	Asn	Lys	Arg	Tyr	Val	Met	Met	Ile	Gly
		260						265					270		
Asp	Gly	Ile	Asn	Gln	Thr	Val	Ile	Thr	Gly	Asn	Arg	Ser	Val	Val	Asp
		275					280					285			
Gly	Trp	Thr	Thr	Phe	Asn	Ser	Ala	Thr	Phe	Ile	Leu	Ser	Gly	Pro	Asn
		290				295						300			
Phe	Ile	Gly	Val	Asn	Ile	Thr	Ile	Arg	Asn	Thr	Ala	Gly	Pro	Thr	Lys
305				310					315						320
Gly	Gln	Ala	Val	Ala	Leu	Arg	Ser	Gly	Gly	Asp	Leu	Ser	Val	Phe	Tyr
			325						330					335	
Ser	Cys	Ser	Phe	Glu	Ala	Tyr	Gln	Asp	Thr	Leu	Tyr	Thr	His	Ser	Leu
			340					345					350		
Arg	Gln	Phe	Tyr	Arg	Glu	Cys	Asp	Val	Tyr	Gly	Thr	Val	Asp	Phe	Ile
		355					360						365		



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Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg
370 375 380
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr
385 390 395 400
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg
405 410 415
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu
420 425 430
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr
435 440 445
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp
450 455 460
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro
465 470 475 480
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile
485 490 495
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly
500 505 510
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile
515 520 525
Ala

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(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

Met Ile Asp Ala Glu Leu Asp Arg Lys Gly Lys Val Ala Ala Lys Ser
1 5 10 15
Thr Val Gly Ala Leu Glu Asp Cys Lys Phe Leu Ala Ser Leu Thr Met
20 25 30
Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr Leu
35 40 45
Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala Ile
50 55 60
Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser Glu
65 70 75 80
Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly Val
85 90 95
Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg Ser
100 105 110
Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly Phe
115 120 125
Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala Val
130 135 140
Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp Ala
145 150 155 160
Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly Asn
165 170 175
Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Ala Pro Asn Lys Thr Asp
180 185 190
Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr Glu
195 200 205
Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile Gly

```

210	215	220
Asp Gly Ile Asn Gln Thr Val Ile Thr Gly	Asn Arg Ser Val Val Asp	
225	230	235
Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe	Ile Leu Ser Gly Pro Asn	240
	245	250
Phe Ile Gly Val Asn Ile Thr Ile Arg Asn	Thr Ala Gly Pro Thr Lys	255
	260	265
Gly Gln Ala Val Ala Leu Arg Ser Gly Gly	Asp Leu Ser Val Phe Tyr	270
	275	280
Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr	Leu Tyr Thr His Ser Leu	285
290	295	300
Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr	Gly Thr Val Asp Phe Ile	
305	310	315
Phe Gly Asn Ala Ala Val Val Leu Gln Asn	Cys Asn Leu Tyr Pro Arg	320
	325	330
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val	Thr Ala Gln Gly Arg Thr	335
	340	345
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile	His Gly Cys Thr Ile Arg	350
	355	360
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr	Thr Val Lys Thr Tyr Leu	365
370	375	380
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr	Val Val Met Gln Thr Tyr	
385	390	395
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp	Asn Ala Trp Ser Gly Asp	400
	405	410
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu	Tyr Asn Asn Thr Gly Pro	415
	420	425
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp	Pro Gly Tyr His Val Ile	430
	435	440
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val	Thr Asn Phe Leu Val Gly	445
450	455	460
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro	Phe Val Gly Gly Leu Ile	465
465	470	475
Ala		480

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1498414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr	
1	5 10 15
Leu Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala	
	20 25 30
Ile Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser	
	35 40 45
Glu Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly	
	50 55 60
Val Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg	
65	70 75 80
Ser Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly	
	85 90 95
Phe Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala	
	100 105 110

Val	Tyr	Asn	Thr	Val	Thr	Arg	Arg	Lys	Leu	Leu	Gln	Ser	Asp	Ala	Asp		
		115					120					125					
Ala	Val	Gln	Val	Ser	Asp	Ile	Val	Thr	Val	Ile	Gln	Asn	Gly	Thr	Gly		
		130				135					140						
Asn	Phe	Thr	Thr	Ile	Asn	Ala	Ala	Ile	Ala	Ala	Ala	Pro	Asn	Lys	Thr		
					150					155					160		
Asp	Gly	Ser	Asn	Gly	Tyr	Phe	Leu	Ile	Tyr	Val	Thr	Ala	Gly	Leu	Tyr		
				165					170					175			
Glu	Glu	Tyr	Val	Glu	Val	Pro	Lys	Asn	Lys	Arg	Tyr	Val	Met	Met	Ile		
			180					185					190				
Gly	Asp	Gly	Ile	Asn	Gln	Thr	Val	Ile	Thr	Gly	Asn	Arg	Ser	Val	Val		
		195					200				205						
Asp	Gly	Trp	Thr	Thr	Phe	Asn	Ser	Ala	Thr	Phe	Ile	Leu	Ser	Gly	Pro		
		210				215					220						
Asn	Phe	Ile	Gly	Val	Asn	Ile	Thr	Ile	Arg	Asn	Thr	Ala	Gly	Pro	Thr		
					230					235					240		
Lys	Gly	Gln	Ala	Val	Ala	Leu	Arg	Ser	Gly	Gly	Asp	Leu	Ser	Val	Phe		
				245					250					255			
Tyr	Ser	Cys	Ser	Phe	Glu	Ala	Tyr	Gln	Asp	Thr	Leu	Tyr	Thr	His	Ser		
			260					265					270				
Leu	Arg	Gln	Phe	Tyr	Arg	Glu	Cys	Asp	Val	Tyr	Gly	Thr	Val	Asp	Phe		
		275					280					285					
Ile	Phe	Gly	Asn	Ala	Ala	Val	Val	Leu	Gln	Asn	Cys	Asn	Leu	Tyr	Pro		
		290				295				300							
Arg	Gln	Pro	Arg	Lys	Gly	Gln	Ser	Asn	Glu	Val	Thr	Ala	Gln	Gly	Arg		
				310						315					320		
Thr	Asp	Pro	Asn	Gln	Asn	Thr	Gly	Thr	Ala	Ile	His	Gly	Cys	Thr	Ile		
				325					330					335			
Arg	Pro	Ala	Asp	Asp	Leu	Ala	Thr	Ser	Asn	Tyr	Thr	Val	Lys	Thr	Tyr		
			340					345					350				
Leu	Gly	Arg	Pro	Trp	Lys	Glu	Tyr	Ser	Arg	Thr	Val	Val	Met	Gln	Thr		
		355					360					365					
Tyr	Ile	Asp	Gly	Phe	Leu	Glu	Pro	Ser	Gly	Trp	Asn	Ala	Trp	Ser	Gly		
		370				375					380						
Asp	Phe	Ala	Leu	Ser	Thr	Leu	Tyr	Tyr	Ala	Glu	Tyr	Asn	Asn	Thr	Gly		
					390					395					400		
Pro	Gly	Ser	Asp	Thr	Thr	Asn	Arg	Val	Thr	Trp	Pro	Gly	Tyr	His	Val		
				405					410					415			
Ile	Asn	Ala	Thr	Asp	Ala	Ser	Asn	Phe	Thr	Val	Thr	Asn	Phe	Leu	Val		
			420					425					430				
Gly	Glu	Gly	Trp	Ile	Gly	Gln	Thr	Gly	Val	Pro	Phe	Val	Gly	Gly	Leu		
		435					440					445					
Ile	Ala																
		450															

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

attttttgcc cctcgaaaga aagtcaaatt actcaacagc gtcgtttctt cttgtttatc	60
gccaatcgcc attattatcg cggtgcctct tctcacctct cgccgtctct ttgaaccgga	120
ggtttcctcc accccttgaa aattccatca tcgattgacc tatagctccg agatctgctc	180
ttcaatttga tgctcttcca ttagttagaa aagttgcttt tgatcggagc aactatgggg	240
tcgtcttttg agaccatcga tatcggtagc agtgctcgga gaattggcgt agataatcgt	300

attttctctca	aattttacttt	caggatcgct	gataatatcc	tcaaacaggc	caacatatatt	360
cgggcagaga	agaatgttat	tgatttatat	gtcatgcttc	tgcggttttc	aagcttggct	420
ctcgagacta	taccgtccca	tcgagattac	agaacatctc	taaaaagcaa	taaagagtat	480
ttgagaatga	gactactaga	tgtcttgacg	gagctggaga	agttgaaacc	agttgtacag	540
caaaggattg	atgaactgta	tccaagctc	aaacctcgat	ataacgttca	agctcatcca	600
gcaaattggtt	ccctaggctg	gtcttctgcc	gtgaaaccgt	catttaatag	ctatgatcat	660
gcaaaggtaa	gaaatcctcc	tggacataat	tctggctaca	tgggttccag	gggtcagcaa	720
tttttgaacg	ctgcaccact	tgaagagcgt	ttccgaaaga	tgtcggtgaa	cttccgacca	780
aatgaagaaa	ccctttccaa	gcattctatc	ttgggtccag	gtggactctc	tgcacagtgg	840
cagccaccaa	agtatgatac	aaaggttcaa	tatccaagca	atatagattt	ttcgctgtt	900
gtaatcccaa	gcttccaaca	acttgtggac	agcaaaccaa	tgataacgaa	tggcagtaac	960
gatgaacctg	aaaagccaat	tgtggaacc	agtgttgcat	ctaataaaaa	aatccagaaa	1020
aattacactg	aagagctttc	ttccatgatt	tctttcgaag	agccagaaag	cgттаатgag	1080
aacaatctca	ttaggcaacc	ttcaccacct	ccagtgctag	cagaagttca	agacttgggt	1140
cctgctttat	gtcctgaagt	tagagaaccg	gaatgtatga	tagaaaactc	tctgccggat	1200
gagtctctac	ggtcggagtc	tcctcttgaa	cttcatattg	cgacttcaat	gatggatacc	1260
tttatgaggc	ttgccaagtc	aaacactaaa	aagaatttag	agacgtgtgg	tattcttgcc	1320
ggttcactaa	aaaacagaaa	attttacatt	acagctctca	tcataccaaa	gcaggaatcg	1380
acatctgact	cgtgtcaggc	cacgaacgaa	gaagagatat	ttgaagtaca	ggacaagcaa	1440
tcctttttcc	cactoggatg	gattcatacg	catccgacac	agtcttggtt	catgtcatcc	1500
attgatgttc	acacacacta	ttcataccag	attatgttac	cagaagctgt	ggcaatcggt	1560
atggcgccac	aagactcttc	aaggaatcac	ggaatatattc	ggctgacgac	gccgggagga	1620
atgacgggtga	taaggaattg	tgaccggcgt	gggtttcatg	cgcacagttc	accggaggac	1680
ggaggaccaa	tttacaatac	ctgtaaggaa	gtttacatga	acccaaatct	caagtttgat	1740
gtcattgatc	tcagatagca	tcacttgcgc	gtttgaaagt	gaaactatgt	tctcaaggcc	1800
atcttttctc	tacgattgta	acaattatgt	atctgtttat	atcccgattt	taatatgatc	1860
tacgtaagtt	ttcgctgc					

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..507

(D) OTHER INFORMATION: / Ceres Seq. ID 1498424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met	Gly	Ser	Ser	Phe	Glu	Thr	Ile	Asp	Ile	Gly	Thr	Ser	Ala	Arg	Arg
1				5					10					15	
Ile	Gly	Val	Asp	Asn	Arg	Ile	Ser	Leu	Lys	Phe	Tyr	Phe	Arg	Ile	Ala
			20					25					30		
Asp	Asn	Ile	Leu	Lys	Gln	Ala	Asn	Ile	Phe	Arg	Ala	Glu	Lys	Asn	Val
		35					40					45			
Ile	Asp	Leu	Tyr	Val	Met	Leu	Leu	Arg	Phe	Ser	Ser	Leu	Ala	Leu	Glu
	50					55				60					
Thr	Ile	Pro	Ser	His	Arg	Asp	Tyr	Arg	Thr	Ser	Leu	Lys	Ser	Asn	Lys
65				70					75					80	
Glu	Tyr	Leu	Arg	Met	Arg	Leu	Leu	Asp	Val	Leu	Thr	Glu	Leu	Glu	Lys
			85					90						95	
Leu	Lys	Pro	Val	Val	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Tyr	Pro	Lys	Leu
		100					105						110		
Lys	Pro	Arg	Tyr	Asn	Val	Gln	Ala	His	Pro	Ala	Asn	Gly	Ser	Leu	Gly
		115				120						125			
Trp	Ser	Ser	Ala	Val	Lys	Pro	Ser	Phe	Asn	Ser	Tyr	Asp	His	Ala	Lys
	130					135					140				
Val	Arg	Asn	Pro	Pro	Gly	His	Asn	Ser	Gly	Tyr	Met	Gly	Ser	Arg	Gly
145					150				155					160	
Gln	Gln	Phe	Leu	Asn	Ala	Ala	Pro	Leu	Glu	Arg	Phe	Arg	Lys	Met	
			165					170					175		

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Ser Val Asn Phe Arg Pro Asn Glu Glu Thr Leu Ser Lys His Ser Ile
      180      185      190
Leu Gly Pro Gly Gly Leu Ser Ala Gln Trp Gln Pro Pro Lys Tyr Asp
      195      200      205
Thr Lys Val Gln Tyr Pro Ser Asn Ile Asp Phe Ser Pro Val Val Ile
      210      215      220
Pro Ser Phe Gln Gln Leu Val Asp Ser Lys Pro Met Ile Thr Asn Gly
225      230      235      240
Ser Asn Asp Glu Pro Glu Lys Pro Ile Val Glu Pro Ser Val Ala Ser
      245      250      255
Asn Glu Lys Ile Gln Lys Asn Tyr Thr Glu Glu Leu Ser Ser Met Ile
      260      265      270
Ser Phe Glu Glu Pro Glu Ser Val Asn Glu Asn Asn Leu Ile Arg Gln
      275      280      285
Pro Ser Pro Pro Pro Val Leu Ala Glu Val Gln Asp Leu Val Pro Ala
      290      295      300
Leu Cys Pro Glu Val Arg Glu Pro Glu Cys Met Ile Glu Asn Ser Leu
305      310      315      320
Pro Asp Glu Ser Leu Arg Ser Glu Ser Pro Leu Glu Leu His Ile Ala
      325      330      335
Thr Ser Met Met Asp Thr Phe Met Arg Leu Ala Lys Ser Asn Thr Lys
      340      345      350
Lys Asn Leu Glu Thr Cys Gly Ile Leu Ala Gly Ser Leu Lys Asn Arg
      355      360      365
Lys Phe Tyr Ile Thr Ala Leu Ile Ile Pro Lys Gln Glu Ser Thr Ser
      370      375      380
Asp Ser Cys Gln Ala Thr Asn Glu Glu Glu Ile Phe Glu Val Gln Asp
385      390      395      400
Lys Gln Ser Leu Phe Pro Leu Gly Trp Ile His Thr His Pro Thr Gln
      405      410      415
Ser Cys Phe Met Ser Ser Ile Asp Val His Thr His Tyr Ser Tyr Gln
      420      425      430
Ile Met Leu Pro Glu Ala Val Ala Ile Val Met Ala Pro Gln Asp Ser
      435      440      445
Ser Arg Asn His Gly Ile Phe Arg Leu Thr Thr Pro Gly Gly Met Thr
      450      455      460
Val Ile Arg Asn Cys Asp Arg Arg Gly Phe His Ala His Ser Ser Pro
465      470      475      480
Glu Asp Gly Gly Pro Ile Tyr Asn Thr Cys Lys Glu Val Tyr Met Asn
      485      490      495
Pro Asn Leu Lys Phe Asp Val Ile Asp Leu Arg
      500      505

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(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

Met Leu Leu Arg Phe Ser Ser Leu Ala Leu Glu Thr Ile Pro Ser His
1      5      10      15
Arg Asp Tyr Arg Thr Ser Leu Lys Ser Asn Lys Glu Tyr Leu Arg Met
      20      25      30
Arg Leu Leu Asp Val Leu Thr Glu Leu Glu Lys Leu Lys Pro Val Val
      35      40      45
Gln Gln Arg Ile Asp Glu Leu Tyr Pro Lys Leu Lys Pro Arg Tyr Asn

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50	55	60
Val Gln Ala His Pro	Ala Asn Gly Ser Leu Gly	Trp Ser Ser Ala Val
65	70	75
Lys Pro Ser Phe Asn	Ser Tyr Asp His Ala Lys	Val Arg Asn Pro Pro
85	90	95
Gly His Asn Ser Gly	Tyr Met Gly Ser Arg Gly	Gln Gln Phe Leu Asn
100	105	110
Ala Ala Pro Leu Glu	Glu Arg Phe Arg Lys Met	Ser Val Asn Phe Arg
115	120	125
Pro Asn Glu Glu Thr	Leu Ser Lys His Ser Ile	Leu Gly Pro Gly Gly
130	135	140
Leu Ser Ala Gln Trp	Gln Pro Pro Lys Tyr Asp	Thr Lys Val Gln Tyr
145	150	155
Pro Ser Asn Ile Asp	Phe Ser Pro Val Val Ile	Pro Ser Phe Gln Gln
165	170	175
Leu Val Asp Ser Lys	Pro Met Ile Thr Asn Gly	Ser Asn Asp Glu Pro
180	185	190
Glu Lys Pro Ile Val	Glu Pro Ser Val Ala Ser	Asn Glu Lys Ile Gln
195	200	205
Lys Asn Tyr Thr Glu	Glu Leu Ser Ser Met Ile	Ser Phe Glu Glu Pro
210	215	220
Glu Ser Val Asn Glu	Asn Asn Leu Ile Arg Gln	Pro Ser Pro Pro Pro
225	230	235
Val Leu Ala Glu Val	Gln Asp Leu Val Pro Ala	Leu Cys Pro Glu Val
245	250	255
Arg Glu Pro Glu Cys	Met Ile Glu Asn Ser Leu	Pro Asp Glu Ser Leu
260	265	270
Arg Ser Glu Ser Pro	Leu Glu Leu His Ile Ala	Thr Ser Met Met Asp
275	280	285
Thr Phe Met Arg Leu	Ala Lys Ser Asn Thr Lys	Lys Asn Leu Glu Thr
290	295	300
Cys Gly Ile Leu Ala	Gly Ser Leu Lys Asn Arg	Lys Phe Tyr Ile Thr
305	310	315
Ala Leu Ile Ile Pro	Lys Gln Glu Ser Thr Ser	Asp Ser Cys Gln Ala
325	330	335
Thr Asn Glu Glu Glu	Ile Phe Glu Val Gln Asp	Lys Gln Ser Leu Phe
340	345	350
Pro Leu Gly Trp Ile	His Thr His Pro Thr Gln	Ser Cys Phe Met Ser
355	360	365
Ser Ile Asp Val His	Thr His Tyr Ser Tyr Gln	Ile Met Leu Pro Glu
370	375	380
Ala Val Ala Ile Val	Met Ala Pro Gln Asp Ser	Ser Arg Asn His Gly
385	390	395
Ile Phe Arg Leu Thr	Thr Pro Gly Gly Met Thr	Val Ile Arg Asn Cys
405	410	415
Asp Arg Arg Gly Phe	His Ala His Ser Ser Pro	Glu Asp Gly Gly Pro
420	425	430
Ile Tyr Asn Thr Cys	Lys Glu Val Tyr Met Asn	Pro Asn Leu Lys Phe
435	440	445
Asp Val Ile Asp Leu	Arg	
450		

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1498426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met	Arg	Leu	Leu	Asp	Val	Leu	Thr	Glu	Leu	Glu	Lys	Leu	Lys	Pro	Val
1				5					10					15	
Val	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Tyr	Pro	Lys	Leu	Lys	Pro	Arg	Tyr
			20					25					30		
Asn	Val	Gln	Ala	His	Pro	Ala	Asn	Gly	Ser	Leu	Gly	Trp	Ser	Ser	Ala
			35				40					45			
Val	Lys	Pro	Ser	Phe	Asn	Ser	Tyr	Asp	His	Ala	Lys	Val	Arg	Asn	Pro
	50					55					60				
Pro	Gly	His	Asn	Ser	Gly	Tyr	Met	Gly	Ser	Arg	Gly	Gln	Gln	Phe	Leu
65					70					75					80
Asn	Ala	Ala	Pro	Leu	Glu	Glu	Arg	Phe	Arg	Lys	Met	Ser	Val	Asn	Phe
				85					90					95	
Arg	Pro	Asn	Glu	Glu	Thr	Leu	Ser	Lys	His	Ser	Ile	Leu	Gly	Pro	Gly
			100					105					110		
Gly	Leu	Ser	Ala	Gln	Trp	Gln	Pro	Pro	Lys	Tyr	Asp	Thr	Lys	Val	Gln
			115				120					125			
Tyr	Pro	Ser	Asn	Ile	Asp	Phe	Ser	Pro	Val	Val	Ile	Pro	Ser	Phe	Gln
	130					135					140				
Gln	Leu	Val	Asp	Ser	Lys	Pro	Met	Ile	Thr	Asn	Gly	Ser	Asn	Asp	Glu
145					150					155					160
Pro	Glu	Lys	Pro	Ile	Val	Glu	Pro	Ser	Val	Ala	Ser	Asn	Glu	Lys	Ile
				165					170					175	
Gln	Lys	Asn	Tyr	Thr	Glu	Glu	Leu	Ser	Ser	Met	Ile	Ser	Phe	Glu	Glu
			180					185					190		
Pro	Glu	Ser	Val	Asn	Glu	Asn	Asn	Leu	Ile	Arg	Gln	Pro	Ser	Pro	Pro
	195						200					205			
Pro	Val	Leu	Ala	Glu	Val	Gln	Asp	Leu	Val	Pro	Ala	Leu	Cys	Pro	Glu
	210					215					220				
Val	Arg	Glu	Pro	Glu	Cys	Met	Ile	Glu	Asn	Ser	Leu	Pro	Asp	Glu	Ser
225					230					235					240
Leu	Arg	Ser	Glu	Ser	Pro	Leu	Glu	Leu	His	Ile	Ala	Thr	Ser	Met	Met
				245					250					255	
Asp	Thr	Phe	Met	Arg	Leu	Ala	Lys	Ser	Asn	Thr	Lys	Lys	Asn	Leu	Glu
			260					265					270		
Thr	Cys	Gly	Ile	Leu	Ala	Gly	Ser	Leu	Lys	Asn	Arg	Lys	Phe	Tyr	Ile
	275						280					285			
Thr	Ala	Leu	Ile	Ile	Pro	Lys	Gln	Glu	Ser	Thr	Ser	Asp	Ser	Cys	Gln
	290					295						300			
Ala	Thr	Asn	Glu	Glu	Glu	Ile	Phe	Glu	Val	Gln	Asp	Lys	Gln	Ser	Leu
305					310					315					320
Phe	Pro	Leu	Gly	Trp	Ile	His	Thr	His	Pro	Thr	Gln	Ser	Cys	Phe	Met
				325					330					335	
Ser	Ser	Ile	Asp	Val	His	Thr	His	Tyr	Ser	Tyr	Gln	Ile	Met	Leu	Pro
			340					345					350		
Glu	Ala	Val	Ala	Ile	Val	Met	Ala	Pro	Gln	Asp	Ser	Ser	Arg	Asn	His
			355				360					365			
Gly	Ile	Phe	Arg	Leu	Thr	Thr	Pro	Gly	Gly	Met	Thr	Val	Ile	Arg	Asn
	370					375					380				
Cys	Asp	Arg	Arg	Gly	Phe	His	Ala	His	Ser	Ser	Pro	Glu	Asp	Gly	Gly
385					390					395					400
Pro	Ile	Tyr	Asn	Thr	Cys	Lys	Glu	Val	Tyr	Met	Asn	Pro	Asn	Leu	Lys
				405					410					415	
Phe	Asp	Val	Ile	Asp	Leu	Arg									
				420											

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1321  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

ttttcatcat	catctcagtc	tctctcgaag	tttcaagttc	gcgactatgg	cagcagcgat	60
gtctttcttct	tggttgcgctt	cctcgcttcg	tttaatccca	ttcaaaccga	ccttggttttc	120
ttcaatccat	tatccggcca	aaacccttct	tctacgacca	ctaaaaccgt	cggaagttcc	180
ttccttttcgc	cggacgatca	tcacttttcca	gaaaatttca	accgggattg	ttcctccacc	240
atcggettca	tcactctcgt	cgagctatgg	agaccttcaa	ccaatcgaag	agcttccacc	300
gaagctacaa	gagatcgta	agcttttcca	atcgggtacaa	gagccaaagg	ctaaatacga	360
gcagcttatg	ttctacggga	agaatctgac	acctctcgat	tctcaattca	agacgagggga	420
gaataaagta	gaaggatgtg	tttctcaggt	ttgggttagg	gctttctttg	atgaggaacg	480
taatgttggtg	tatgaagctg	attctgattc	ggttctcact	aaagggttag	ctgctctatt	540
agtcaaggggt	ttatctggaa	gacctgtccc	tgagattttg	aggataacac	ctgatttcgc	600
tgttcttcttc	gggttgacgc	agagtctgtc	tccttctaga	aacaatggat	tacttaatat	660
gcttaagctg	atgcagaaaa	aggctcttca	tttggaagtc	aaaggtgagg	aagattcaag	720
ttctggagag	agttcagaat	ccagctttgt	gtctattcct	gagactaagg	acgaagctaa	780
tggtccggag	gtggatttgg	agtctaaacc	tgatctagtt	gaggatttgg	gaacagaaaa	840
gattgatgat	tctgagagtg	gggtcaaatgt	tggtgcttta	gggagtagag	ggatgaggat	900
aagagagaaaa	ttggagaagg	agctagatcc	tggtgagtta	gaagttgaag	atgtttctta	960
ccagcacgca	ggacatgccg	ctgtagaggg	tagtgctggg	gatgatgggg	aaacacattt	1020
caacttgcca	atcgtttcgg	atgctttcca	aggtaaaagc	ttgggtcaaga	gacataggct	1080
gatatatgac	ttggtgcaag	atgagttgaa	gagcgggtta	catgctctct	ctattgtggc	1140
aaagactcct	gctgaggttt	gaggggtgta	cattggaaga	agtcagggtc	tgattctttt	1200
acttcttttg	gtccatttgc	tttgatatt	gttctctgga	ccttctaata	atgttaagag	1260
ctcgatcagg	attgtgttaa	atgagagata	gatattgaag	gatataaata	atgttttcgt	1320

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 386 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..386  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Phe	His	His	His	Leu	Ser	Leu	Ser	Arg	Ser	Phe	Lys	Phe	Ala	Thr	Met
1				5				10						15	
Ala	Ala	Ala	Met	Ser	Ser	Ser	Cys	Cys	Ala	Ser	Ser	Leu	Arg	Leu	Ile
			20					25					30		
Pro	Phe	Lys	Arg	Thr	Leu	Phe	Ser	Ser	Ile	His	Tyr	Pro	Ala	Lys	Thr
			35				40						45		
Leu	Leu	Leu	Arg	Pro	Leu	Lys	Pro	Ser	Glu	Val	Pro	Ser	Phe	Arg	Arg
			50				55					60			
Thr	Ile	Ile	Thr	Phe	Gln	Lys	Ile	Ser	Thr	Gly	Ile	Val	Pro	Pro	Pro
			65				70					75			80
Ser	Ala	Ser	Ser	Ser	Pro	Ser	Ser	Tyr	Gly	Asp	Leu	Gln	Pro	Ile	Glu
				85					90					95	
Glu	Leu	Pro	Pro	Lys	Leu	Gln	Glu	Ile	Val	Lys	Leu	Phe	Gln	Ser	Val
				100				105					110		
Gln	Glu	Pro	Lys	Ala	Lys	Tyr	Glu	Gln	Leu	Met	Phe	Tyr	Gly	Lys	Asn
				115				120					125		
Leu	Thr	Pro	Leu	Asp	Ser	Gln	Phe	Lys	Thr	Arg	Glu	Asn	Lys	Val	Glu
				130				135				140			
Gly	Cys	Val	Ser	Gln	Val	Trp	Val	Arg	Ala	Phe	Phe	Asp	Glu	Glu	Arg



```

145          150          155          160
Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly Leu
          165          170          175
Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu Ile
          180          185          190
Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln Ser
          195          200          205
Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu Met
          210          215          220
Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser Ser
          225          230          235          240
Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr Lys
          245          250          255
Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp Leu
          260          265          270
Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly Ser
          275          280          285
Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys Leu
          290          295          300
Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser Tyr
          305          310          315          320
Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp Gly
          325          330          335
Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly Lys
          340          345          350
Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp Glu
          355          360          365
Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro Ala
          370          375          380
Glu Val
385

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..371
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

Met Ala Ala Ala Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu
1          5          10          15
Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys
          20          25          30
Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg
          35          40          45
Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro
          50          55          60
Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile
          65          70          75          80
Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser
          85          90          95
Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys
          100          105          110
Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val
          115          120          125
Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu
          130          135          140

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Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
145          150          155          160
Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
          165          170          175
Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln
          180          185          190
Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu
          195          200          205
Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser
          210          215          220
Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr
225          230          235          240
Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp
          245          250          255
Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly
          260          265          270
Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys
          275          280          285
Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser
          290          295          300
Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp
305          310          315          320
Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly
          325          330          335
Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp
          340          345          350
Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro
          355          360          365
Ala Glu Val
          370

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu Ile Pro Phe Lys
1          5          10          15
Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys Thr Leu Leu
          20          25          30
Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg Arg Thr Ile Ile
          35          40          45
Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro Pro Ser Ala Ser
          50          55          60
Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile Glu Glu Leu Pro
          65          70          75          80
Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser Val Gln Glu Pro
          85          90          95
Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys Asn Leu Thr Pro
          100          105          110
Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val Glu Gly Cys Val
          115          120          125
Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu Arg Asn Val Val
          130          135          140
Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly Leu Ala Ala Leu

```

145 150 155 160  
Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu Ile Leu Arg Ile  
165 170 175  
Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln Ser Leu Ser Pro  
180 185 190  
Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu Met Gln Lys Lys  
195 200 205  
Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser Ser Ser Gly Glu  
210 215 220  
Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr Lys Asp Glu Ala  
225 230 235 240  
Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp Leu Val Glu Asp  
245 250 255  
Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly Ser Asn Val Val  
260 265 270  
Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys Leu Glu Lys Glu  
275 280 285  
Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser Tyr Gln His Ala  
290 295 300  
Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp Gly Glu Thr His  
305 310 315 320  
Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly Lys Ser Leu Val  
325 330 335  
Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp Glu Leu Lys Ser  
340 345 350  
Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro Ala Glu Val  
355 360 365

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1725
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

attttcttaa cattgttcca ccaactcctc ccacattctc tccgcctctc tcggtttacaa	60
atcccacctc aaaggtcgac tctttatctc tctttctacc aacccaactt ctccaatggc	120
ttctcagagt tcagtcgccc tcatctcctc cgccgcccgc agaggtgaat cattcccaga	180
ttcaaagaaa ccaatcgggt cagttcgggt ccaacaaccc ctccgtctct ccttctcgtg	240
ctgtaagtca gggaatatgt catctagaat ctgcgctatg gccaaaccaa atgatgctga	300
gactctttca tcatcagtag atatgtcact tagcccgcca gttcagtcct taaaaccttc	360
caagactatg gttataaccg atcttgcagc cactcttggt caatccgggtg ttccgggtat	420
tagactagct gcgggagAAC cggatttcga cactcccaaa gtcgtagctg aggtcgggat	480
caacgcgatt cgagaagggt ttactaggta tacgttaaAT gcagggtatta cagaactcag	540
agaagcaata tgtcgaaagc taaaagagga gaatggattg tcttatgcgc ctgatcagat	600
cttggttagt aatggagcta aacaaagtct cttacaagca gtgcttgagc tttgttctcc	660
tggagatgaa gttataattc ctgcaccgta ttgggtgagt tacacagAAC aggcgagatt	720
ggctgatgca acgcccgtgg ttattcttac caagatttct aacaattttt tgttgatcc	780
aaaggatctt gagtctaaat tgactgaaaa atctagactt cttattctct gctctccttc	840
caaccctact ggatctgttt accccaagag tttgctcgaa gagattgcac ggatcattgc	900
taagcatcca agacttctgg tgctttcgga tgaaatatat gaacacatta tttatgcacc	960
tgcaacacac acaagctttg cttctttgcc tgacatgtat gaaagaactt tgacagtaaa	1020
cggtttctca aaggctttcg caatgacggg ttggaggctt ggatatcttg ctggtcctaa	1080
acatattgtg gcagcttgca gtaaattaca aggccagggt agttcaggag ctagtagcat	1140
tgctcagaaa gcaggtgttg ctgcgcttgg gtaggcaaa gctggaggag aaacgggtgc	1200
agagatgggt aaagcttata gagaaagacg agatttcttg gttaaaagct taggtgatat	1260
caaagggtgtt aagatctctg aacctcaggg agctttttat ctctttattg acttcagtgc	1320

ttactatgga tcagaagctg aagggttttg tttgatcaat gattcgtcgt ctcttgcact 1380  
atacttttctt gacaagtttc aggttgcaat ggttcctggt gatgcttttg gagatcatag 1440  
ttgtatccga atatcttatg ccacatctct cgacgttctt caagcagctg ttgagaagat 1500  
caggaaagcc cttgagccac tccgtgccac tgtctccgtt taacagttcg gacacagaaa 1560  
tgtgtttaag attgtttatg atatgttgta acttatttat cagctttgtc tccaatccaa 1620  
taaaaagtct ttttctatgc tttgttcggt ctttcaaatt catatataac cataaacaat 1680  
tatcttaatt gtaaatacatt tattagtatt taaggttgct tgtgc

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1498432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met	Ala	Ser	Gln	Ser	Ser	Val	Ala	Val	Ile	Ser	Ser	Ala	Ala	Ala	Arg	
1			5						10					15		
Gly	Glu	Ser	Phe	Pro	Asp	Ser	Lys	Lys	Pro	Ile	Gly	Ser	Val	Arg	Phe	
			20					25					30			
Gln	Gln	Pro	Leu	Arg	Leu	Ser	Phe	Ser	Tyr	Cys	Lys	Ser	Gly	Asn	Met	
			35				40					45				
Ser	Ser	Arg	Ile	Cys	Ala	Met	Ala	Lys	Pro	Asn	Asp	Ala	Glu	Thr	Leu	
			50				55				60					
Ser	Ser	Ser	Val	Asp	Met	Ser	Leu	Ser	Pro	Arg	Val	Gln	Ser	Leu	Lys	
65							70			75					80	
Pro	Ser	Lys	Thr	Met	Val	Ile	Thr	Asp	Leu	Ala	Ala	Thr	Leu	Val	Gln	
							85			90					95	
Ser	Gly	Val	Pro	Val	Ile	Arg	Leu	Ala	Ala	Gly	Glu	Pro	Asp	Phe	Asp	
			100					105					110			
Thr	Pro	Lys	Val	Val	Ala	Glu	Ala	Gly	Ile	Asn	Ala	Ile	Arg	Glu	Gly	
			115				120					125				
Phe	Thr	Arg	Tyr	Thr	Leu	Asn	Ala	Gly	Ile	Thr	Glu	Leu	Arg	Glu	Ala	
			130				135					140				
Ile	Cys	Arg	Lys	Leu	Lys	Glu	Glu	Asn	Gly	Leu	Ser	Tyr	Ala	Pro	Asp	
145							150				155				160	
Gln	Ile	Leu	Val	Ser	Asn	Gly	Ala	Lys	Gln	Ser	Leu	Leu	Gln	Ala	Val	
							165				170				175	
Leu	Ala	Val	Cys	Ser	Pro	Gly	Asp	Glu	Val	Ile	Ile	Pro	Ala	Pro	Tyr	
			180					185					190			
Trp	Val	Ser	Tyr	Thr	Glu	Gln	Ala	Arg	Leu	Ala	Asp	Ala	Thr	Pro	Val	
			195				200					205				
Val	Ile	Pro	Thr	Lys	Ile	Ser	Asn	Asn	Phe	Leu	Leu	Asp	Pro	Lys	Asp	
			210				215					220				
Leu	Glu	Ser	Lys	Leu	Thr	Glu	Lys	Ser	Arg	Leu	Leu	Ile	Leu	Cys	Ser	
225							230				235				240	
Pro	Ser	Asn	Pro	Thr	Gly	Ser	Val	Tyr	Pro	Lys	Ser	Leu	Leu	Glu	Glu	
							245				250				255	
Ile	Ala	Arg	Ile	Ile	Ala	Lys	His	Pro	Arg	Leu	Leu	Val	Leu	Ser	Asp	
			260					265						270		
Glu	Ile	Tyr	Glu	His	Ile	Ile	Tyr	Ala	Pro	Ala	Thr	His	Thr	Ser	Phe	
			275					280					285			
Ala	Ser	Leu	Pro	Asp	Met	Tyr	Glu	Arg	Thr	Leu	Thr	Val	Asn	Gly	Phe	
			290				295					300				
Ser	Lys	Ala	Phe	Ala	Met	Thr	Gly	Trp	Arg	Leu	Gly	Tyr	Leu	Ala	Gly	
305							310				315				320	
Pro	Lys	His	Ile	Val	Ala	Ala	Cys	Ser	Lys	Leu	Gln	Gly	Gln	Val	Ser	
							325				330				335	

Ser Gly Ala Ser Ser Ile Ala Gln Lys Ala Gly Val Ala Ala Leu Gly  
340 345 350  
Leu Gly Lys Ala Gly Gly Glu Thr Val Ala Glu Met Val Lys Ala Tyr  
355 360 365  
Arg Glu Arg Arg Asp Phe Leu Val Lys Ser Leu Gly Asp Ile Lys Gly  
370 375 380  
Val Lys Ile Ser Glu Pro Gln Gly Ala Phe Tyr Leu Phe Ile Asp Phe  
385 390 395 400  
Ser Ala Tyr Tyr Gly Ser Glu Ala Glu Gly Phe Gly Leu Ile Asn Asp  
405 410 415  
Ser Ser Ser Leu Ala Leu Tyr Phe Leu Asp Lys Phe Gln Val Ala Met  
420 425 430  
Val Pro Gly Asp Ala Phe Gly Asp His Ser Cys Ile Arg Ile Ser Tyr  
435 440 445  
Ala Thr Ser Leu Asp Val Leu Gln Ala Ala Val Glu Lys Ile Arg Lys  
450 455 460  
Ala Leu Glu Pro Leu Arg Ala Thr Val Ser Val  
465 470 475

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Ser Ser Arg Ile Cys Ala Met Ala Lys Pro Asn Asp Ala Glu Thr  
1 5 10 15  
Leu Ser Ser Ser Val Asp Met Ser Leu Ser Pro Arg Val Gln Ser Leu  
20 25 30  
Lys Pro Ser Lys Thr Met Val Ile Thr Asp Leu Ala Ala Thr Leu Val  
35 40 45  
Gln Ser Gly Val Pro Val Ile Arg Leu Ala Ala Gly Glu Pro Asp Phe  
50 55 60  
Asp Thr Pro Lys Val Val Ala Glu Ala Gly Ile Asn Ala Ile Arg Glu  
65 70 75 80  
Gly Phe Thr Arg Tyr Thr Leu Asn Ala Gly Ile Thr Glu Leu Arg Glu  
85 90 95  
Ala Ile Cys Arg Lys Leu Lys Glu Glu Asn Gly Leu Ser Tyr Ala Pro  
100 105 110  
Asp Gln Ile Leu Val Ser Asn Gly Ala Lys Gln Ser Leu Leu Gln Ala  
115 120 125  
Val Leu Ala Val Cys Ser Pro Gly Asp Glu Val Ile Ile Pro Ala Pro  
130 135 140  
Tyr Trp Val Ser Tyr Thr Glu Gln Ala Arg Leu Ala Asp Ala Thr Pro  
145 150 155 160  
Val Val Ile Pro Thr Lys Ile Ser Asn Asn Phe Leu Leu Asp Pro Lys  
165 170 175  
Asp Leu Glu Ser Lys Leu Thr Glu Lys Ser Arg Leu Leu Ile Leu Cys  
180 185 190  
Ser Pro Ser Asn Pro Thr Gly Ser Val Tyr Pro Lys Ser Leu Leu Glu  
195 200 205  
Glu Ile Ala Arg Ile Ile Ala Lys His Pro Arg Leu Leu Val Leu Ser  
210 215 220  
Asp Glu Ile Tyr Glu His Ile Ile Tyr Ala Pro Ala Thr His Thr Ser  
225 230 235 240  
Phe Ala Ser Leu Pro Asp Met Tyr Glu Arg Thr Leu Thr Val Asn Gly

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1																
Met	Ala	Lys	Pro	Asn	Asp	Ala	Glu	Thr	Leu	Ser	Ser	Ser	Val	Asp	Met	
1				5					10					15		
Ser	Leu	Ser	Pro	Arg	Val	Gln	Ser	Leu	Lys	Pro	Ser	Lys	Thr	Met	Val	
			20					25					30			
Ile	Thr	Asp	Leu	Ala	Ala	Thr	Leu	Val	Gln	Ser	Gly	Val	Pro	Val	Ile	
		35				40						45				
Arg	Leu	Ala	Ala	Gly	Glu	Pro	Asp	Phe	Asp	Thr	Pro	Lys	Val	Val	Ala	
	50					55					60					
Glu	Ala	Gly	Ile	Asn	Ala	Ile	Arg	Glu	Gly	Phe	Thr	Arg	Tyr	Thr	Leu	
65				70						75					80	
Asn	Ala	Gly	Ile	Thr	Glu	Leu	Arg	Glu	Ala	Ile	Cys	Arg	Lys	Leu	Lys	
				85					90					95		
Glu	Glu	Asn	Gly	Leu	Ser	Tyr	Ala	Pro	Asp	Gln	Ile	Leu	Val	Ser	Asn	
			100					105					110			
Gly	Ala	Lys	Gln	Ser	Leu	Leu	Gln	Ala	Val	Leu	Ala	Val	Cys	Ser	Pro	
		115					120					125				
Gly	Asp	Glu	Val	Ile	Ile	Pro	Ala	Pro	Tyr	Trp	Val	Ser	Tyr	Thr	Glu	
	130					135					140					
Gln	Ala	Arg	Leu	Ala	Asp	Ala	Thr	Pro	Val	Val	Ile	Pro	Thr	Lys	Ile	
145				150						155				160		
Ser	Asn	Asn	Phe	Leu	Leu	Asp	Pro	Lys	Asp	Leu	Glu	Ser	Lys	Leu	Thr	
			165					170						175		
Glu	Lys	Ser	Arg	Leu	Leu	Ile	Leu	Cys	Ser	Pro	Ser	Asn	Pro	Thr	Gly	
			180				185						190			
Ser	Val	Tyr	Pro	Lys	Ser	Leu	Leu	Glu	Ile	Ala	Arg	Ile	Ile	Ala		
		195				200					205					

Lys His Pro Arg Leu Leu Val Leu Ser Asp Glu Ile Tyr Glu His Ile  
210 215 220  
Ile Tyr Ala Pro Ala Thr His Thr Ser Phe Ala Ser Leu Pro Asp Met  
225 230 235 240  
Tyr Glu Arg Thr Leu Thr Val Asn Gly Phe Ser Lys Ala Phe Ala Met  
245 250 255  
Thr Gly Trp Arg Leu Gly Tyr Leu Ala Gly Pro Lys His Ile Val Ala  
260 265 270  
Ala Cys Ser Lys Leu Gln Gly Gln Val Ser Ser Gly Ala Ser Ser Ile  
275 280 285  
Ala Gln Lys Ala Gly Val Ala Ala Leu Gly Leu Gly Lys Ala Gly Gly  
290 295 300  
Glu Thr Val Ala Glu Met Val Lys Ala Tyr Arg Glu Arg Arg Asp Phe  
305 310 315 320  
Leu Val Lys Ser Leu Gly Asp Ile Lys Gly Val Lys Ile Ser Glu Pro  
325 330 335  
Gln Gly Ala Phe Tyr Leu Phe Ile Asp Phe Ser Ala Tyr Tyr Gly Ser  
340 345 350  
Glu Ala Glu Gly Phe Gly Leu Ile Asn Asp Ser Ser Ser Leu Ala Leu  
355 360 365  
Tyr Phe Leu Asp Lys Phe Gln Val Ala Met Val Pro Gly Asp Ala Phe  
370 375 380  
Gly Asp His Ser Cys Ile Arg Ile Ser Tyr Ala Thr Ser Leu Asp Val  
385 390 395 400  
Leu Gln Ala Ala Val Glu Lys Ile Arg Lys Ala Leu Glu Pro Leu Arg  
405 410 415  
Ala Thr Val Ser Val  
420

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1052
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

cctagtccaa aaattttctca tactataaaa agattttttt ttttgcttcg ctccctcttt	60
ttcacttcgt taacggcccc gcctccactc taccctaccg ccgacgtccg tgatcgccga	120
aatgactgaa gcagagtcca agactgttgt tcctgagtcg gtgttggaaga agagaaagag	180
ggaggaagaa tgggcacttg ccaagaaaca ggagcttgag gctgccaaaa agcagaatgc	240
tgagaagagg aaactcatat ttaaccgggc taaacagtac tccaaggagt accaggagaa	300
agaaagggaa ttaatccagc tgaagcgtga ggcaaaattg aaaggaggct tttatgttga	360
cccagaagct aaactgcttt tcattatccg tatccgtggg atcaatgcca ttgacccaaa	420
gacaaagaag attttgcaac ttttgctttt aagacagatt tkcaatgggtg tgktcttgaa	480
ggtcaacaag gcaaccatta acatgcttcg ccgtgttgaa ccctatgtaa cctatggata	540
cccgaactta aaaagtgtga aggaattgat ttacaaacga ggttttggaa agcttaacca	600
ccagaggatt gccttaacag acaattctat tgtagatcag gggctaggaa agcatggcat	660
catctgcgtt gaggatctga tccatgagat catgacggtt gggccacatt tcaaggaagc	720
caataacttt ttgtggccat tccagttgaa ggctccattg ggagggatga agaagaagag	780
gaaccattac gtggaaggag gagatgctgg aaaccgcgag aacttcatca acgagctcgt	840
taggagaatg aactgaagcg taagcgttat tgctctgaaa ctccctagga aacgttttgc	900
tataggtgga aaacttctgt tcgcttgctt gtgttgccat tgaggcgaag taaacattta	960
cggtgaaaga ctttgatatt ttataagttg gcaattgtaa gaacacatca tttatttcct	1020
tccacattac atcgtcactt gcattgcatt tt	

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..244  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498436  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Met	Thr	Glu	Ala	Glu	Ser	Lys	Thr	Val	Val	Pro	Glu	Ser	Val	Leu	Lys
1				5				10						15	
Lys	Arg	Lys	Arg	Glu	Glu	Glu	Trp	Ala	Leu	Ala	Lys	Lys	Gln	Glu	Leu
			20					25					30		
Glu	Ala	Ala	Lys	Lys	Gln	Asn	Ala	Glu	Lys	Arg	Lys	Leu	Ile	Phe	Asn
			35				40					45			
Arg	Ala	Lys	Gln	Tyr	Ser	Lys	Glu	Tyr	Gln	Glu	Lys	Glu	Arg	Glu	Leu
	50					55				60					
Ile	Gln	Leu	Lys	Arg	Glu	Ala	Lys	Leu	Lys	Gly	Gly	Phe	Tyr	Val	Asp
65					70				75					80	
Pro	Glu	Ala	Lys	Leu	Phe	Ile	Ile	Arg	Ile	Arg	Gly	Ile	Asn	Ala	
				85				90					95		
Ile	Asp	Pro	Lys	Thr	Lys	Lys	Ile	Leu	Gln	Leu	Leu	Arg	Leu	Arg	Gln
			100					105					110		
Ile	Xaa	Asn	Gly	Val	Xaa	Leu	Lys	Val	Asn	Lys	Ala	Thr	Ile	Asn	Met
		115					120					125			
Leu	Arg	Arg	Val	Glu	Pro	Tyr	Val	Thr	Tyr	Gly	Tyr	Pro	Asn	Leu	Lys
	130					135					140				
Ser	Val	Lys	Glu	Leu	Ile	Tyr	Lys	Arg	Gly	Phe	Gly	Lys	Leu	Asn	His
145					150				155					160	
Gln	Arg	Ile	Ala	Leu	Thr	Asp	Asn	Ser	Ile	Val	Asp	Gln	Gly	Leu	Gly
				165					170					175	
Lys	His	Gly	Ile	Ile	Cys	Val	Glu	Asp	Leu	Ile	His	Glu	Ile	Met	Thr
			180					185					190		
Val	Gly	Pro	His	Phe	Lys	Glu	Ala	Asn	Asn	Phe	Leu	Trp	Pro	Phe	Gln
		195					200					205			
Leu	Lys	Ala	Pro	Leu	Gly	Gly	Met	Lys	Lys	Lys	Arg	Asn	His	Tyr	Val
	210					215					220				
Glu	Gly	Gly	Asp	Ala	Gly	Asn	Arg	Glu	Asn	Phe	Ile	Asn	Glu	Leu	Val
225					230					235				240	
Arg	Arg	Met	Asn												

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1252  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

attgttttgg	gatacttgaa	ctccttggtg	ggtgttgagc	acgatcagct	taatgctgct	60
tccaaagctg	aagacgatgt	gaacttttat	caaacagtga	atcctgatgt	tgcaaagatg	120
tttcaccttg	atccggagtc	taaaaggcct	gctcttgctc	tagttaagaa	ggaagaggag	180
aaaatttagcc	attttgatgc	agaatttggt	aagtctgctc	tagttagttt	tgtgtctgcc	240
aacaagcttg	cttttgtctc	tgttttcacc	agagagactg	ctccggaaat	ttttgagagt	300
gcaatcaaga	aacagttggt	gttgtttgta	acaaaaaatg	aatctgaaaa	ggttcttacg	360
gaatttcaag	aagcagcgaa	atcattcaaa	ggaaagctca	tctttgtatc	tgtggatctg	420
gataatgagg	attatgggaa	gccagtcgct	gaatactttg	gtgtgtctgg	aaatggtcct	480



```
aaacttattg gctacacagg gaatgaagac cctaaaaaat acttttttcga tggcgagatc 540
cagtcagata aaattaagat atttggggag gatttcctga acgacaagtt aaagcctttc 600
tataagtcag accccattcc tgaaaagaac gatgaagatg tgaaaatagt gggttgagat 660
aactttgatg aaattgttct ggacgattct aaagatgtgc ttctcgaggt ctacgcacca 720
tggtgtggcc attgccaagc ccttgagcca atgtataaca aacttgccaa gcatttacga 780
agtattgatt ctctcgtcat aaccgagatg gatggaacaa ccaatgaaca tccaaggca 840
aaggctgagg ggttccctac cattctcttc ttccctgcgg gcaacaagac ttcagagccg 900
attactgtag atacagaccg cactgtggtt gcattttaca agttcttaag gaaacacgca 960
acgatcccat tcaaactgga gaaacctgca tcaaccgaaw cacctaaaac tgcagagtcc 1020
acaccaaag tagaaactac cgagaccaa gaatcacccg atagcacgac aaagagtagc 1080
caaagtgact cgaaggacga attgtgatca gaaaagggtg taatatatat tacatgtctc 1140
cttaagttgt tatatgtatg atcagaattg tcacatcatg agtttgact agataaagat 1200
gggaattaaa gtaattttag ttttgagaaa gacaatttct tttgatttgg tc
```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```
Ile Val Leu Gly Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln
1           5           10           15
Leu Asn Ala Ala Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr
          20           25           30
Val Asn Pro Asp Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys
          35           40           45
Arg Pro Ala Leu Val Leu Val Lys Lys Glu Glu Glu Lys Ile Ser His
          50           55           60
Phe Asp Gly Glu Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala
65           70           75           80
Asn Lys Leu Ala Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu
          85           90           95
Ile Phe Glu Ser Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys
          100          105          110
Asn Glu Ser Glu Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser
          115          120          125
Phe Lys Gly Lys Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp
          130          135          140
Tyr Gly Lys Pro Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro
          145          150          155          160
Lys Leu Ile Gly Tyr Thr Gly Asn Glu Asp Pro Lys Lys Tyr Phe Phe
          165          170          175
Asp Gly Glu Ile Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe
          180          185          190
Leu Asn Asp Lys Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu
          195          200          205
Lys Asn Asp Glu Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu
          210          215          220
Ile Val Leu Asp Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro
          225          230          235          240
Trp Cys Gly His Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala
          245          250          255
Lys His Leu Arg Ser Ile Asp Ser Leu Val Ile Thr Glu Met Asp Gly
          260          265          270
Thr Thr Asn Glu His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile
          275          280          285
```

Leu Phe Phe Pro Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp  
290 295 300  
Thr Asp Arg Thr Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala  
305 310 315 320  
Thr Ile Pro Phe Lys Leu Glu Lys Pro Ala Ser Thr Glu Xaa Pro Lys  
325 330 335  
Thr Ala Glu Ser Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser  
340 345 350  
Pro Asp Ser Thr Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu  
355 360 365

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..329

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala Leu Val Leu Val  
1 5 10 15  
Lys Lys Glu Glu Glu Lys Ile Ser His Phe Asp Gly Glu Phe Val Lys  
20 25 30  
Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu Ala Leu Val Ser  
35 40 45  
Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu Ser Ala Ile Lys  
50 55 60  
Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser Glu Lys Val Leu  
65 70 75 80  
Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly Lys Leu Ile Phe  
85 90 95  
Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys Pro Val Ala Glu  
100 105 110  
Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile Gly Tyr Thr Gly  
115 120 125  
Asn Glu Asp Pro Lys Lys Tyr Phe Phe Asp Gly Glu Ile Gln Ser Asp  
130 135 140  
Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp Lys Leu Lys Pro  
145 150 155 160  
Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp Glu Asp Val Lys  
165 170 175  
Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu Asp Asp Ser Lys  
180 185 190  
Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly His Cys Gln Ala  
195 200 205  
Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu Arg Ser Ile Asp  
210 215 220  
Ser Leu Val Ile Thr Glu Met Asp Gly Thr Thr Asn Glu His Pro Lys  
225 230 235 240  
Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe Pro Ala Gly Asn  
245 250 255  
Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala  
260 265 270  
Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro Phe Lys Leu Glu  
275 280 285  
Lys Pro Ala Ser Thr Glu Xaa Pro Lys Thr Ala Glu Ser Thr Pro Lys

290 295 300  
Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser Thr Thr Lys Ser  
305 310 315 320  
Ser Gln Ser Asp Ser Lys Asp Glu Leu  
325

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1755  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```
aaacaagggt tcttgctccg acacgacaac aaatccagat tctgagctta gggaaacttg      60
agaaggagaa aaaaatgtcg aacatagaca tagaagggat cttgaaggat ctacctaatg      120
atgggaggat cccaaagacg aagatagttt gcacattagg accagcttct cgcactgttt      180
ccatgatcga aaagcttttg aaagccggtg tgaatgtggc tcgcttcaac ttctcacatg      240
gaagccatga ataccatcaa gagacactcg acaacctccg ctctgctatg cataataaccg      300
gcattctcgc tgctgtcatg cttgatacta aggggcctga gattcgtact ggtttcttga      360
aagatgggaa ccctatacaa ctgaaggaag gtcaagagat tactataacc actgattatg      420
acattcaagg agacgaatca acgatatcca tgagctataa aaagctgcct ttggatgtga      480
agcccggaag caccatactc tgtgcagatg gaagcataag tctagctgtc ttgtcatgtg      540
atcctgagtc tggaaactgt aggtgccggt gtgaaaactc ggcatgctt ggtgaaagaa      600
agaatgtgaa tottctctggc gttgttgttg atcttcccac ttgacagat aaggatatgt      660
aagatattct cggttggggg gttccgaaca gcattgatat gattgctctt tcgtttgtcc      720
gtaaagggtt ggaattgtgt aatgtccgca aggttcttg atctcatgct aaaagcataa      780
tgctcatgtc aaaggttgag aaccaggaag gtgtgattaa ctttgatgag atcttgctgt      840
aaacagatgc gttcatgggt gcccggtgtg atctcgggat ggagattccg atagagaaga      900
tcttcttggc tcaaaagttg atgatctaca agtgtaacct tgcgggtaaa ccggtggtca      960
cagccactca gatgctggag tcaatgatca aatcacctcg gccaaaccga gctgaagcca      1020
cagatgttgc aaatgctgtt cttgatggta ctgactgtgt gatgcttagc ggtgagagtg      1080
cagcaggagc ttatccggaa atagctgtga aagtcattgg taagatctgc attgaagccg      1140
aatcctcgtc tgattacaac acaatcttta aagagatgat ccgagcaact ccacttccaa      1200
tgagcccact cgagagtctt gcacatccg ctgtacggac tgctaacaaa gcgagggcaa      1260
aactcatcat tgtgttgaca cgtggagggt caactgctaa tctcgtggct aaatacagac      1320
cggctgttcc gattctgtca gtggttgtcc cggttatgac cactgattcc tttgactggt      1380
ctttagtgta cgagtcacct gcaaggcata gtctgatata cagaggtcta atccctatgt      1440
tggtgtaagg atctgcaaag gcaacagata gtgaagccac cgaagttatc attgaagctg      1500
ctctgaagtc ggctactcag agaggactgt gcaaccgtgg tgatgcaatc gtggcgctgc      1560
accgtattgg agctgcctca gttattaaga tctgtgtggt taagtgaagt tacagacttc      1620
tttcaatacc tcaaactctt gattgttggt aatcgtaact gagattttgc tttgtagcat      1680
gaaataaaga aaacaggtca caatagttcc tgaaactctg ttacttttaa gatattcttc      1740
tctctttttt ttttc
```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..534  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Thr Arg Val Leu Ala Pro Thr Arg Gln Ile Gln Ile Leu Ser Leu  
1 5 10 15

Gly	Lys	Leu	Glu	Lys	Glu	Lys	Lys	Met	Ser	Asn	Ile	Asp	Ile	Glu	Gly	20	25	30
Ile	Leu	Lys	Asp	Leu	Pro	Asn	Asp	Gly	Arg	Ile	Pro	Lys	Thr	Lys	Ile	35	40	45
Val	Cys	Thr	Leu	Gly	Pro	Ala	Ser	Arg	Thr	Val	Ser	Met	Ile	Glu	Lys	50	55	60
Leu	Leu	Lys	Ala	Gly	Met	Asn	Val	Ala	Arg	Phe	Asn	Phe	Ser	His	Gly	65	70	75
Ser	His	Glu	Tyr	His	Gln	Glu	Thr	Leu	Asp	Asn	Leu	Arg	Ser	Ala	Met	85	90	95
His	Asn	Thr	Gly	Ile	Leu	Ala	Ala	Val	Met	Leu	Asp	Thr	Lys	Gly	Pro	100	105	110
Glu	Ile	Arg	Thr	Gly	Phe	Leu	Lys	Asp	Gly	Asn	Pro	Ile	Gln	Leu	Lys	115	120	125
Glu	Gly	Gln	Glu	Ile	Thr	Ile	Thr	Thr	Asp	Tyr	Asp	Ile	Gln	Gly	Asp	130	135	140
Glu	Ser	Thr	Ile	Ser	Met	Ser	Tyr	Lys	Lys	Leu	Pro	Leu	Asp	Val	Lys	145	150	155
Pro	Gly	Asn	Thr	Ile	Leu	Cys	Ala	Asp	Gly	Ser	Ile	Ser	Leu	Ala	Val	165	170	175
Leu	Ser	Cys	Asp	Pro	Glu	Ser	Gly	Thr	Val	Arg	Cys	Arg	Cys	Glu	Asn	180	185	190
Ser	Ala	Met	Leu	Gly	Glu	Arg	Lys	Asn	Val	Asn	Leu	Pro	Gly	Val	Val	195	200	205
Val	Asp	Leu	Pro	Thr	Leu	Thr	Asp	Lys	Asp	Ile	Glu	Asp	Ile	Leu	Gly	210	215	220
Trp	Gly	Val	Pro	Asn	Ser	Ile	Asp	Met	Ile	Ala	Leu	Ser	Phe	Val	Arg	225	230	235
Lys	Gly	Ser	Asp	Leu	Val	Asn	Val	Arg	Lys	Val	Leu	Gly	Ser	His	Ala	245	250	255
Lys	Ser	Ile	Met	Leu	Met	Ser	Lys	Val	Glu	Asn	Gln	Glu	Gly	Val	Ile	260	265	270
Asn	Phe	Asp	Glu	Ile	Leu	Arg	Glu	Thr	Asp	Ala	Phe	Met	Val	Ala	Arg	275	280	285
Gly	Asp	Leu	Gly	Met	Glu	Ile	Pro	Ile	Glu	Lys	Ile	Phe	Leu	Ala	Gln	290	295	300
Lys	Leu	Met	Ile	Tyr	Lys	Cys	Asn	Leu	Ala	Gly	Lys	Pro	Val	Val	Thr	305	310	315
Ala	Thr	Gln	Met	Leu	Glu	Ser	Met	Ile	Lys	Ser	Pro	Arg	Pro	Thr	Arg	325	330	335
Ala	Glu	Ala	Thr	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp	Gly	Thr	Asp	Cys	340	345	350
Val	Met	Leu	Ser	Gly	Glu	Ser	Ala	Ala	Gly	Ala	Tyr	Pro	Glu	Ile	Ala	355	360	365
Val	Lys	Val	Met	Ala	Lys	Ile	Cys	Ile	Glu	Ala	Glu	Ser	Ser	Leu	Asp	370	375	380
Tyr	Asn	Thr	Ile	Phe	Lys	Glu	Met	Ile	Arg	Ala	Thr	Pro	Leu	Pro	Met	385	390	395
Ser	Pro	Leu	Glu	Ser	Leu	Ala	Ser	Ser	Ala	Val	Arg	Thr	Ala	Asn	Lys	405	410	415
Ala	Arg	Ala	Lys	Leu	Ile	Ile	Val	Leu	Thr	Arg	Gly	Gly	Ser	Thr	Ala	420	425	430
Asn	Leu	Val	Ala	Lys	Tyr	Arg	Pro	Ala	Val	Pro	Ile	Leu	Ser	Val	Val	435	440	445
Val	Pro	Val	Met	Thr	Thr	Asp	Ser	Phe	Asp	Trp	Ser	Cys	Ser	Asp	Glu	450	455	460
Ser	Pro	Ala	Arg	His	Ser	Leu	Ile	Tyr	Arg	Gly	Leu	Ile	Pro	Met	Leu	465	470	475
Ala	Glu	Gly	Ser	Ala	Lys	Ala	Thr	Asp	Ser	Glu	Ala	Thr	Glu	Val	Ile	485	490	495
Ile	Glu	Ala	Ala	Leu	Lys	Ser	Ala	Thr	Gln	Arg	Gly	Leu	Cys	Asn	Arg			

500 505 510  
Gly Asp Ala Ile Val Ala Leu His Arg Ile Gly Ala Ala Ser Val Ile  
515 520 525  
Lys Ile Cys Val Val Lys  
530

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met	Ser	Asn	Ile	Asp	Ile	Glu	Gly	Ile	Leu	Lys	Asp	Leu	Pro	Asn	Asp	
1				5					10					15		
Gly	Arg	Ile	Pro	Lys	Thr	Lys	Ile	Val	Cys	Thr	Leu	Gly	Pro	Ala	Ser	
			20					25					30			
Arg	Thr	Val	Ser	Met	Ile	Glu	Lys	Leu	Leu	Lys	Ala	Gly	Met	Asn	Val	
			35				40					45				
Ala	Arg	Phe	Asn	Phe	Ser	His	Gly	Ser	His	Glu	Tyr	His	Gln	Glu	Thr	
			50				55				60					
Leu	Asp	Asn	Leu	Arg	Ser	Ala	Met	His	Asn	Thr	Gly	Ile	Leu	Ala	Ala	
65					70					75				80		
Val	Met	Leu	Asp	Thr	Lys	Gly	Pro	Glu	Ile	Arg	Thr	Gly	Phe	Leu	Lys	
				85					90					95		
Asp	Gly	Asn	Pro	Ile	Gln	Leu	Lys	Glu	Gly	Gln	Glu	Ile	Thr	Ile	Thr	
			100					105					110			
Thr	Asp	Tyr	Asp	Ile	Gln	Gly	Asp	Glu	Ser	Thr	Ile	Ser	Met	Ser	Tyr	
			115				120					125				
Lys	Lys	Leu	Pro	Leu	Asp	Val	Lys	Pro	Gly	Asn	Thr	Ile	Leu	Cys	Ala	
			130				135				140					
Asp	Gly	Ser	Ile	Ser	Leu	Ala	Val	Leu	Ser	Cys	Asp	Pro	Glu	Ser	Gly	
145					150					155				160		
Thr	Val	Arg	Cys	Arg	Cys	Glu	Asn	Ser	Ala	Met	Leu	Gly	Glu	Arg	Lys	
				165					170					175		
Asn	Val	Asn	Leu	Pro	Gly	Val	Val	Val	Asp	Leu	Pro	Thr	Leu	Thr	Asp	
			180					185					190			
Lys	Asp	Ile	Glu	Asp	Ile	Leu	Gly	Trp	Gly	Val	Pro	Asn	Ser	Ile	Asp	
			195				200					205				
Met	Ile	Ala	Leu	Ser	Phe	Val	Arg	Lys	Gly	Ser	Asp	Leu	Val	Asn	Val	
			210			215					220					
Arg	Lys	Val	Leu	Gly	Ser	His	Ala	Lys	Ser	Ile	Met	Leu	Met	Ser	Lys	
225					230					235				240		
Val	Glu	Asn	Gln	Glu	Gly	Val	Ile	Asn	Phe	Asp	Glu	Ile	Leu	Arg	Glu	
				245					250					255		
Thr	Asp	Ala	Phe	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Met	Glu	Ile	Pro	
			260					265					270			
Ile	Glu	Lys	Ile	Phe	Leu	Ala	Gln	Lys	Leu	Met	Ile	Tyr	Lys	Cys	Asn	
			275				280					285				
Leu	Ala	Gly	Lys	Pro	Val	Val	Thr	Ala	Thr	Gln	Met	Leu	Glu	Ser	Met	
			290			295					300					
Ile	Lys	Ser	Pro	Arg	Pro	Thr	Arg	Ala	Glu	Ala	Thr	Asp	Val	Ala	Asn	
305				310						315				320		
Ala	Val	Leu	Asp	Gly	Thr	Asp	Cys	Val	Met	Leu	Ser	Gly	Glu	Ser	Ala	
				325					330					335		
Ala	Gly	Ala	Tyr	Pro	Glu	Ile	Ala	Val	Lys	Val	Met	Ala	Lys	Ile	Cys	
			340					345					350			

Ile Glu Ala Glu Ser Ser Leu Asp Tyr Asn Thr Ile Phe Lys Glu Met  
355 360 365  
Ile Arg Ala Thr Pro Leu Pro Met Ser Pro Leu Glu Ser Leu Ala Ser  
370 375 380  
Ser Ala Val Arg Thr Ala Asn Lys Ala Arg Ala Lys Leu Ile Ile Val  
385 390 395 400  
Leu Thr Arg Gly Gly Ser Thr Ala Asn Leu Val Ala Lys Tyr Arg Pro  
405 410 415  
Ala Val Pro Ile Leu Ser Val Val Val Pro Val Met Thr Thr Asp Ser  
420 425 430  
Phe Asp Trp Ser Cys Ser Asp Glu Ser Pro Ala Arg His Ser Leu Ile  
435 440 445  
Tyr Arg Gly Leu Ile Pro Met Leu Ala Glu Gly Ser Ala Lys Ala Thr  
450 455 460  
Asp Ser Glu Ala Thr Glu Val Ile Ile Glu Ala Ala Leu Lys Ser Ala  
465 470 475 480  
Thr Gln Arg Gly Leu Cys Asn Arg Gly Asp Ala Ile Val Ala Leu His  
485 490 495  
Arg Ile Gly Ala Ala Ser Val Ile Lys Ile Cys Val Val Lys  
500 505 510

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Ile Glu Lys Leu Leu Lys Ala Gly Met Asn Val Ala Arg Phe Asn  
1 5 10 15  
Phe Ser His Gly Ser His Glu Tyr His Gln Glu Thr Leu Asp Asn Leu  
20 25 30  
Arg Ser Ala Met His Asn Thr Gly Ile Leu Ala Ala Val Met Leu Asp  
35 40 45  
Thr Lys Gly Pro Glu Ile Arg Thr Gly Phe Leu Lys Asp Gly Asn Pro  
50 55 60  
Ile Gln Leu Lys Glu Gly Gln Glu Ile Thr Ile Thr Thr Asp Tyr Asp  
65 70 75 80  
Ile Gln Gly Asp Glu Ser Thr Ile Ser Met Ser Tyr Lys Lys Leu Pro  
85 90 95  
Leu Asp Val Lys Pro Gly Asn Thr Ile Leu Cys Ala Asp Gly Ser Ile  
100 105 110  
Ser Leu Ala Val Leu Ser Cys Asp Pro Glu Ser Gly Thr Val Arg Cys  
115 120 125  
Arg Cys Glu Asn Ser Ala Met Leu Gly Glu Arg Lys Asn Val Asn Leu  
130 135 140  
Pro Gly Val Val Val Asp Leu Pro Thr Leu Thr Asp Lys Asp Ile Glu  
145 150 155 160  
Asp Ile Leu Gly Trp Gly Val Pro Asn Ser Ile Asp Met Ile Ala Leu  
165 170 175  
Ser Phe Val Arg Lys Gly Ser Asp Leu Val Asn Val Arg Lys Val Leu  
180 185 190  
Gly Ser His Ala Lys Ser Ile Met Leu Met Ser Lys Val Glu Asn Gln  
195 200 205  
Glu Gly Val Ile Asn Phe Asp Glu Ile Leu Arg Glu Thr Asp Ala Phe  
210 215 220  
Met Val Ala Arg Gly Asp Leu Gly Met Glu Ile Pro Ile Glu Lys Ile

225					230					235					240
Phe	Leu	Ala	Gln	Lys	Leu	Met	Ile	Tyr	Lys	Cys	Asn	Leu	Ala	Gly	Lys
				245					250					255	
Pro	Val	Val	Thr	Ala	Thr	Gln	Met	Leu	Glu	Ser	Met	Ile	Lys	Ser	Pro
			260					265					270		
Arg	Pro	Thr	Arg	Ala	Glu	Ala	Thr	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp
		275					280				285				
Gly	Thr	Asp	Cys	Val	Met	Leu	Ser	Gly	Glu	Ser	Ala	Ala	Gly	Ala	Tyr
	290					295				300					
Pro	Glu	Ile	Ala	Val	Lys	Val	Met	Ala	Lys	Ile	Cys	Ile	Glu	Ala	Glu
305					310					315					320
Ser	Ser	Leu	Asp	Tyr	Asn	Thr	Ile	Phe	Lys	Glu	Met	Ile	Arg	Ala	Thr
			325					330					335		
Pro	Leu	Pro	Met	Ser	Pro	Leu	Glu	Ser	Leu	Ala	Ser	Ser	Ala	Val	Arg
			340					345					350		
Thr	Ala	Asn	Lys	Ala	Arg	Ala	Lys	Leu	Ile	Ile	Val	Leu	Thr	Arg	Gly
		355					360					365			
Gly	Ser	Thr	Ala	Asn	Leu	Val	Ala	Lys	Tyr	Arg	Pro	Ala	Val	Pro	Ile
	370					375				380					
Leu	Ser	Val	Val	Val	Pro	Val	Met	Thr	Thr	Asp	Ser	Phe	Asp	Trp	Ser
385					390					395					400
Cys	Ser	Asp	Glu	Ser	Pro	Ala	Arg	His	Ser	Leu	Ile	Tyr	Arg	Gly	Leu
			405					410					415		
Ile	Pro	Met	Leu	Ala	Glu	Gly	Ser	Ala	Lys	Ala	Thr	Asp	Ser	Glu	Ala
		420					425					430			
Thr	Glu	Val	Ile	Ile	Glu	Ala	Ala	Leu	Lys	Ser	Ala	Thr	Gln	Arg	Gly
	435					440						445			
Leu	Cys	Asn	Arg	Gly	Asp	Ala	Ile	Val	Ala	Leu	His	Arg	Ile	Gly	Ala
	450					455					460				
Ala	Ser	Val	Ile	Lys	Ile	Cys	Val	Val	Lys						
465					470										

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1397
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

caagctgttc	gagattcttc	cagtcttacg	atatctcatc	tatactccaa	cgtaccatag	60
tctgcatcat	caagaaatgg	ggaccaactt	ttgtctatct	atgcctctct	ttgatgtttt	120
gggcgataca	caaaacccaa	actcatggga	actccaaaag	aagattcggt	tgagtgcagg	180
ggaacggaag	agagtgcggg	agtttgtgtt	cttagctcac	ggagttgatg	taatgtcggc	240
gatgcatgca	ccgttcgtgt	tcagatcttt	tgcttcaatg	ccatatacca	caaggatatt	300
cttgctaccg	atgtggccat	tcacgttctg	tgttatgttg	ggcatgtggg	cttgggtcaaa	360
gacttttctt	ttcagcttct	ataccctcag	gaacaatctt	tgtcagactt	ggggcgttcc	420
tagattcgga	ttccaatact	tcttaccgtt	tgctacaaaa	ggaattaatg	atcaaatgga	480
ggctgcgatt	cttagagctg	ataagattgg	tgttaaagtt	ataagcttgg	ctgctctcaa	540
caagaacgaa	gctctaaatg	gtggtggaac	actgtttgtc	aacaagcatc	ctgaccttag	600
agttcgtgtg	gttcatggga	acactttaac	tgacgcagtg	attctctatg	aaattccaaa	660
agatgtgaat	gaggttttct	tgactggagc	cacttctaag	ctgggaagag	ctattgtctct	720
ttacctttgt	cgccgtggag	tgagagttct	catgttgaca	ttgtctatgg	aaaggttcca	780
aaagattcag	aaagaggctc	ctgttgagtt	ccagaacaac	cttgtacaag	tgaccaaata	840
caatgctgct	caacactgca	agacttggat	cgttggaaaa	tggttaaacac	caagagagca	900
gagctgggct	cctgcaggga	cgcatttcca	tcagtttgtg	gtgccaccaa	tccttaagtt	960
tagaagggaac	tgcaattacg	gtgatctagc	agctatgaag	ctccctaaag	atgttgaagg	1020
actcggaact	tgcgagtaca	cgatggagag	aggggtggta	catgcgtgcc	atgcaggagg	1080

```
agtggttcat atgcttgagg gttggaagca tcatgagggtt ggagccattg atgttgaccg      1140
tatcgatttg gtgtgggaag cagccatgaa gtatgggtctt agtgctgttt cttcactcac      1200
aaattgagtg aagagagaga cacgtttcat tggtgtcttt tgactctccc aagattgggtc      1260
attctttgta caggtgaaaag gagatgcaag caggaaaaaa aagtagaatt tcaccttatg      1320
tattgtttta tcttttatta atgatgtatt actttctttt tagatttcct taatattaat      1380
atatgcacct aatttcc
```

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1498449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```
Lys Leu Phe Glu Ile Leu Pro Val Leu Arg Tyr Leu Ile Tyr Thr Pro
1      5      10      15
Thr Tyr His Ser Leu His His Gln Glu Met Gly Thr Asn Phe Cys Leu
20     25     30
Phe Met Pro Leu Phe Asp Val Leu Gly Asp Thr Gln Asn Pro Asn Ser
35     40     45
Trp Glu Leu Gln Lys Lys Ile Arg Leu Ser Ala Gly Glu Arg Lys Arg
50     55     60
Val Pro Glu Phe Val Phe Leu Ala His Gly Val Asp Val Met Ser Ala
65     70     75     80
Met His Ala Pro Phe Val Phe Arg Ser Phe Ala Ser Met Pro Tyr Thr
85     90     95
Thr Arg Ile Phe Leu Leu Pro Met Trp Pro Phe Thr Phe Cys Val Met
100    105    110
Leu Gly Met Trp Ala Trp Ser Lys Thr Phe Leu Phe Ser Phe Tyr Thr
115    120    125
Leu Arg Asn Asn Leu Cys Gln Thr Trp Gly Val Pro Arg Phe Gly Phe
130    135    140
Gln Tyr Phe Leu Pro Phe Ala Thr Lys Gly Ile Asn Asp Gln Ile Glu
145    150    155    160
Ala Ala Ile Leu Arg Ala Asp Lys Ile Gly Val Lys Val Ile Ser Leu
165    170    175
Ala Ala Leu Asn Lys Asn Glu Ala Leu Asn Gly Gly Gly Thr Leu Phe
180    185    190
Val Asn Lys His Pro Asp Leu Arg Val Arg Val Val His Gly Asn Thr
195    200    205
Leu Thr Ala Ala Val Ile Leu Tyr Glu Ile Pro Lys Asp Val Asn Glu
210    215    220
Val Phe Leu Thr Gly Ala Thr Ser Lys Leu Gly Arg Ala Ile Ala Leu
225    230    235    240
Tyr Leu Cys Arg Arg Gly Val Arg Val Leu Met Leu Thr Leu Ser Met
245    250    255
Glu Arg Phe Gln Lys Ile Gln Lys Glu Ala Pro Val Glu Phe Gln Asn
260    265    270
Asn Leu Val Gln Val Thr Lys Tyr Asn Ala Ala Gln His Cys Lys Thr
275    280    285
Trp Ile Val Gly Lys Trp Leu Thr Pro Arg Glu Gln Ser Trp Ala Pro
290    295    300
Ala Gly Thr His Phe His Gln Phe Val Val Pro Pro Ile Leu Lys Phe
305    310    315    320
Arg Arg Asn Cys Thr Tyr Gly Asp Leu Ala Ala Met Lys Leu Pro Lys
325    330    335
Asp Val Glu Gly Leu Gly Thr Cys Glu Tyr Thr Met Glu Arg Gly Val
```



	340		345		350										
Val	His	Ala	Cys	His	Ala	Gly	Gly	Val	Val	His	Met	Leu	Glu	Gly	Trp
	355					360						365			
Lys	His	His	Glu	Val	Gly	Ala	Ile	Asp	Val	Asp	Arg	Ile	Asp	Leu	Val
	370					375					380				
Trp	Glu	Ala	Ala	Met	Lys	Tyr	Gly	Leu	Ser	Ala	Val	Ser	Ser	Leu	Thr
385					390					395					400
Asn															

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1498450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met	Gly	Thr	Asn	Phe	Cys	Leu	Phe	Met	Pro	Leu	Phe	Asp	Val	Leu	Gly
1			5					10					15		
Asp	Thr	Gln	Asn	Pro	Asn	Ser	Trp	Glu	Leu	Gln	Lys	Lys	Ile	Arg	Leu
		20					25						30		
Ser	Ala	Gly	Glu	Arg	Lys	Arg	Val	Pro	Glu	Phe	Val	Phe	Leu	Ala	His
	35					40					45				
Gly	Val	Asp	Val	Met	Ser	Ala	Met	His	Ala	Pro	Phe	Val	Phe	Arg	Ser
	50				55					60					
Phe	Ala	Ser	Met	Pro	Tyr	Thr	Thr	Arg	Ile	Phe	Leu	Leu	Pro	Met	Trp
65					70				75						80
Pro	Phe	Thr	Phe	Cys	Val	Met	Leu	Gly	Met	Trp	Ala	Trp	Ser	Lys	Thr
			85					90					95		
Phe	Leu	Phe	Ser	Phe	Tyr	Thr	Leu	Arg	Asn	Asn	Leu	Cys	Gln	Thr	Trp
		100					105					110			
Gly	Val	Pro	Arg	Phe	Gly	Phe	Gln	Tyr	Phe	Leu	Pro	Phe	Ala	Thr	Lys
	115					120					125				
Gly	Ile	Asn	Asp	Gln	Ile	Glu	Ala	Ala	Ile	Leu	Arg	Ala	Asp	Lys	Ile
	130				135						140				
Gly	Val	Lys	Val	Ile	Ser	Leu	Ala	Ala	Leu	Asn	Lys	Asn	Glu	Ala	Leu
145					150					155					160
Asn	Gly	Gly	Gly	Thr	Leu	Phe	Val	Asn	Lys	His	Pro	Asp	Leu	Arg	Val
			165				170						175		
Arg	Val	Val	His	Gly	Asn	Thr	Leu	Thr	Ala	Ala	Val	Ile	Leu	Tyr	Glu
		180					185						190		
Ile	Pro	Lys	Asp	Val	Asn	Glu	Val	Phe	Leu	Thr	Gly	Ala	Thr	Ser	Lys
	195					200					205				
Leu	Gly	Arg	Ala	Ile	Ala	Leu	Tyr	Leu	Cys	Arg	Arg	Gly	Val	Arg	Val
	210				215					220					
Leu	Met	Leu	Thr	Leu	Ser	Met	Glu	Arg	Phe	Gln	Lys	Ile	Gln	Lys	Glu
225					230					235					240
Ala	Pro	Val	Glu	Phe	Gln	Asn	Asn	Leu	Val	Gln	Val	Thr	Lys	Tyr	Asn
			245					250						255	
Ala	Ala	Gln	His	Cys	Lys	Thr	Trp	Ile	Val	Gly	Lys	Trp	Leu	Thr	Pro
	260						265						270		
Arg	Glu	Gln	Ser	Trp	Ala	Pro	Ala	Gly	Thr	His	Phe	His	Gln	Phe	Val
	275					280						285			
Val	Pro	Pro	Ile	Leu	Lys	Phe	Arg	Arg	Asn	Cys	Thr	Tyr	Gly	Asp	Leu
	290					295				300					
Ala	Ala	Met	Lys	Leu	Pro	Lys	Asp	Val	Glu	Gly	Leu	Gly	Thr	Cys	Glu
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:439:

(A) LENGTH: 368 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:439:

[illegible]

```

                325                330                335
His His Glu Val Gly Ala Ile Asp Val Asp Arg Ile Asp Leu Val Trp
                340                345                350
Glu Ala Ala Met Lys Tyr Gly Leu Ser Ala Val Ser Ser Leu Thr Asn
                355                360                365
```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1424
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

gtattgtgtt gttggagact gaaccatcaa cgctttttcg acacttcttc ttcttctctc      60
tttctctctt catgcaaaat cacagttaca agaaataaac aaaagattat aaatcaaaaac      120
ataaagagac aaaaatgagt gatggtcgag ttaacgcaga tcctcaacaa gaagagaaca      180
tggttaaacc accggttaag agatctctca ctctcctcat cgtgacttac ttttttctct      240
tcttcggctc tatcgcttcg agccttctcg cgaagtacta tttcgtctac ggtggctcga      300
gccggtgggt ctccacgtgg gttcaatctg ctggcttttc cctctcctcc tcataccta      360
ctacttcccc tcaactacgtt ctcaaaaacca ccactcgccg tcctttcacg cgcttcacgc      420
tccgccatct catctttctc gtgttgatcg ggcttgttct cggtttcaac aacttcctct      480
tctcatgggg aacctcgta cttccgggtg ccacgtcatc gcttctcctc tcgacacaac      540
tcgtcttcac tctcattttg tctaggatca ttgtgaaaca gaagatcact ttctcaaaac      600
tcaactgcgt tgtcctggtg acgttaagct ctgttttgtt ggctcttgat tcgagtaaag      660
ataaaccgtc cggtttaacc aaaaccaagt atttcatcgg gtatgtatcc acgatcggag      720
ccggtttact cttcgctctt tacctccccg tgacggagaa gctataccgt accgtttatt      780
gttacgcgat ggtcatggag gtgcaactgg tgatggaatt cgcagcgacg gttttcgcga      840
caatcggtat ggcttgcgaa ggcggggtta aggaaatggt taaggaagcg aacctgttt      900
tcaccaaagg accaacattt tattggacgt ttgcgatact agcaaagtgt gtgacgtggc      960
agctctcttt cgcagccacg tcagggatgg tttacttgac gtcaggtatc accggaggt      1020
tctgcatgac ggcgttgctc gcgatgaatg tgataggagg tgtggtggct tacggtgacg      1080
tgtttggtgg agtgaagatt gtgtcgacgg tgctatgtat ttggggattc tcattctaca      1140
catacgggat gtatatgaag atgaagaagg aggagaagga gaagggagaa tattccggcg      1200
taaagacgac ggaagacagc ggagagatgg aggtggaaat gggaaatgtt aaagatgacg      1260
tggcggcggc ggatgatagg gcttgaagat atctgtgtga ttgagacggc cgttatgatt      1320
attattagga aggaagccaa caaaaaaaaaa aaaagtagta gtatcttttt gtgttctttc      1380
tttttctcac cttatgtttt tttagtaatg catttgcttt tgtc
```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Val Met Glu Val Gln Leu Val Met Glu Phe Ala Ala Thr Val Phe
1           5           10           15
Ala Thr Ile Gly Met Ala Cys Glu Gly Gly Phe Lys Glu Met Val Lys
                20                25                30
Glu Ala Asn His Val Phe Thr Lys Gly Pro Thr Phe Tyr Trp Thr Phe
                35                40                45
```

Ala Ile Leu Ala Asn Val Val Thr Trp Gln Leu Ser Phe Ala Ala Thr  
50 55 60  
Ser Gly Met Val Tyr Leu Thr Ser Gly Ile Thr Gly Gly Ile Cys Met  
65 70 75 80  
Thr Ala Leu Leu Ala Met Asn Val Ile Gly Gly Val Val Ala Tyr Gly  
85 90 95  
Asp Val Phe Gly Gly Val Lys Ile Val Ser Thr Val Leu Cys Ile Trp  
100 105 110  
Gly Phe Ser Ser Tyr Thr Tyr Gly Met Tyr Met Lys Met Lys Lys Glu  
115 120 125  
Glu Lys Glu Lys Gly Glu Tyr Ser Gly Val Lys Thr Thr Glu Asp Ser  
130 135 140  
Gly Glu Met Glu Val Glu Met Gly Asn Val Lys Asp Asp Val Ala Ala  
145 150 155 160  
Ala Asp Asp Arg Ala  
165

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met Glu Val Gln Leu Val Met Glu Phe Ala Thr Val Phe Ala Thr  
1 5 10 15  
Ile Gly Met Ala Cys Glu Gly Gly Phe Lys Glu Met Val Lys Glu Ala  
20 25 30  
Asn His Val Phe Thr Lys Gly Pro Thr Phe Tyr Trp Thr Phe Ala Ile  
35 40 45  
Leu Ala Asn Val Val Thr Trp Gln Leu Ser Phe Ala Ala Thr Ser Gly  
50 55 60  
Met Val Tyr Leu Thr Ser Gly Ile Thr Gly Gly Ile Cys Met Thr Ala  
65 70 75 80  
Leu Leu Ala Met Asn Val Ile Gly Gly Val Val Ala Tyr Gly Asp Val  
85 90 95  
Phe Gly Gly Val Lys Ile Val Ser Thr Val Leu Cys Ile Trp Gly Phe  
100 105 110  
Ser Ser Tyr Thr Tyr Gly Met Tyr Met Lys Met Lys Lys Glu Glu Lys  
115 120 125  
Glu Lys Gly Glu Tyr Ser Gly Val Lys Thr Thr Glu Asp Ser Gly Glu  
130 135 140  
Met Glu Val Glu Met Gly Asn Val Lys Asp Asp Val Ala Ala Ala Asp  
145 150 155 160  
Asp Arg Ala

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1498455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Glu Phe Ala Ala Thr Val Phe Ala Thr Ile Gly Met Ala Cys Glu  
1 5 10 15  
Gly Gly Phe Lys Glu Met Val Lys Glu Ala Asn His Val Phe Thr Lys  
20 25 30  
Gly Pro Thr Phe Tyr Trp Thr Phe Ala Ile Leu Ala Asn Val Val Thr  
35 40 45  
Trp Gln Leu Ser Phe Ala Ala Thr Ser Gly Met Val Tyr Leu Thr Ser  
50 55 60  
Gly Ile Thr Gly Gly Ile Cys Met Thr Ala Leu Ala Met Asn Val  
65 70 75 80  
Ile Gly Gly Val Val Ala Tyr Gly Asp Val Phe Gly Gly Val Lys Ile  
85 90 95  
Val Ser Thr Val Leu Cys Ile Trp Gly Phe Ser Ser Tyr Thr Tyr Gly  
100 105 110  
Met Tyr Met Lys Met Lys Lys Glu Glu Lys Glu Lys Gly Glu Tyr Ser  
115 120 125  
Gly Val Lys Thr Thr Glu Asp Ser Gly Glu Met Glu Val Glu Met Gly  
130 135 140  
Asn Val Lys Asp Asp Val Ala Ala Asp Asp Arg Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1005
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

agggtttttt tcagcggaga ttagcttcag tatccattgg cggattagcc tcagagtgc 60  
ctgatcaagg ttttgagggt tgcatttgag tgaggagatg ttttcggctc agcataagat 120  
tcataaggag aagggtgtgg aactttctga attggatgag caagttgctc aggctttctt 180  
tgatttggag aacaccaatc aagaattgaa aagtgagctg aaggatttat acgtcaactc 240  
ggctgttcaa gttgatatct ctggaggacg caaggcaatt gttgtcaatg ttccttacag 300  
actgagaaaa gcttgaacag ccgagttgrc gtataaatcc ttcagstcac ttkctcaattc 360  
tytcatagtc ktatggctac taaattcatc accctcabc aaatccaccg ccctaaaacc 420  
ttactatcca ccacaaaatc tcgtcgacgc aataataaca aacccaaacc atccaaaacc 480  
ataagcgaac acatgttgaa caacgtcttt tctggcaaaa cgctaacaga aatctaccat 540  
aataagataa attcacaccc acttactaat ccactactgt ttcttgaaga tcagttcgta 600  
aaagaagagg agacgaatca acaagaacac gggaaggctc cgaacaaaga tggttaagtcc 660  
ataaccgcga ccaaatacgg agatttgagg cgtgatgttg ctcgattaag cttgttggtg 720  
tacatgaaat gttccataag ccatatatta aggaaggcaa gagcgtttta caatgagttt 780  
tggtgtgata cttatgctga gagtaacact atggctgtgg tagagccata tttttctatt 840  
ccggttaatta attaatacct ccaaatacgac gtaattaaaa attgtattta taattagtaa 900  
aatgtttcat tagttttgtt gtgttgtaat gtgatgtgct ctctatatat gtcatatatg 960  
tgtaaacaag acgtcaagtt atgtaattaa tggtatatga aaact

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met	Ala	Thr	Lys	Phe	Ile	Thr	Leu	Xaa	Gln	Ile	His	Arg	Pro	Lys	Thr
1				5					10					15	
Leu	Leu	Ser	Thr	Thr	Lys	Ser	Arg	Arg	Arg	Asn	Asn	Asn	Lys	Pro	Lys
			20					25					30		
Pro	Ser	Lys	Thr	Ile	Ser	Glu	Asn	Met	Leu	Asn	Asn	Val	Phe	Ser	Gly
		35					40					45			
Lys	Thr	Leu	Thr	Glu	Ile	Tyr	His	Asn	Lys	Ile	Asn	Ser	His	Pro	Leu
		50				55					60				
Thr	Asn	Pro	Leu	Leu	Phe	Leu	Glu	Asp	Gln	Phe	Val	Lys	Glu	Glu	Glu
65					70					75					80
Thr	Asn	Gln	Gln	Glu	His	Gly	Lys	Val	Ser	Asn	Lys	Asp	Gly	Lys	Ser
			85					90						95	
Ile	Thr	Ala	Thr	Lys	Tyr	Gly	Asp	Leu	Arg	Arg	Asp	Val	Ala	Arg	Leu
			100					105					110		
Ser	Leu	Leu	Trp	Tyr	Met	Lys	Cys	Ser	Ile	Ser	His	Ile	Leu	Arg	Lys
		115					120					125			
Ala	Arg	Ala	Phe	Tyr	Asn	Glu	Phe	Cys	Cys	Asp	Thr	Tyr	Ala	Glu	Ser
		130				135					140				
Asn	Thr	Met	Ala	Val	Val	Glu	Pro	Tyr	Phe	Ser	Ile	Pro	Val	Ile	Asn
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met	Leu	Asn	Asn	Val	Phe	Ser	Gly	Lys	Thr	Leu	Thr	Glu	Ile	Tyr	His
1				5					10					15	
Asn	Lys	Ile	Asn	Ser	His	Pro	Leu	Thr	Asn	Pro	Leu	Leu	Phe	Leu	Glu
			20					25					30		
Asp	Gln	Phe	Val	Lys	Glu	Glu	Glu	Thr	Asn	Gln	Gln	Glu	His	Gly	Lys
		35					40					45			
Val	Ser	Asn	Lys	Asp	Gly	Lys	Ser	Ile	Thr	Ala	Thr	Lys	Tyr	Gly	Asp
		50				55					60				
Leu	Arg	Arg	Asp	Val	Ala	Arg	Leu	Ser	Leu	Leu	Trp	Tyr	Met	Lys	Cys
65					70				75						80
Ser	Ile	Ser	His	Ile	Leu	Arg	Lys	Ala	Arg	Ala	Phe	Tyr	Asn	Glu	Phe
			85					90					95		
Cys	Cys	Asp	Thr	Tyr	Ala	Glu	Ser	Asn	Thr	Met	Ala	Val	Val	Glu	Pro
		100						105					110		
Tyr	Phe	Ser	Ile	Pro	Val	Ile	Asn								
		115					120								

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1802

(D) OTHER INFORMATION: / Ceres Seq. ID 1498459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

aaacttagcc	aaacgtcaca	aatccaaaac	ccaaaaccga	atcgtttttt	agcctccaag	60
agagagatct	acagatagag	aatgatagaa	ccgtcgatgg	agagagagaa	tggtgcttta	120
acggcggcga	caacaacgac	gacggcgggtg	acttctcctc	ctccgatggc	ttcttcaccg	180
cgtcaagctt	tagttgagag	attgaaagat	tatggacaag	aagatatattt	ctctcttttg	240
gatgaacttt	caccagacga	gaaagatttt	ctcgtagag	atattgagaa	tttgatctt	300
ccaagaatag	atcgatcat	tagatgttca	cttcactctc	aaggtttacc	ggttgcggcg	360
attgaaccgg	taccggagaa	ttgggtttcg	acagtagatg	gtagaacaat	ggaagataga	420
gagaaatggt	ggaaaatggg	attaaaaact	atctatgaag	gcaaattagg	tggtgtgctt	480
ttatctgggtg	gacaggggaa	aaggcttgga	agctcagatc	caaaaggatg	tttcaaatc	540
ggattaccat	caggggaaatc	gctctttcag	attcaagcag	agagaatctt	gtgtgttcaa	600
agacttgctg	ctcaagtagt	gagtgaaagt	ccaattcgtc	cagttacaaa	tacattggta	660
tattatgact	tagtccattt	actgatgaan	gcgacacgaa	aatatttctc	gangtcacaa	720
gtactttggt	cttgaaccag	atcaaatcag	ttttttccaa	caaggtactt	tgccctgcgt	780
tacaaaggat	ggaaagttaa	ttatggagac	acctttcagt	ctagctaaag	ctccagatgg	840
taacggcggga	gtctatgcag	cgctaaagtg	ttcaaggcta	ttagaggata	tggtctctag	900
ggggattaaa	tacgtcgatt	gctatggcgt	tgacaatgtc	ctgggtcgag	tagctgatcc	960
tacttttctt	ggatacttca	tcgataaagg	ggctgcttcg	gctgcaaaag	ttgtgcggaa	1020
ggcatatyc	cmagaacagg	taggagtggt	tgtagaaga	ggtaaaggag	gaccgttgac	1080
agtagttgag	tatagtgcag	ttgatcagtc	tatggcttct	gctattaatc	aacgaacagg	1140
acgtcttcaa	tattgctgga	gtaacgtgtg	cttacacatg	tttactttag	atttccttaa	1200
tcaagtcgct	accggcctag	aaaaagatag	cgtgtaccat	ttggcggaga	agaagatacc	1260
atctatgaat	ggatacacaa	tgggactaaa	actagaacaa	ttcatttttg	attcgtttcc	1320
ttatgctcct	tcaaccgcac	tttttgaggt	tttaagggaa	gaggagtttg	caccagtga	1380
gaatgttaac	gggtcgatt	tcgatacacc	ggaaagtgcg	aggcttttgg	ttctaagggt	1440
acacacacgt	tgggttatag	cagctggtgg	atttctaaca	cattctgtgc	ctttatatgc	1500
tactggtgta	gagggtttcac	ctttgtgctc	atagcccgga	gaaaatcttg	aagctatttg	1560
tcgaggaaga	acgtttcatg	caccttggtg	aatttccttc	taatgggttt	tggtgttttg	1620
ttttgggggt	ttaaaatctt	ttcttcattt	ttatgtgatt	tgttttcttt	gtttccggtt	1680
gtgggtttata	tatataaact	gattatcttc	ccatgagaga	gagaaagaga	gagtcaaaga	1740
gggtcttggcg	ttttgtatcc	attaatgtaa	catatcta	aaaaatttta	tggtggtttt	1800

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1498460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met	Ile	Glu	Pro	Ser	Met	Glu	Arg	Glu	Asn	Gly	Ala	Leu	Thr	Ala	Ala
1				5				10						15	
Thr	Thr	Thr	Thr	Thr	Ala	Val	Thr	Ser	Pro	Pro	Pro	Met	Ala	Ser	Ser
				20				25					30		
Pro	Arg	Gln	Ala	Leu	Val	Glu	Arg	Leu	Lys	Asp	Tyr	Gly	Gln	Glu	Asp
		35					40					45			
Ile	Phe	Ser	Leu	Trp	Asp	Glu	Leu	Ser	Pro	Asp	Glu	Lys	Asp	Phe	Leu
	50					55				60					
Val	Arg	Asp	Ile	Glu	Asn	Leu	Asp	Leu	Pro	Arg	Ile	Asp	Arg	Ile	Ile
65				70						75				80	
Arg	Cys	Ser	Leu	His	Ser	Gln	Gly	Leu	Pro	Val	Ala	Ala	Ile	Glu	Pro
				85				90						95	
Val	Pro	Glu	Asn	Trp	Val	Ser	Thr	Val	Asp	Gly	Arg	Thr	Met	Glu	Asp
			100					105					110		
Arg	Glu	Lys	Trp	Trp	Lys	Met	Gly	Leu	Lys	Thr	Ile	Tyr	Glu	Gly	Lys
			115				120						125		

Leu Gly Val Val Leu Leu Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser  
130 135 140  
Ser Asp Pro Lys Gly Cys Phe Asn Ile Gly Leu Pro Ser Gly Lys Ser  
145 150 155 160  
Leu Phe Gln Ile Gln Ala Glu Arg Ile Leu Cys Val Gln Arg Leu Ala  
165 170 175  
Ala Gln Val Val Ser Glu Gly Pro Ile Arg Pro Val Thr Asn Thr Leu  
180 185 190  
Val Tyr Tyr Asp Leu Val His Leu Leu Met Xaa Ala Thr Arg Lys Tyr  
195 200 205  
Phe Ser Xaa Ser Gln Val Leu Trp Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Glu Thr Pro Phe Ser Leu Ala Lys Ala Pro Asp Gly Asn Gly Gly  
1 5 10 15  
Val Tyr Ala Ala Leu Lys Cys Ser Arg Leu Leu Glu Asp Met Ala Ser  
20 25 30  
Arg Gly Ile Lys Tyr Val Asp Cys Tyr Gly Val Asp Asn Val Leu Val  
35 40 45  
Arg Val Ala Asp Pro Thr Phe Leu Gly Tyr Phe Ile Asp Lys Gly Ala  
50 55 60  
Ala Ser Ala Ala Lys Val Val Arg Lys Ala Tyr Xaa Xaa Glu Gln Val  
65 70 75 80  
Gly Val Xaa Val Arg Arg Gly Lys Gly Gly Pro Leu Thr Val Val Glu  
85 90 95  
Tyr Ser Glu Leu Asp Gln Ser Met Ala Ser Ala Ile Asn Gln Arg Thr  
100 105 110  
Gly Arg Leu Gln Tyr Cys Trp Ser Asn Val Cys Leu His Met Phe Thr  
115 120 125  
Leu Asp Phe Leu Asn Gln Val Ala Thr Gly Leu Glu Lys Asp Ser Val  
130 135 140  
Tyr His Leu Ala Glu Lys Lys Ile Pro Ser Met Asn Gly Tyr Thr Met  
145 150 155 160  
Gly Leu Lys Leu Glu Gln Phe Ile Phe Asp Ser Phe Pro Tyr Ala Pro  
165 170 175  
Ser Thr Ala Leu Phe Glu Val Leu Arg Glu Glu Glu Phe Ala Pro Val  
180 185 190  
Lys Asn Val Asn Gly Ser Asn Phe Asp Thr Pro Glu Ser Ala Arg Leu  
195 200 205  
Leu Val Leu Arg Leu His Thr Arg Trp Val Ile Ala Ala Gly Gly Phe  
210 215 220  
Leu Thr His Ser Val Pro Leu Tyr Ala Thr Gly Val Glu Val Ser Pro  
225 230 235 240  
Leu Cys Ser Tyr Ala Gly Glu Asn Leu Glu Ala Ile Cys Arg Gly Arg  
245 250 255  
Thr Phe His Ala Pro Cys Glu Ile Ser Leu  
260 265

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..237
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met	Ala	Ser	Arg	Gly	Ile	Lys	Tyr	Val	Asp	Cys	Tyr	Gly	Val	Asp	Asn
1				5					10					15	
Val	Leu	Val	Arg	Val	Ala	Asp	Pro	Thr	Phe	Leu	Gly	Tyr	Phe	Ile	Asp
			20					25					30		
Lys	Gly	Ala	Ala	Ser	Ala	Ala	Lys	Val	Val	Arg	Lys	Ala	Tyr	Xaa	Xaa
		35					40					45			
Glu	Gln	Val	Gly	Val	Xaa	Val	Arg	Arg	Gly	Lys	Gly	Gly	Pro	Leu	Thr
	50					55					60				
Val	Val	Glu	Tyr	Ser	Glu	Leu	Asp	Gln	Ser	Met	Ala	Ser	Ala	Ile	Asn
65					70					75				80	
Gln	Arg	Thr	Gly	Arg	Leu	Gln	Tyr	Cys	Trp	Ser	Asn	Val	Cys	Leu	His
			85						90				95		
Met	Phe	Thr	Leu	Asp	Phe	Leu	Asn	Gln	Val	Ala	Thr	Gly	Leu	Glu	Lys
			100					105					110		
Asp	Ser	Val	Tyr	His	Leu	Ala	Glu	Lys	Lys	Ile	Pro	Ser	Met	Asn	Gly
		115					120					125			
Tyr	Thr	Met	Gly	Leu	Lys	Leu	Glu	Gln	Phe	Ile	Phe	Asp	Ser	Phe	Pro
	130					135					140				
Tyr	Ala	Pro	Ser	Thr	Ala	Leu	Phe	Glu	Val	Leu	Arg	Glu	Glu	Glu	Phe
145					150					155				160	
Ala	Pro	Val	Lys	Asn	Val	Asn	Gly	Ser	Asn	Phe	Asp	Thr	Pro	Glu	Ser
			165						170					175	
Ala	Arg	Leu	Leu	Val	Leu	Arg	Leu	His	Thr	Arg	Trp	Val	Ile	Ala	Ala
		180						185					190		
Gly	Gly	Phe	Leu	Thr	His	Ser	Val	Pro	Leu	Tyr	Ala	Thr	Gly	Val	Glu
		195					200					205			
Val	Ser	Pro	Leu	Cys	Ser	Tyr	Ala	Gly	Glu	Asn	Leu	Glu	Ala	Ile	Cys
	210					215					220				
Arg	Gly	Arg	Thr	Phe	His	Ala	Pro	Cys	Glu	Ile	Ser	Leu			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

ctaacttctc	tgttcatctt	tttctctctt	tatttataaa	tttatctgca	tagtactctc	60
tgaatctata	tcttcaaaaa	aaaaaaacgt	ccaagatcaa	atcaagaaac	ccattaaaaa	120
aaaaaatcag	gttttggttt	cagttttaag	ggtttaaggt	ttcttgaggga	agaaacgatg	180
gagacttttt	gtgggtttca	aaaggaggaa	gagcagatgg	atttacctcc	tgggttcagg	240
tttcatccaa	cagatgaaga	actcataaac	tcactatctc	cataagaagg	ttcttgacac	300
cagctttctca	gctaaagcta	tcggtgaagt	tgattttaa	aaatcagagc	catgggagtt	360
accatggatg	gcaaaaatgg	gtgagaaaga	atgggtat	ttctgtgtga	gagacagaaa	420
gtatcccacc	ggtttaagaa	ctaaccgagc	aactgaagcc	ggttattgga	aggcgaccgg	480
gaaggataaa	gagatatacc	gaggcaaata	acttggtggg	atgaagaaga	cacttgtttt	540
ctatagagga	agagctccta	aaggtcagaa	aaccaactgg	gtgatgcatg	agtacaggct	600

tgaaaaaaat	tctctgccc	taacttgccg	aaaaccgcaa	agaatgaatg	ggtgatatgc	660
agggtgttcc	aaaagagtgc	tggagggaag	aagatcccga	tttcgagtc	aatccgaatc	720
ggttcactcg	gaaccgactt	taacccttcg	cttttgccct	ctttaaccga	ttcttcgcct	780
tacaacgata	aaacccaaaac	agaaccggtc	tacgtgccct	gcttctccaa	ccaaacggat	840
caaaaccaag	gaaccacact	caattgcttc	agcagccctg	ttcttaactc	gatccaagcc	900
gacatttttc	acaggattcc	actctatcaa	actcagtccc	tccaggtttc	tatgaatcta	960
cagagcccgg	ttctcacgca	agaacactca	gttctacatg	ctatgatcga	gaacaacaga	1020
agacaaagtc	tcaaaacgat	gagtgtctca	caagaaaccg	gagtttcaac	tgacatgaac	1080
actgatatct	catcggattt	tgaatttgg	aagaggcggt	ttgattctca	agaagatccg	1140
tcttcctcta	ctggaccgg	tgatcttgaa	cctttctgga	attactgaag	atgattcaag	1200
attctcatgt	ccattaattt	actgtgggtg	gttaaagttt	gtataggcta	ttgtcatata	1260
ctctcatatc	aacttcact	atatattata	acaatttaaa	gaaacttaaa	aatatgattt	1320
gatatatgac	taaagtatta	taatacaatt	ttgtacccc			

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met	Ala	Lys	Met	Gly	Glu	Lys	Glu	Trp	Tyr	Phe	Phe	Cys	Val	Arg	Asp
1				5					10					15	
Arg	Lys	Tyr	Pro	Thr	Gly	Leu	Arg	Thr	Asn	Arg	Ala	Thr	Glu	Ala	Gly
			20					25					30		
Tyr	Trp	Lys	Ala	Thr	Gly	Lys	Asp	Lys	Glu	Ile	Tyr	Arg	Gly	Lys	Ser
		35					40					45			
Leu	Val	Gly	Met	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Arg	Gly	Arg	Ala	Pro
	50					55				60					
Lys	Gly	Gln	Lys	Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Glu	Lys
65					70					75				80	
Asn	Ser	Leu	Pro	Ile	Thr	Cys	Arg	Lys	Pro	Gln	Arg	Met	Asn	Gly	
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met	Gly	Glu	Lys	Glu	Trp	Tyr	Phe	Phe	Cys	Val	Arg	Asp	Arg	Lys	Tyr
1				5					10					15	
Pro	Thr	Gly	Leu	Arg	Thr	Asn	Arg	Ala	Thr	Glu	Ala	Gly	Tyr	Trp	Lys
			20					25					30		
Ala	Thr	Gly	Lys	Asp	Lys	Glu	Ile	Tyr	Arg	Gly	Lys	Ser	Leu	Val	Gly
		35					40					45			
Met	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Arg	Gly	Arg	Ala	Pro	Lys	Gly	Gln
	50					55				60					
Lys	Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Glu	Lys	Asn	Ser	Leu
65					70					75				80	
Pro	Ile	Thr	Cys	Arg	Lys	Pro	Gln	Arg	Met	Asn	Gly				
			85						90						

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

```
Met Asn Leu Gln Ser Pro Val Leu Thr Gln Glu His Ser Val Leu His
1           5           10           15
Ala Met Ile Glu Asn Asn Arg Arg Gln Ser Leu Lys Thr Met Ser Val
20           25           30
Ser Gln Glu Thr Gly Val Ser Thr Asp Met Asn Thr Asp Ile Ser Ser
35           40           45
Asp Phe Glu Phe Gly Lys Arg Arg Phe Asp Ser Gln Glu Asp Pro Ser
50           55           60
Ser Ser Thr Gly Pro Val Asp Leu Glu Pro Phe Trp Asn Tyr
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1879
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

```
acttctctct ctctctctct ctcttttctc aaatcttggg ggagaagaag caaagaatta 60
gactactctg caacaatggc tattttattct gtccataacg ggcacaagaa gcattgggtgg 120
ttcactcaca agaagattgt tgataagtac attaaggacg caagatcttt aatggagagt 180
gaggagcaaa acgacgttgc ttcagccatt catttactag acgcggtctt atcaatatcc 240
ccgcgttcgg aaactgcgtt agaacttaaa gccagatctt tgctctttct acgtcgcttc 300
aaagatgtag ttgatatgct tcaagattat atcccaagcc tcaagcttgc cgtgaacgag 360
gaagatggat cttattcata cgaagggttct tcttactctt cctcctcttc tcagctctcc 420
cggaaacttc tctctgactc atctcctcgc cgtgactcat ccttcaagtg cttctctggt 480
tcttacctga aaaagaaaat tatggctggg atttgtaaaa atcgcgatca agataaacia 540
tgagatacag ttgttttagg acaagcttgt tgccacctag gattaatgga ggacgcattg 600
gttcttcttt aaaccggaaa acgtctcgca acagtcgagt tccgcgctct aagtgtgaagc 660
ttgtcagatg atagcgtctc actcctcctc tctgaatcgt catcatcatc atcctcatcc 720
tcttatgctt ttcctccacg caaagtctcc gaatgcgaaa ccgtcactaa ccttctcgcc 780
cacacgaaaa atctcctccg gcgtcgctcc gccggattcg ccgcctttga cgttggaactt 840
ttcgccgact cgatacgtca cttctccaaa attctcgacg gtctgtctcg tcccgcgcca 900
caaggattcc tcgctgattg ctatatgcac cgcgccgccc cttacaaatc cgccgggaaa 960
atcgcggaag cgatcgccga ttgtaataaa acctagctc ttgagccgtc gtgtatccat 1020
gcgttgagga ctagagccac tcttttgga acggttcggt gtctaccgga ttcgcttcac 1080
gatttagagc atttgaagat actctacaac actatcttac gtgatcgga acttcccgga 1140
ccaccgtgga aacgacacaa tgtgaaatac agagagatac cgggaaaagt atgcgaactg 1200
acgacgaaat cgaagaaact gaaagcaaaa atggcgaatg gagaatcgg aaacgttgat 1260
tattacggat tggctcgagt tagacgcggt tgcacgagat cggagcttga tcgagcaaat 1320
ctcttgctct gtctcaggca taaaccggac aaggctttag cattcatgga acgttgcgat 1380
ttcttcgata agagttagat tagttccgtt aaagatcgag cgaagatgtc ttctttgttg 1440
ctttaccgat tgattcagag aggttatata gctttggcgg cagcgatagc tgaggaggaa 1500
cagaggaaga agatgatggt gttgactcaa atgtcaacga aaacggttga agaacaatgaa 1560
ccggttgaaa aatccggttc aattacttta accgattttg cagaaattaa gccgggggaat 1620
```

```
tcgaacgcgt accaaggagt tttctgccga ggtcttgctg ctggtgggag tttgttatct 1680
aggaccggat ttaaccaacc gataccaatg aaatacgaatg cgatcagttg ttaaccggga 1740
atcttagttt gtatataatt aagaattttt tgtcacttta aaatattcgt ctcttttgag 1800
ttaattctcc tactttctct ttatttctgt gcagaaaatg ctttacttgt cgaatatcaa 1860
atcaaagtag tgtgagatt
```

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```
Thr Ser Leu Ser Leu Ser Leu Ser Phe Leu Lys Ser Trp Arg Arg Arg
1          5          10          15
Ser Lys Glu Leu Asp Tyr Ser Ala Thr Met Ala Ile Tyr Ser Val His
20          25          30
Asn Gly Asp Lys Lys His Trp Trp Phe Thr His Lys Lys Ile Val Asp
35          40          45
Lys Tyr Ile Lys Asp Ala Arg Ser Leu Met Glu Ser Glu Glu Gln Asn
50          55          60
Asp Val Ala Ser Ala Ile His Leu Leu Asp Ala Ala Leu Ser Ile Ser
65          70          75          80
Pro Arg Ser Glu Thr Ala Leu Glu Leu Lys Ala Arg Ser Leu Leu Phe
85          90          95
Leu Arg Arg Phe Lys Asp Val Val Asp Met Leu Gln Asp Tyr Ile Pro
100          105          110
Ser Leu Lys Leu Ala Val Asn Glu Glu Asp Gly Ser Tyr Ser Tyr Glu
115          120          125
Gly Ser Ser Tyr Ser Ser Ser Ser Ser Gln Leu Ser Arg Lys Leu Leu
130          135          140
Ser Asp Ser Ser Pro Arg Arg Asp Ser Ser Phe Lys Cys Phe Ser Val
145          150          155          160
Ser Tyr Leu Lys Lys Lys Ile Met Ala Gly Ile Cys Lys Asn Arg Asp
165          170          175
Gln Asp Lys Gln Trp Arg Tyr Val Val Leu Gly Gln Ala Cys Cys His
180          185          190
Leu Gly Leu Met Glu Asp Ala Leu Val Leu Leu
195          200
```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```
Met Ala Ile Tyr Ser Val His Asn Gly Asp Lys Lys His Trp Trp Phe
1          5          10          15
Thr His Lys Lys Ile Val Asp Lys Tyr Ile Lys Asp Ala Arg Ser Leu
20          25          30
Met Glu Ser Glu Glu Gln Asn Asp Val Ala Ser Ala Ile His Leu Leu
35          40          45
```

Asp Ala Ala Leu Ser Ile Ser Pro Arg Ser Glu Thr Ala Leu Glu Leu  
50 55 60  
Lys Ala Arg Ser Leu Leu Phe Leu Arg Arg Phe Lys Asp Val Val Asp  
65 70 75 80  
Met Leu Gln Asp Tyr Ile Pro Ser Leu Lys Leu Ala Val Asn Glu Glu  
85 90 95  
Asp Gly Ser Tyr Ser Tyr Glu Gly Ser Ser Tyr Ser Ser Ser Ser Ser  
100 105 110  
Gln Leu Ser Arg Lys Leu Leu Ser Asp Ser Ser Pro Arg Arg Asp Ser  
115 120 125  
Ser Phe Lys Cys Phe Ser Val Ser Tyr Leu Lys Lys Lys Ile Met Ala  
130 135 140  
Gly Ile Cys Lys Asn Arg Asp Gln Asp Lys Gln Trp Arg Tyr Val Val  
145 150 155 160  
Leu Gly Gln Ala Cys Cys His Leu Gly Leu Met Glu Asp Ala Leu Val  
165 170 175  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1498478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met His Arg Ala Ala Tyr Lys Ser Ala Gly Lys Ile Ala Glu Ala  
1 5 10 15  
Ile Ala Asp Cys Asn Lys Thr Leu Ala Leu Glu Pro Ser Cys Ile His  
20 25 30  
Ala Leu Glu Thr Arg Ala Thr Leu Leu Glu Thr Val Arg Cys Leu Pro  
35 40 45  
Asp Ser Leu His Asp Leu Glu His Leu Lys Ile Leu Tyr Asn Thr Ile  
50 55 60  
Leu Arg Asp Arg Lys Leu Pro Gly Pro Pro Trp Lys Arg His Asn Val  
65 70 75 80  
Lys Tyr Arg Glu Ile Pro Gly Lys Leu Cys Glu Leu Thr Thr Lys Ser  
85 90 95  
Lys Lys Leu Lys Ala Lys Met Ala Asn Gly Glu Ile Gly Asn Val Asp  
100 105 110  
Tyr Tyr Gly Leu Val Gly Val Arg Arg Gly Cys Thr Arg Ser Glu Leu  
115 120 125  
Asp Arg Ala Asn Leu Leu Leu Cys Leu Arg His Lys Pro Asp Lys Ala  
130 135 140  
Leu Ala Phe Met Glu Arg Cys Asp Phe Phe Asp Gln Ser Glu Ile Ser  
145 150 155 160  
Ser Val Lys Asp Arg Ala Lys Met Ser Ser Leu Leu Leu Tyr Arg Leu  
165 170 175  
Ile Gln Arg Gly Tyr Thr Ala Leu Ala Ala Ala Ile Ala Glu Glu Glu  
180 185 190  
Gln Arg Lys Lys Met Met Val Leu Thr Gln Met Ser Thr Lys Thr Val  
195 200 205  
Glu Glu His Glu Pro Val Glu Lys Ser Gly Ser Ile Thr Leu Thr Asp  
210 215 220  
Phe Ala Glu Ile Lys Pro Gly Asn Ser Asn Ala Tyr Gln Gly Val Phe  
225 230 235 240  
Cys Arg Gly Leu Ala Ala Val Gly Ser Leu Leu Ser Arg Thr Gly Phe

245 250 255  
Asn Gln Pro Ile Pro Met Lys Tyr Asp Ala Ile Ser Cys  
260 265

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1751
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```
aatctctctc cctctctatc tctctcttac aaaattccat ttcacgggga aaataataat 60
acgacttttg aaatctctcg ctaatatctt ccaagaaaac ctgatgaatt aaaagttcat 120
atcttcttgg tgttggttgg tattagatga ctatttcttg gtattagtca attctctgtt 180
tccatcttat atggatagtc tagacacaga gcaaagatcc ttctttggag aaaaagaaga 240
tgagagacga gagaggatcg tttcttcacg tattggtcgt agatagatct taatcgataa 300
ccatctaggc cttgatctaa ccattcaata taaactttat ttccttcttc ttttcgatct 360
caattgttcc gaccaaacaa gatgaagaga tcacgtggaa gctccgattc tttatccggt 420
ttcttaccac ttgcgcattc tacaacagac aaacaaataa gcccaagacc aacaactacc 480
ggctttctct attccggcgc cggagactac tcccagatgt ttgacgcatt agaagacgac 540
ggaagtctag aggacctcgg cggcggttga caccgctctt ctacggcggc ggagaaaaaa 600
cggcggttgg gtgtagagca agtgaaagcg ttagagaaga atttcgagat tgataacaag 660
ttagagccag agaggaaagt gaagctggct caagagcttg ggttgacgcc acgccaagtc 720
gcgatctggt ttcaaaaccg ccgtgctcgg tggaaaacaa agcagcttga acgtgattac 780
ggcgttctta agtcaaactt tgatgcactc aaacgcaacc gcgactcgct tcaacgcgat 840
aacgattcac tccttggaac gattaaagag ctgaaagcaa aacttaacgt ggaagggttt 900
aaaggtatag aagagaacgg cgctttaaaa gtagtggaag caaatcagac ggtgatggct 960
aataatgaag tcttagagct aagccaccgt tctccatcgc caccaccgca tattcctacg 1020
gaagctccga catcgagct cgcattcgaa atgttttagc tttttccacg cacggaaaac 1080
ttcagagaag atcctgccga tagcagcgac tcaagcgagg ttttgaacga agagtatagt 1140
cccaatacgg ttgaagcagc gggcgagtg gcgccacga ctgtagaaat gtcgacgatg 1200
gattgtttta gccaatcgt gaaaatggaa gagcatgaag atctgtttag tggagaggaa 1260
gcttgcaagt tgtttgcgga caatgagcaa tggattgct ccgatcagtg gaattcgtaa 1320
aatgtggggg cagaaataaa aacatagaaa agtcgaaggg gatatgtgga aatattactg 1380
aagtcattat gggtcgaaa atgcattact caaaatatta ggggttttgt tgagaaaatg 1440
gaatatgacg cgagagggtg gtaaaaacga gcgtgtggtg ttccatgcac gtgtggccgt 1500
aatcttttca aggttgaaat agagaggaca acaatgtctg aaatcatcgg gaataaaaaa 1560
aatatgtgac gaagaaatcg ttttttcgtc gtttataata ttatttgaat aattttactt 1620
aggtgaatgt aatcgtcaaa aatctttaaa ttccgaaggg ttaaagattc tgagcacgac 1680
tatctatcta tcctctttta ttgttctcgt cgtccattga cgactatgca caattcataa 1740
gattattccc t
```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```
Met Lys Arg Ser Arg Gly Ser Ser Asp Ser Leu Ser Gly Phe Leu Pro
1 5 10 15
Ile Arg His Ser Thr Thr Asp Lys Gln Ile Ser Pro Arg Pro Thr Thr
20 25 30
```

Thr Gly Phe Leu Tyr Ser Gly Ala Gly Asp Tyr Ser Gln Met Phe Asp  
35 40 45  
Ala Leu Glu Asp Asp Gly Ser Leu Glu Asp Leu Gly Gly Val Gly His  
50 55 60  
Ala Ser Ser Thr Ala Ala Glu Lys Lys Arg Arg Leu Gly Val Glu Gln  
65 70 75 80  
Val Lys Ala Leu Glu Lys Asn Phe Glu Ile Asp Asn Lys Leu Glu Pro  
85 90 95  
Glu Arg Lys Val Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln  
100 105 110  
Val Ala Ile Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln  
115 120 125  
Leu Glu Arg Asp Tyr Gly Val Leu Lys Ser Asn Phe Asp Ala Leu Lys  
130 135 140  
Arg Asn Arg Asp Ser Leu Gln Arg Asp Asn Asp Ser Leu Leu Gly Gln  
145 150 155 160  
Ile Lys Glu Leu Lys Ala Lys Leu Asn Val Glu Gly Phe Lys Gly Ile  
165 170 175  
Glu Glu Asn Gly Ala Leu Lys Val Val Glu Ala Asn Gln Thr Val Met  
180 185 190  
Ala Asn Asn Glu Val Leu Glu Leu Ser His Arg Ser Pro Ser Pro Pro  
195 200 205  
Pro His Ile Pro Thr Glu Ala Pro Thr Ser Glu Leu Ala Phe Glu Met  
210 215 220  
Phe Ser Ile Phe Pro Arg Thr Glu Asn Phe Arg Glu Asp Pro Ala Asp  
225 230 235 240  
Ser Ser Asp Ser Ser Ala Val Leu Asn Glu Glu Tyr Ser Pro Asn Thr  
245 250 255  
Val Glu Ala Ala Gly Ala Val Ala Ala Thr Thr Val Glu Met Ser Thr  
260 265 270  
Met Asp Cys Phe Ser Gln Phe Val Lys Met Glu Glu His Glu Asp Leu  
275 280 285  
Phe Ser Gly Glu Glu Ala Cys Lys Leu Phe Ala Asp Asn Glu Gln Trp  
290 295 300  
Tyr Cys Ser Asp Gln Trp Asn Ser  
305 310

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1498489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Phe Asp Ala Leu Glu Asp Asp Gly Ser Leu Glu Asp Leu Gly Gly  
1 5 10 15  
Val Gly His Ala Ser Ser Thr Ala Ala Glu Lys Lys Arg Arg Leu Gly  
20 25 30  
Val Glu Gln Val Lys Ala Leu Glu Lys Asn Phe Glu Ile Asp Asn Lys  
35 40 45  
Leu Glu Pro Glu Arg Lys Val Lys Leu Ala Gln Glu Leu Gly Leu Gln  
50 55 60  
Pro Arg Gln Val Ala Ile Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys  
65 70 75 80  
Thr Lys Gln Leu Glu Arg Asp Tyr Gly Val Leu Lys Ser Asn Phe Asp  
85 90 95  
Ala Leu Lys Arg Asn Arg Asp Ser Leu Gln Arg Asp Asn Asp Ser Leu

100	105	110
Leu Gly Gln Ile Lys Glu Leu Lys Ala Lys Leu Asn Val Glu Gly Phe		
115	120	125
Lys Gly Ile Glu Glu Asn Gly Ala Leu Lys Val Val Glu Ala Asn Gln		
130	135	140
Thr Val Met Ala Asn Asn Glu Val Leu Glu Leu Ser His Arg Ser Pro		
145	150	155
Ser Pro Pro Pro His Ile Pro Thr Glu Ala Pro Thr Ser Glu Leu Ala		
165	170	175
Phe Glu Met Phe Ser Ile Phe Pro Arg Thr Glu Asn Phe Arg Glu Asp		
180	185	190
Pro Ala Asp Ser Ser Asp Ser Ser Ala Val Leu Asn Glu Glu Tyr Ser		
195	200	205
Pro Asn Thr Val Glu Ala Ala Gly Ala Val Ala Ala Thr Thr Val Glu		
210	215	220
Met Ser Thr Met Asp Cys Phe Ser Gln Phe Val Lys Met Glu Glu His		
225	230	235
Glu Asp Leu Phe Ser Gly Glu Glu Ala Cys Lys Leu Phe Ala Asp Asn		
245	250	255
Glu Gln Trp Tyr Cys Ser Asp Gln Trp Asn Ser		
260	265	

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

atttttcttg agagatccaa aaaaagtatc agaaagaaga agaagacgac tccaaaaawc	60
gatgccgtat tacaccaacg acgacaatga cgtcgacgat ttcaccgaat acgatccgat	120
gccttatagt ggaggtacg acatcacggt gacatacggc cggtcaattc caccgtccga	180
cgagacttgt taccctctct cctctctctc cggcgacgcc tttagtatc agcgacctaa	240
tttctcttct aacaacgatt cttctgctta tgacgaccaa gctcttaaaa ccgagtacag	300
tagctatgca cgaccggac ccgttggatc tggatctgat ttggccgga aacctaatc	360
tggatatgga gggagaacgg aggttgagta tggccggaaa actgaatcg agcatggatc	420
tggctatggt gggagaattg agagcgatta cgtgaagcct agctatggcg gtcacgagga	480
tgatggtgac gatggtcaca aaaaacatag tggtaaggat tatgatgat gagatgagaa	540
gagtaagaag aaggagaagg agaagaagaa ggataagaag aaagatggta ataactctga	600
agatgatgag tttaagaaga agaagaagaa atagcagtac aaggagcatc atgatgatga	660
tgattatgat gagaagaaga agaagaagaa agactataat gatgatgatg agaagaagaa	720
gaagaagcat tataatgatg atgatgatga gaagaagaag aagcattaca atgatgatga	780
tgatgagaag aagaagaaga aggagtatca tgatgatgag gataagaaga agaagaagca	840
ctatgataat gatgatgatg agaagaagaa gaagaaggat catcgtgatg atgatgatga	900
gaagaagaag aagaaggata accaccacaa gggacatgac taaaaaagggt ttatgatttg	960
ggatttgcat tcttatgact aaataagtaa caacaactta agcacacttc tgctctctac	1020
gtttatgtca attgtgttt tggttttgct tctgtgtttt gctgctaact tcaatgagat	1080
cttcataagt catatgtaat atgttttagtg tacgtgtttt ctagtgatgt cgtttggctt	1140

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: peptide  
(B) LOCATION: 1..210  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```
Phe Phe Leu Arg Asp Pro Lys Lys Val Ser Glu Arg Arg Arg Arg Arg
1          5          10          15
Leu Gln Lys Xaa Met Pro Tyr Tyr Thr Asn Asp Asp Asn Asp Val Asp
20          25          30
Asp Phe Thr Glu Tyr Asp Pro Met Pro Tyr Ser Gly Gly Tyr Asp Ile
35          40          45
Thr Val Thr Tyr Gly Arg Ser Ile Pro Pro Ser Asp Glu Thr Cys Tyr
50          55          60
Pro Leu Ser Ser Leu Ser Gly Asp Ala Phe Glu Tyr Gln Arg Pro Asn
65          70          75          80
Phe Ser Ser Asn Asn Asp Ser Ser Ala Tyr Asp Asp Gln Ala Leu Lys
85          90          95
Thr Glu Tyr Ser Ser Tyr Ala Arg Pro Gly Pro Val Gly Ser Gly Ser
100         105         110
Asp Phe Gly Arg Lys Pro Asn Ser Gly Tyr Gly Gly Arg Thr Glu Val
115         120         125
Glu Tyr Gly Arg Lys Thr Glu Ser Glu His Gly Ser Gly Tyr Gly Gly
130         135         140
Arg Ile Glu Ser Asp Tyr Val Lys Pro Ser Tyr Gly Gly His Glu Asp
145         150         155         160
Asp Gly Asp Asp Gly His Lys Lys His Ser Gly Lys Asp Tyr Asp Asp
165         170         175
Gly Asp Glu Lys Ser Lys Lys Lys Glu Lys Glu Lys Lys Lys Asp Lys
180         185         190
Lys Lys Asp Gly Asn Asn Ser Glu Asp Asp Glu Phe Lys Lys Lys Lys
195         200         205
Lys Lys
210
```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..190  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```
Met Pro Tyr Tyr Thr Asn Asp Asp Asn Asp Val Asp Asp Phe Thr Glu
1          5          10          15
Tyr Asp Pro Met Pro Tyr Ser Gly Gly Tyr Asp Ile Thr Val Thr Tyr
20          25          30
Gly Arg Ser Ile Pro Pro Ser Asp Glu Thr Cys Tyr Pro Leu Ser Ser
35          40          45
Leu Ser Gly Asp Ala Phe Glu Tyr Gln Arg Pro Asn Phe Ser Ser Asn
50          55          60
Asn Asp Ser Ser Ala Tyr Asp Asp Gln Ala Leu Lys Thr Glu Tyr Ser
65          70          75          80
Ser Tyr Ala Arg Pro Gly Pro Val Gly Ser Gly Ser Asp Phe Gly Arg
85          90          95
Lys Pro Asn Ser Gly Tyr Gly Gly Arg Thr Glu Val Glu Tyr Gly Arg
100         105         110
Lys Thr Glu Ser Glu His Gly Ser Gly Tyr Gly Gly Arg Ile Glu Ser
115         120         125
Asp Tyr Val Lys Pro Ser Tyr Gly Gly His Glu Asp Asp Gly Asp Asp
```

130	135	140
Gly His Lys Lys His Ser Gly Lys Asp Tyr Asp Asp Gly Asp Glu Lys		
145	150	155
Ser Lys Lys Lys Glu Lys Glu Lys Lys Lys Asp Lys Lys Lys Asp Gly		
	165	170
Asn Asn Ser Glu Asp Asp Glu Phe Lys Lys Lys Lys Lys Lys		
	180	185
		190

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1498496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met	Pro	Tyr	Ser	Gly	Gly	Tyr	Asp	Ile	Thr	Val	Thr	Tyr	Gly	Arg	Ser
1			5					10						15	
Ile	Pro	Pro	Ser	Asp	Glu	Thr	Cys	Tyr	Pro	Leu	Ser	Ser	Leu	Ser	Gly
			20					25					30		
Asp	Ala	Phe	Glu	Tyr	Gln	Arg	Pro	Asn	Phe	Ser	Ser	Asn	Asn	Asp	Ser
		35					40					45			
Ser	Ala	Tyr	Asp	Asp	Gln	Ala	Leu	Lys	Thr	Glu	Tyr	Ser	Ser	Tyr	Ala
		50				55				60					
Arg	Pro	Gly	Pro	Val	Gly	Ser	Gly	Ser	Asp	Phe	Gly	Arg	Lys	Pro	Asn
65					70					75					80
Ser	Gly	Tyr	Gly	Gly	Arg	Thr	Glu	Val	Glu	Tyr	Gly	Arg	Lys	Thr	Glu
			85					90						95	
Ser	Glu	His	Gly	Ser	Gly	Tyr	Gly	Gly	Arg	Ile	Glu	Ser	Asp	Tyr	Val
			100					105					110		
Lys	Pro	Ser	Tyr	Gly	Gly	His	Glu	Asp	Asp	Gly	Asp	Asp	Gly	His	Lys
		115					120						125		
Lys	His	Ser	Gly	Lys	Asp	Tyr	Asp	Asp	Gly	Asp	Glu	Lys	Ser	Lys	Lys
		130					135				140				
Lys	Glu	Lys	Glu	Lys	Lys	Lys	Asp	Lys	Lys	Lys	Asp	Gly	Asn	Asn	Ser
145					150					155					160
Glu	Asp	Asp	Glu	Phe	Lys	Lys	Lys	Lys	Lys	Lys					
					165					170					

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1332

(D) OTHER INFORMATION: / Ceres Seq. ID 1498497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

gatacatctc	ctcgctcgccg	ttcttcggat	tttcaactctt	ctgctcgaaa	ggtctctcac	60
tcttctcttt	tttaattctat	tgaattgaa	acttcccttc	tcttctcttc	tcttctctgt	120
agcactcctg	cttctagttt	agctgctctt	cttcttctac	ttgctgcaac	aactccaaat	180
catcatttct	cttggtccag	gcagtgttg	agaatcattg	aagaaggtag	tcgctggtgc	240
tgttttgata	actcaaagcc	gttttgctga	aagagggtta	ccaaagttag	aagctcaaga	300
acttgagact	gtgtcttctt	tttgtatcat	gccatatttt	attcagaggc	ttttcaatac	360
ttgcaagtca	tctctctcac	ctaattggcc	tgtgtctgag	gaggccttag	acaagggtcg	420
caatgtcttg	gagaaaatca	agccgtctga	tgttggtctc	gaacaggaag	ctcaattggt	480

```
gcgtaattgg cctggctcctg ggaacgagcg taatggaaac aatcattctc tgccagcaat 540
aaaatacctt cagttacatg agtgtgacag cttctcgatt ggaattttct gcatgccacc 600
tgggtctatc ataccacttc ataatcatcc aggcatagaca gtgctaagca agcttggtta 660
tgggttcaatg cacgttaagt catatgattg ggctgagcct gaccaatcag agctagacga 720
tccattacaa gcaagaccgg cgaagctggt caaggatatt gatatgactt cccctagccc 780
agcaaccact ctatatccaa caaccggtgg caacattcat tgtttcaaag ccattactca 840
ttgtgcaatc tttgacatct tatctcctcc atactcttct actcatggca gacactgcaa 900
ctacttccga aaatccccaa tgctagactt acctggtgag attgaagtga tgaatggaga 960
agtgatctca aatgtgacat ggcttgaaga gtatcaacct ccagataact ttgtgatatg 1020
gagagttccg tacagaggtc cagtgmmtag aaaatgagaa atacaaaaag gattaaacat 1080
attaaaaaag agcagaaaga gaaagggtgct tatgatcagg agaataattg gtaaaccatt 1140
cagaggctgg ctgcataatg gtcgaggttc ttacataatt gtgaccacat taagttccag 1200
cctatgtcgt tgtatgataa tgattacttc actagtttaa tattataatt tttttccct 1260
atttttatat gcagctacac aaaaaattgc tcataaacag tgttatatat agttatcata 1320
aattttgttt cc
```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```
Met Pro Tyr Phe Ile Gln Arg Leu Phe Asn Thr Cys Lys Ser Ser Leu
1          5          10          15
Ser Pro Asn Gly Pro Val Ser Glu Glu Ala Leu Asp Lys Val Arg Asn
20          25          30
Val Leu Glu Lys Ile Lys Pro Ser Asp Val Gly Leu Glu Gln Glu Ala
35          40          45
Gln Leu Val Arg Asn Trp Pro Gly Pro Gly Asn Glu Arg Asn Gly Asn
50          55          60
Asn His Ser Leu Pro Ala Ile Lys Tyr Leu Gln Leu His Glu Cys Asp
65          70          75          80
Ser Phe Ser Ile Gly Ile Phe Cys Met Pro Pro Gly Ser Ile Ile Pro
85          90          95
Leu His Asn His Pro Gly Met Thr Val Leu Ser Lys Leu Val Tyr Gly
100          105          110
Ser Met His Val Lys Ser Tyr Asp Trp Ala Glu Pro Asp Gln Ser Glu
115          120          125
Leu Asp Asp Pro Leu Gln Ala Arg Pro Ala Lys Leu Val Lys Asp Ile
130          135          140
Asp Met Thr Ser Pro Ser Pro Ala Thr Thr Leu Tyr Pro Thr Thr Gly
145          150          155          160
Gly Asn Ile His Cys Phe Lys Ala Ile Thr His Cys Ala Ile Phe Asp
165          170          175
Ile Leu Ser Pro Pro Tyr Ser Ser Thr His Gly Arg His Cys Asn Tyr
180          185          190
Phe Arg Lys Ser Pro Met Leu Asp Leu Pro Gly Glu Ile Glu Val Met
195          200          205
Asn Gly Glu Val Ile Ser Asn Val Thr Trp Leu Glu Glu Tyr Gln Pro
210          215          220
Pro Asp Asn Phe Val Ile Trp Arg Val Pro Tyr Arg Gly Pro Val Xaa
225          230          235          240
Arg Lys
```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..154  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498499  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:  
Met Pro Pro Gly Ser Ile Ile Pro Leu His Asn His Pro Gly Met Thr  
1 5 10 15  
Val Leu Ser Lys Leu Val Tyr Gly Ser Met His Val Lys Ser Tyr Asp  
20 25 30  
Trp Ala Glu Pro Asp Gln Ser Glu Leu Asp Asp Pro Leu Gln Ala Arg  
35 40 45  
Pro Ala Lys Leu Val Lys Asp Ile Asp Met Thr Ser Pro Ser Pro Ala  
50 55 60  
Thr Thr Leu Tyr Pro Thr Thr Gly Gly Asn Ile His Cys Phe Lys Ala  
65 70 75 80  
Ile Thr His Cys Ala Ile Phe Asp Ile Leu Ser Pro Pro Tyr Ser Ser  
85 90 95  
Thr His Gly Arg His Cys Asn Tyr Phe Arg Lys Ser Pro Met Leu Asp  
100 105 110  
Leu Pro Gly Glu Ile Glu Val Met Asn Gly Glu Val Ile Ser Asn Val  
115 120 125  
Thr Trp Leu Glu Glu Tyr Gln Pro Pro Asp Asn Phe Val Ile Trp Arg  
130 135 140  
Val Pro Tyr Arg Gly Pro Val Xaa Arg Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1498500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Met Thr Val Leu Ser Lys Leu Val Tyr Gly Ser Met His Val Lys Ser  
1 5 10 15  
Tyr Asp Trp Ala Glu Pro Asp Gln Ser Glu Leu Asp Asp Pro Leu Gln  
20 25 30  
Ala Arg Pro Ala Lys Leu Val Lys Asp Ile Asp Met Thr Ser Pro Ser  
35 40 45  
Pro Ala Thr Thr Leu Tyr Pro Thr Thr Gly Gly Asn Ile His Cys Phe  
50 55 60  
Lys Ala Ile Thr His Cys Ala Ile Phe Asp Ile Leu Ser Pro Pro Tyr  
65 70 75 80  
Ser Ser Thr His Gly Arg His Cys Asn Tyr Phe Arg Lys Ser Pro Met  
85 90 95  
Leu Asp Leu Pro Gly Glu Ile Glu Val Met Asn Gly Glu Val Ile Ser  
100 105 110  
Asn Val Thr Trp Leu Glu Glu Tyr Gln Pro Pro Asp Asn Phe Val Ile  
115 120 125  
Trp Arg Val Pro Tyr Arg Gly Pro Val Xaa Arg Lys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 984 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..984  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498501  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```
agattcgcga gttcttcggt cttcggtctg cttttwtttt ttttattttt tttgtgtggt      60
tgagagatgt ctgccctttga agacgattcc ttcgtcatat tcaacgatga tgcgtctgag      120
tctgtttccag tctcaggctc ttttgacgcc actgattctt tctcagcttt cgacgggtca      180
ctccaagtcg aggactccgt cgacgatgtt tttgcagcgc cgtcttctga ctacgggtgct      240
tactccaacg gtgacggcat cttcggatcc aacggggatc acgacgggtcc tatcttgcca      300
ccaccgtcgg agatggaatc agatgaggga tttgctctta gagaatggag aagacaaaat      360
gcaattcaac ttgaggagaa ggagaagaga gaaaaggaat tgttgaagca aattattgag      420
gaagctgata aatacaaaag agagtttcat aagaagattg aagtaacttg tgaaaacaac      480
aaagcagcta acagagagaa ggaaaagctg tatctggaga accaagagaa gttctacgcg      540
gaatccagca agaattactg gaaggcaata gcagagctag ttcctaaaag agttccaaca      600
atagagaaaa ggagaggaaa aaaagagcaa caagatccta agaagccaac agtctctgtg      660
attcaagggtc caaagcccg taagccaacc gatctaaca gaatgagaca aatattggtg      720
aagctcaaac acaaccacc ttctcacctg aaactcact ctcaacctcc atcggaggag      780
gcggtgctc ctccaaagaa tgttcccgaa accaagccca ctgaggcagt tactgctgct      840
taaaaacctc ttttgttttc ttattcggtg cttacatctg tgtgaattca gtctttgcat      900
ttcattatgt gttataaaca gctgagagat tttatggttc atgtgtgtta ttaacataat      960
tatgtcatat tggaatgata actt
```

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 134 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..134  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```
Asp Ser Arg Val Leu Arg Ser Ser Phe Cys Leu Xaa Phe Phe Tyr Phe
1           5           10           15
Phe Cys Val Phe Glu Arg Cys Leu Pro Leu Lys Thr Ile Pro Ser Ser
20           25           30
Tyr Ser Thr Met Met Arg Leu Ser Leu Phe Gln Ser Gln Ala Leu Leu
35           40           45
Thr Pro Leu Ile Leu Ser Gln Leu Ser Thr Ala His Ser Lys Ser Arg
50           55           60
Thr Pro Ser Thr Met Phe Leu Gln Arg Arg Leu Leu Thr Thr Val Leu
65           70           75           80
Thr Pro Thr Val Thr Ala Ser Ser Asp Pro Thr Gly Ile Thr Thr Val
85           90           95
Leu Ser Cys His His Arg Arg Arg Trp Asn Gln Met Arg Asp Leu Leu
100          105          110
Leu Glu Asn Gly Glu Asp Lys Met Gln Phe Asn Leu Arg Arg Arg Arg
115          120          125
Arg Glu Lys Arg Asn Cys
130
```

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 258 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..258
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Met	Ser	Ala	Phe	Glu	Asp	Asp	Ser	Phe	Val	Ile	Leu	Asn	Asp	Asp	Ala	
1				5					10						15	
Ser	Glu	Ser	Val	Pro	Val	Ser	Gly	Ser	Phe	Asp	Ala	Thr	Asp	Ser	Phe	
			20					25					30			
Ser	Ala	Phe	Asp	Gly	Ser	Leu	Gln	Val	Glu	Asp	Ser	Val	Asp	Asp	Val	
		35					40					45				
Phe	Ala	Ala	Pro	Ser	Ser	Asp	Tyr	Gly	Ala	Tyr	Ser	Asn	Gly	Asp	Gly	
	50					55				60						
Ile	Phe	Gly	Ser	Asn	Gly	Asp	His	Asp	Gly	Pro	Ile	Leu	Pro	Pro	Pro	
65					70				75					80		
Ser	Glu	Met	Glu	Ser	Asp	Glu	Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	
			85						90				95			
Gln	Asn	Ala	Ile	Gln	Leu	Glu	Glu	Lys	Glu	Lys	Arg	Glu	Lys	Glu	Leu	
			100					105					110			
Leu	Lys	Gln	Ile	Ile	Glu	Glu	Ala	Asp	Gln	Tyr	Lys	Glu	Glu	Phe	His	
		115					120					125				
Lys	Lys	Ile	Glu	Val	Thr	Cys	Glu	Asn	Asn	Lys	Ala	Ala	Asn	Arg	Glu	
	130					135					140					
Lys	Glu	Lys	Leu	Tyr	Leu	Glu	Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ser	
145					150					155					160	
Ser	Lys	Asn	Tyr	Trp	Lys	Ala	Ile	Ala	Glu	Leu	Val	Pro	Lys	Glu	Val	
			165						170					175		
Pro	Thr	Ile	Glu	Lys	Arg	Arg	Gly	Lys	Lys	Glu	Gln	Gln	Asp	Pro	Lys	
			180					185					190			
Lys	Pro	Thr	Val	Ser	Val	Ile	Gln	Gly	Pro	Lys	Pro	Gly	Lys	Pro	Thr	
		195					200					205				
Asp	Leu	Thr	Arg	Met	Arg	Gln	Ile	Leu	Val	Lys	Leu	Lys	His	Asn	Pro	
	210					215					220					
Pro	Ser	His	Leu	Lys	Leu	Thr	Ser	Gln	Pro	Pro	Ser	Glu	Glu	Ala	Ala	
225					230					235					240	
Ala	Pro	Pro	Lys	Asn	Val	Pro	Glu	Thr	Lys	Pro	Thr	Glu	Ala	Val	Thr	
			245						250					255		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..176
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met	Glu	Ser	Asp	Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Gln	Asn	
1			5						10				15		
Ala	Ile	Gln	Leu	Glu	Glu	Lys	Glu	Lys	Arg	Glu	Lys	Glu	Leu	Leu	Lys
		20					25					30			
Gln	Ile	Ile	Glu	Glu	Ala	Asp	Gln	Tyr	Lys	Glu	Glu	Phe	His	Lys	Lys
		35					40					45			

Ile	Glu	Val	Thr	Cys	Glu	Asn	Asn	Lys	Ala	Ala	Asn	Arg	Glu	Lys	Glu
50						55					60				
Lys	Leu	Tyr	Leu	Glu	Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ser	Ser	Lys
65					70					75					80
Asn	Tyr	Trp	Lys	Ala	Ile	Ala	Glu	Leu	Val	Pro	Lys	Glu	Val	Pro	Thr
				85					90					95	
Ile	Glu	Lys	Arg	Arg	Gly	Lys	Lys	Glu	Gln	Gln	Asp	Pro	Lys	Lys	Pro
			100					105					110		
Thr	Val	Ser	Val	Ile	Gln	Gly	Pro	Lys	Pro	Gly	Lys	Pro	Thr	Asp	Leu
		115					120						125		
Thr	Arg	Met	Arg	Gln	Ile	Leu	Val	Lys	Leu	Lys	His	Asn	Pro	Pro	Ser
	130					135					140				
His	Leu	Lys	Leu	Thr	Ser	Gln	Pro	Pro	Ser	Glu	Glu	Ala	Ala	Ala	Pro
145					150					155					160
Pro	Lys	Asn	Val	Pro	Glu	Thr	Lys	Pro	Thr	Glu	Ala	Val	Thr	Ala	Ala
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

catctttttc	tctcttttatt	tataaattta	tctgcatagt	actctctgaa	tctatatctt	60
caaaaaaaaa	aaacgtccaa	gatcaaatca	agaaacccat	taaaaaaaaa	aatcagggtt	120
tggtttcagt	tttaagggtt	taaggtttct	tggggaagaa	acgatggaga	ctttttgtgg	180
gtttcaaaag	gaggaagagc	agatggattt	acctcctggg	ttcagggttc	atccaacaga	240
tgaagaactc	ataactcact	atctccataa	gaaggttctt	gacaccagct	tctcagctaa	300
agctatcggt	gaagttgatt	taaacaaatc	agagccatgg	gagttaccat	ggatggcaaa	360
aatgggtgag	aaagaatggt	atttttttctg	tgtgagagac	agaaagtatc	ccaccggttt	420
aagaactaac	cgagcaactg	aagccggtta	ttggaaggcg	accgggaagg	ataaagagat	480
ataccgaggc	aaatcacttg	ttgggatgaa	gaagacactt	gttttctata	gaggaagagc	540
tcctaaaggt	cagaaaacca	actgggtgat	gcatgagtac	aggcttgaag	gaaaattctc	600
tgcccataac	ttgccgaaaa	ccgcaaagaa	tgaatgggtg	atatgcaggg	tgwtccaaaa	660
gagtgtctgga	gggcaagaag	atcccgat	cgagtcta	ccgaatcggt	tcactcggaa	720
ccgactttta	cccttcgctt	ttgccctctt	taaccgattc	ttcgcccttac	aacgataaar	780
ccraaacaga	ascggtctac	gtgccctgct	tctccaacca	aacggatcaa	aaccaaggaa	840
ccacactcaa	ttgcttcagc	agccctgttc	ttaactcgat	ccaagccgac	atttttcmca	900
ggattccact	ctatcaaact	cagtcctctc	aggtttctat	gaatctacag	agcccggttc	960
tcacgcaaga	acactcagtt	ctacatgcta	tgatcgagaa	caacagaaga	caaagtctca	1020
aaacgatgag	tgtctcacia	gaaaccggag	tttcaactga	catgaacact	gatatctcat	1080
cggattttga	atttggttaag	agacggtttg	attctcaaga	agatccgtct	tcctctactg	1140
gaccggttga	tcttgaacct	ttctggaatt	actgaagatg	attcaagatt	ctcatgtcca	1200
ttaatttact	gtggtgtgtt	aaagtttgta	taggctattg	tcataactc	tcatatcaac	1260
ttccactata	tattataaca	atttaaagaa	acttaaaaat	atgatttg		

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

```
Met Glu Thr Phe Cys Gly Phe Gln Lys Glu Glu Glu Gln Met Asp Leu
1      5      10      15
Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile Thr His
      20      25      30
Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala Lys Ala Ile
      35      40      45
Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu Pro Trp Met
      50      55      60
Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp Arg
65      70      75      80
Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly Tyr
      85      90      95
Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser Leu
      100      105      110
Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys
      115      120      125
Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys
      130      135      140
Phe Ser Ala His Asn Leu Pro Lys Thr Ala Lys Asn Glu Trp Val Ile
145      150      155      160
Cys Arg Val Xaa Gln Lys Ser Ala Gly Gly Gln Glu Asp Pro Asp Phe
      165      170      175
Glu Ser Asn Pro Asn Arg Phe Thr Arg Asn Arg Leu
      180      185
```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```
Met Asp Leu Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu
1      5      10      15
Ile Thr His Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala
      20      25      30
Lys Ala Ile Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu
      35      40      45
Pro Trp Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val
      50      55      60
Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu
65      70      75      80
Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly
      85      90      95
Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg
      100      105      110
Ala Pro Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu
      115      120      125
Glu Gly Lys Phe Ser Ala His Asn Leu Pro Lys Thr Ala Lys Asn Glu
      130      135      140
Trp Val Ile Cys Arg Val Xaa Gln Lys Ser Ala Gly Gly Gln Glu Asp
145      150      155      160
Pro Asp Phe Glu Ser Asn Pro Asn Arg Phe Thr Arg Asn Arg Leu
      165      170      175
```



(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met	Ala	Lys	Met	Gly	Glu	Lys	Glu	Trp	Tyr	Phe	Phe	Cys	Val	Arg	Asp
1			5						10					15	
Arg	Lys	Tyr	Pro	Thr	Gly	Leu	Arg	Thr	Asn	Arg	Ala	Thr	Glu	Ala	Gly
			20					25					30		
Tyr	Trp	Lys	Ala	Thr	Gly	Lys	Asp	Lys	Glu	Ile	Tyr	Arg	Gly	Lys	Ser
		35					40					45			
Leu	Val	Gly	Met	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Arg	Gly	Arg	Ala	Pro
	50					55				60					
Lys	Gly	Gln	Lys	Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Glu	Gly
65					70					75				80	
Lys	Phe	Ser	Ala	His	Asn	Leu	Pro	Lys	Thr	Ala	Lys	Asn	Glu	Trp	Val
			85						90				95		
Ile	Cys	Arg	Val	Xaa	Gln	Lys	Ser	Ala	Gly	Gly	Gln	Glu	Asp	Pro	Asp
			100					105				110			
Phe	Glu	Ser	Asn	Pro	Asn	Arg	Phe	Thr	Arg	Asn	Arg	Leu			
	115					120						125			

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

attctctaga	tgcttgaaag	ctgtgtagg	attgtagaag	aggaggcgat	atttttcaat	60
cgctcgctcg	ttgggaaatt	cctcacatct	cagatgaact	ccaatcgctt	cgagaaactc	120
taattcctcg	ggagttttcg	atagcatcat	cgagaaattg	ttttcccgtt	gaacaatgga	180
tggttaacaaa	gatgacgcgt	tgaaatgcct	aaaaatcggc	aaggatgcta	taaaagcagg	240
agatagatct	cgcgctttga	aattttcttga	gaaagcttgt	cgctcttgatc	caaattcttct	300
gatcgatgat	cttgtttcgg	atctgaagaa	gcaatcgcat	gaaccagcgg	cggaggagga	360
ttcgccctgga	tctggcgcca	acgagtcctt	taagccgtcg	gatcgacctt	ctcttcgtca	420
acgtggatct	tcgtcatcag	ccgcgggatc	gtcatcatct	tcgtcttcca	cggaagaaca	480
acgaacgatc	gtgaggggaga	taaagtcgaa	gaaggattac	tatgagatcc	ttggattgaa	540
aagaaactgt	tcagtggag	atttgaggaa	atcttatcgg	aaactctcgt	tgaaagttca	600
tcccgataag	aataaagctc	ctgcttctga	agaagctttt	aaattcgtct	ctaaagcttt	660
ccaatgctta	aagcaacaaa	gacactagcc	gaaagtacga	cgtcagtggt	tccgatgagc	720
ctgcttatca	accatgccga	gctgcgagaa	gaaacaacgg	attcaacggc	ttctctgatg	780
atgaatttga	tgctgatgag	attttcagaa	gcttctttgg	tggtggtgga	atgaatcctg	840
ctactactca	attccgatca	ttcaatttcg	gtggaggaac	tagaacagct	aattaagctt	900
ctgatacagg	attcaatcct	cgtgtactcc	ttcaataact	tcctgtttgtg	ttcatactac	960
ttctcaactt	tttgctttct	cctcaaccaa	tttactcgct	ttctccatcg	tataactacg	1020
agcacaaatt	caccactcat	aggggtgtca	attactttgt	gagatcagcc	aagttcgagc	1080
aggaataccc	gataagtagc	ttctagagac	agagggttga	agagcaagtt	gatagagatt	1140
acttgtctat	acttgccag	aattgtcgcc	atgagcttca	gagacaacaa	tggggatata	1200
tccgcgaagc	gccacattgt	gacatgatga	agaggtttga	tgcagctgct	gcataaacca	1260

```
tccatgtcag agagagactg aagcaccaag ttagtaaact caaatccaag aaacttggtt 1320
ggattgttct gagacatagc tatggtactt actaacttct gagcattttt gttgatgctt 1380
cagtgaagttt gatttctaag tcccaaactc atatacgttg attactgtgc tccttatgat 1440
gttagtatga aacatattat gtgtg
```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```
Met Asp Gly Asn Lys Asp Asp Ala Leu Lys Cys Leu Lys Ile Gly Lys
1          5          10          15
Asp Ala Ile Lys Ala Gly Asp Arg Ser Arg Ala Leu Lys Phe Leu Glu
20          25          30
Lys Ala Cys Arg Leu Asp Pro Asn Leu Leu Ile Asp Asp Leu Val Ser
35          40          45
Asp Leu Lys Lys Gln Ser Asp Glu Pro Ala Ala Glu Glu Asp Ser Pro
50          55          60
Gly Ser Gly Ala Asn Glu Ser Ser Lys Pro Ser Asp Arg Pro Ser Leu
65          70          75          80
Arg Gln Arg Gly Ser Ser Ser Ser Ala Ala Gly Ser Ser Ser Ser
85          90          95
Ser Ser Thr Glu Gln Arg Thr Ile Val Arg Glu Ile Lys Ser Lys
100         105         110
Lys Asp Tyr Tyr Glu Ile Leu Gly Leu Lys Arg Asn Cys Ser Val Glu
115         120         125
Asp Leu Arg Lys Ser Tyr Arg Lys Leu Ser Leu Lys Val His Pro Asp
130         135         140
Lys Asn Lys Ala Pro Ala Ser Glu Glu Ala Phe Lys Phe Val Ser Lys
145         150         155         160
Ala Phe Gln Cys Leu Lys Gln Gln Arg His
165         170
```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..778
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

```
ctctctctta ggtttttttt ccttctctcc aatctcatct tctccgaaaa ctttctttct 60
ctcaaatttc tgggtgaaaac atgtctgacg acgagcacca ctttgaggcc agcgaatccg 120
gagcttccaa gacctatcct caatcagccg gtaacatccg taaaggtggt cacatcgta 180
tcaaaaaccg tccctgcaag gttgttgagg ttctgacttc caaaactggc aagcacggtc 240
acgccaaatg tcactttgtt gctattgata tcttcactgc taagaagctt gaagatattg 300
ttccatcttc ccacaattgt gatgttcac atgtgaaccg tgttgattac cagttgattg 360
atatcactga ggatggcttc gtgagccttc tcaactgacag tgggtggcacc aaggatgatc 420
tcaagcttcc caccgatgat ggtctcaccg nccagttgtt gtgttttgtt aatgcacatg 480
agscttggtt tcgatgaggg aaaggatatt gtggtgtctg tcatgtcttc catgggagag 540
gagcagatct gtgccgtcaa ggaagttggt ggtggcaagt aaacaagtat cattcgatat 600
attattacca gtttgacaac ggacgtcaat gttataagaa ccaaaagatg tttttctttt 660
```

tcctaattta gaccctttgt gtgtgtttct tgttgcaaga caaccatatac tattggtttt 720  
ggattgttg aaaagtttgt gttgaaacat tcaaagtttc ttatgagatg ttattctc

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Leu	Ser	Leu	Arg	Phe	Phe	Phe	Pro	Ser	Pro	Asn	Leu	Ile	Phe	Ser	Glu
1				5					10					15	
Asn	Leu	Ser	Ser	Leu	Lys	Phe	Leu	Val	Lys	Thr	Cys	Leu	Thr	Thr	Ser
			20					25					30		
Thr	Thr	Leu	Arg	Pro	Ala	Asn	Pro	Glu	Leu	Pro	Arg	Pro	Ile	Leu	Asn
		35					40					45			
Gln	Pro	Val	Thr	Ser	Val	Lys	Val	Val	Thr	Ser	Ser	Ser	Lys	Thr	Val
	50					55					60				
Pro	Ala	Arg	Leu	Leu	Arg	Phe	Arg	Leu	Pro	Lys	Leu	Ala	Ser	Thr	Val
65					70					75				80	
Thr	Pro	Asn	Val	Thr	Leu	Leu	Leu	Leu	Ile	Ser	Ser	Leu	Leu	Arg	Ser
			85						90					95	
Leu	Lys	Ile	Leu	Phe	His	Leu	Pro	Thr	Ile	Val	Met	Phe	His	Met	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

Met	Ser	Asp	Asp	Glu	His	His	Phe	Glu	Ala	Ser	Glu	Ser	Gly	Ala	Ser
1				5					10					15	
Lys	Thr	Tyr	Pro	Gln	Ser	Ala	Gly	Asn	Ile	Arg	Lys	Gly	Gly	His	Ile
			20					25					30		
Val	Ile	Lys	Asn	Arg	Pro	Cys	Lys	Val	Val	Glu	Val	Ser	Thr	Ser	Lys
		35					40					45			
Thr	Gly	Lys	His	Gly	His	Ala	Lys	Cys	His	Phe	Val	Ala	Ile	Asp	Ile
	50					55					60				
Phe	Thr	Ala	Lys	Lys	Leu	Glu	Asp	Ile	Val	Pro	Ser	Ser	His	Asn	Cys
65					70					75				80	
Asp	Val	Pro	His	Val	Asn	Arg	Val	Asp	Tyr	Gln	Leu	Ile	Asp	Ile	Thr
			85					90						95	
Glu	Asp	Gly	Phe	Val	Ser	Leu	Leu	Thr	Asp	Ser	Gly	Gly	Thr	Lys	Asp
			100					105					110		
Asp	Leu	Lys	Leu	Pro	Thr	Asp	Asp	Gly	Leu	Thr	Xaa	Gln	Leu	Leu	Cys
		115					120						125		
Phe	Val	Asn	Ala	His	Glu	Xaa	Trp	Ile	Arg						
	130						135								

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

(2) INFORMATION FOR SEQ ID NO:484:

(A) LENGTH: 310 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1498523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

Met	Lys	Thr	Met	Thr	Gln	Leu	Asn	Ile	Ala	Val	Xaa	Val	Val	Val	Thr
1				5					10					15	
Val	Leu	Ile	Gly	Met	Leu	Arg	Ser	Ser	Glu	Ala	Gln	Leu	Gln	Met	Asn
			20					25					30		
Phe	Tyr	Ala	Lys	Ser	Cys	Pro	Asn	Ala	Glu	Lys	Ile	Ile	Ser	Asp	His
		35					40					45			
Ile	Gln	Asn	His	Ile	His	Asn	Gly	Pro	Ser	Leu	Ala	Ala	Pro	Leu	Ile
		50				55					60				
Arg	Met	His	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser	Val
					70					75					80
Leu	Ile	Asn	Ser	Thr	Ser	Gly	Asn	Ala	Glu	Arg	Asp	Ala	Pro	Pro	Asn
				85					90					95	
Leu	Thr	Leu	Arg	Gly	Phe	Gly	Phe	Val	Glu	Arg	Ile	Lys	Ala	Leu	Leu
			100					105					110		
Glu	Lys	Val	Cys	Pro	Lys	Thr	Val	Ser	Cys	Ala	Asp	Ile	Ile	Ala	Leu
		115					120					125			
Thr	Ala	Arg	Asp	Thr	Val	Val	Ala	Thr	Gly	Gly	Pro	Ser	Trp	Ser	Val
	130					135					140				
Pro	Thr	Gly	Arg	Arg	Asp	Gly	Arg	Ile	Ser	Asn	Leu	Lys	Glu	Ala	Thr

145					150					155					160
Asn	Asn	Ile	Pro	Pro	Thr	Ser	Asn	Phe	Thr	Thr	Leu	Arg	Arg	Leu	
				165					170					175	
Phe	Lys	Asn	Gln	Gly	Leu	Asn	Leu	Lys	Asp	Leu	Val	Leu	Leu	Ser	Gly
			180					185					190		
Ala	His	Thr	Ile	Gly	Val	Ser	His	Cys	Ser	Ser	Met	Asn	Thr	Arg	Leu
		195					200					205			
Tyr	Asn	Phe	Ser	Thr	Thr	Val	Lys	Gln	Asp	Pro	Ser	Leu	Asp	Ser	Gln
	210					215					220				
Tyr	Ala	Ala	Asn	Leu	Lys	Ala	Asn	Lys	Cys	Lys	Ser	Leu	Asn	Asp	Asn
225					230					235				240	
Ser	Thr	Ile	Leu	Glu	Met	Asp	Pro	Gly	Ser	Ser	Arg	Ser	Phe	Asp	Leu
			245						250					255	
Ser	Tyr	Tyr	Arg	Leu	Val	Leu	Lys	Arg	Arg	Gly	Leu	Phe	Gln	Ser	Asp
		260						265					270		
Ser	Ala	Leu	Thr	Thr	Asn	Ser	Ala	Thr	Leu	Lys	Val	Ile	Asn	Asp	Leu
	275						280					285			
Val	Asn	Gly	Ser	Glu	Lys	Lys	Phe	Phe	Lys	Ala	Phe	Ala	Lys	Ser	Met
	290					295					300				
Xaa	Glu	Asp	Gly	Glu	Ser										
305					310										

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Met	Thr	Gln	Leu	Asn	Ile	Ala	Val	Xaa	Val	Val	Val	Thr	Val	Leu	Ile
1				5				10						15	
Gly	Met	Leu	Arg	Ser	Ser	Glu	Ala	Gln	Leu	Gln	Met	Asn	Phe	Tyr	Ala
		20						25					30		
Lys	Ser	Cys	Pro	Asn	Ala	Glu	Lys	Ile	Ile	Ser	Asp	His	Ile	Gln	Asn
		35					40					45			
His	Ile	His	Asn	Gly	Pro	Ser	Leu	Ala	Ala	Pro	Leu	Ile	Arg	Met	His
	50					55					60				
Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser	Val	Leu	Ile	Asn
65					70				75					80	
Ser	Thr	Ser	Gly	Asn	Ala	Glu	Arg	Asp	Ala	Pro	Pro	Asn	Leu	Thr	Leu
			85					90						95	
Arg	Gly	Phe	Gly	Phe	Val	Glu	Arg	Ile	Lys	Ala	Leu	Leu	Glu	Lys	Val
		100						105					110		
Cys	Pro	Lys	Thr	Val	Ser	Cys	Ala	Asp	Ile	Ile	Ala	Leu	Thr	Ala	Arg
		115					120					125			
Asp	Thr	Val	Val	Ala	Thr	Gly	Gly	Pro	Ser	Trp	Ser	Val	Pro	Thr	Gly
	130					135					140				
Arg	Arg	Asp	Gly	Arg	Ile	Ser	Asn	Leu	Lys	Glu	Ala	Thr	Asn	Asn	Ile
145					150					155				160	
Pro	Pro	Pro	Thr	Ser	Asn	Phe	Thr	Thr	Leu	Arg	Arg	Leu	Phe	Lys	Asn
			165						170					175	
Gln	Gly	Leu	Asn	Leu	Lys	Asp	Leu	Val	Leu	Leu	Ser	Gly	Ala	His	Thr
		180					185						190		
Ile	Gly	Val	Ser	His	Cys	Ser	Ser	Met	Asn	Thr	Arg	Leu	Tyr	Asn	Phe
	195						200					205			
Ser	Thr	Thr	Val	Lys	Gln	Asp	Pro	Ser	Leu	Asp	Ser	Gln	Tyr	Ala	Ala
	210					215						220			

Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile  
225 230 235 240  
Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr  
245 250 255  
Arg Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu  
260 265 270  
Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly  
275 280 285  
Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp  
290 295 300  
Gly Glu Ser  
305

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala Lys  
1 5 10 15  
Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn His  
20 25 30  
Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His Phe  
35 40 45  
His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn Ser  
50 55 60  
Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu Arg  
65 70 75 80  
Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val Cys  
85 90 95  
Pro Lys Thr Val Ser Cys Ala Asp Ile Ala Leu Thr Ala Arg Asp  
100 105 110  
Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly Arg  
115 120 125  
Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile Pro  
130 135 140  
Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn Gln  
145 150 155 160  
Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr Ile  
165 170 175  
Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe Ser  
180 185 190  
Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala Asn  
195 200 205  
Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile Leu  
210 215 220  
Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr Arg  
225 230 235 240  
Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu Thr  
245 250 255  
Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly Ser  
260 265 270  
Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp Gly  
275 280 285  
Glu Ser

290

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1734
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

atcaatggct	ctggatgcat	tcttcttcat	cgtctctcta	tttcttctgt	ttccgtcacc	60
atccgcgtca	gaatccacta	ctcagttttg	tagtgcaggg	agagagaatg	gtgtggggatc	120
ttgtgggggtt	tcacgcacga	ggattttgat	taaaggaggt	actgttgtca	atgcacacca	180
tcaagaactt	gctgatgttt	atgtggaaaa	tggattatt	gtcgtgtg	agccaaacat	240
taaggttggg	gatgaagtca	ctgtcctcga	tgctactgga	aagtttgtca	tgccaggagg	300
aattgacccc	cacacgcacc	tcgccatgga	atttatgggt	accgagacta	ttgatgattt	360
cttcagtggg	caggcagcgg	cattagctgg	tggacaact	atgcatatag	actttgttat	420
acctgtcaat	gggaatctgg	tggctgggtt	tgaagcctat	gaaaacaaat	ctagagaatc	480
ttgtatggat	tacggttttc	atatggcaat	cacaaagtgg	gatgaagggt	tttccaggga	540
catggagatg	ttggtcaagg	aaaagggtat	caactctttc	aagtttttcc	tagcgtataa	600
aggatctctt	atggtaactg	atgacctact	cctagaagga	cttaaaagat	gcaaatccct	660
cgggtgccttg	gccatggttc	atgctgaaaa	tggagatgca	gtattcgaag	gacagaaaag	720
aatgattgar	ctgggcattt	acagggtccag	agggtcatgc	tcttttcaag	gcctcctgtg	780
ctcgagggag	aggccactgc	tagagcaatt	cgtttggtc	gttttattaa	cacgcctctc	840
tatgttggtc	atgtgatgag	tggtgatgca	atggacgaga	ttgctaaagc	tcgaaaatca	900
ggacagaagg	ttattggaga	gcctgttggt	tctggattaa	tccttgatga	tcattggctt	960
tgggacccctg	acttcacaat	tgctccaag	tatgtcatga	gtccacctat	cagaccagta	1020
ggacatggga	aagccctaca	agatgccctt	tccacaggaa	tccttcagct	tgtaggaact	1080
gatcactgca	ctttcaattc	tacacaaaaa	gctctaggac	ttgatgattt	ccgcaaaata	1140
cctaattggtg	ttaatggcct	tgaggaaacgg	atgcacttga	tatgggacac	gatgggtggag	1200
tctggccaac	tctcagctac	tgattatggt	cgaataacca	gcactgagtg	tgctagaatt	1260
ttcaacatat	atccacggaa	aggagctatc	cttgctgggt	cggatgcaga	tattatcata	1320
ttgaatccaa	actcaagcta	cgagattagc	tcaaagtctc	atcattcaag	atcacagaca	1380
aacgtctacg	agggcagaag	aggaaaggga	aaagttgaag	tgacaatagc	aggaggacga	1440
attgtgtggg	aaaacgagga	acttaaaagt	gttccaagaa	gtggcaagta	tatagagatg	1500
cctcctttca	gttacctttt	cgatgggtatt	gagaaatcag	atgctaatta	tctatcttct	1560
cttcgagctc	cagttaagcg	tgtcagaact	gaagctacgt	aaagtgcagg	tatctatctt	1620
tcgtgattct	gtaagaacaa	ttgtacataa	tttgatttaa	aagtattgaa	agagcgatta	1680
tgaataatgt	gcatgtagtc	tggttttgag	aaaaataaaa	agattgtaaa	at	

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Ser	Met	Ala	Leu	Asp	Ala	Phe	Phe	Phe	Ile	Val	Ser	Leu	Phe	Leu	Leu
1			5						10					15	
Phe	Pro	Ser	Pro	Ser	Ala	Ser	Glu	Ser	Thr	Thr	Gln	Phe	Cys	Ser	Ala
			20						25				30		
Gly	Arg	Glu	Asn	Gly	Val	Gly	Ser	Cys	Gly	Val	Ser	Ser	Thr	Arg	Ile
			35						40				45		
Leu	Ile	Lys	Gly	Gly	Thr	Val	Val	Asn	Ala	His	His	Gln	Glu	Leu	Ala

50	55	60
Asp Val Tyr Val Glu	Asn Gly Ile Ile Val	Ala Val Gln Pro Asn Ile
65	70	75
Lys Val Gly Asp Glu	Val Thr Val Leu Asp	Ala Thr Gly Lys Phe Val
85	90	95
Met Pro Gly Gly Ile	Asp Pro His Thr His	Leu Ala Met Glu Phe Met
100	105	110
Gly Thr Glu Thr Ile	Asp Asp Phe Phe Ser	Gly Gln Ala Ala Leu
115	120	125
Ala Gly Gly Thr Thr	Met His Ile Asp Phe	Val Ile Pro Val Asn Gly
130	135	140
Asn Leu Val Ala Gly	Phe Glu Ala Tyr Glu	Asn Lys Ser Arg Glu Ser
145	150	155
Cys Met Asp Tyr Gly	Phe His Met Ala Ile	Thr Lys Trp Asp Glu Gly
165	170	175
Val Ser Arg Asp Met	Glu Met Leu Val Lys	Glu Lys Gly Ile Asn Ser
180	185	190
Phe Lys Phe Phe Leu	Ala Tyr Lys Gly Ser	Leu Met Val Thr Asp Asp
195	200	205
Leu Leu Leu Glu Gly	Leu Lys Arg Cys Lys	Ser Leu Gly Ala Leu Ala
210	215	220
Met Val His Ala Glu	Asn Gly Asp Ala Val	Phe Glu Gly Gln Lys Arg
225	230	235
Met Ile Xaa Leu Gly	Ile Tyr Arg Ser Arg	Gly Ser Cys Ser Phe Gln
245	250	255
Gly Leu Leu Cys Ser	Arg Glu Arg Pro Leu	Leu Glu Gln Phe Val Trp
260	265	270
Leu Val Leu Leu Thr	Arg Leu Ser Met Leu	Phe Met
275	280	

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Leu Phe	
1	15
Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala Gly	
20	30
Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile Leu	
35	45
Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala Asp	
50	60
Val Tyr Val Glu Asn Gly Ile Ile Val Ala Val Gln Pro Asn Ile Lys	
65	80
Val Gly Asp Glu Val Thr Val Leu Asp Ala Thr Gly Lys Phe Val Met	
85	95
Pro Gly Gly Ile Asp Pro His Thr His Leu Ala Met Glu Phe Met Gly	
100	110
Thr Glu Thr Ile Asp Asp Phe Phe Ser Gly Gln Ala Ala Ala Leu Ala	
115	125
Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly Asn	
130	140
Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser Cys	
145	160



Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly Val  
165 170 175  
Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser Phe  
180 185 190  
Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp Leu  
195 200 205  
Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala Met  
210 215 220  
Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg Met  
225 230 235 240  
Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln Gly  
245 250 255  
Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp Leu  
260 265 270  
Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met  
275 280

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1498529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Leu Phe Ser Arg Pro Pro Val Leu Glu Gly Glu Ala Thr Ala Arg  
1 5 10 15  
Ala Ile Arg Leu Ala Arg Phe Ile Asn Thr Pro Leu Tyr Val Val His  
20 25 30  
Val Met Ser Val Asp Ala Met Asp Glu Ile Ala Lys Ala Arg Lys Ser  
35 40 45  
Gly Gln Lys Val Ile Gly Glu Pro Val Val Ser Gly Leu Ile Leu Asp  
50 55 60  
Asp His Trp Leu Trp Asp Pro Asp Phe Thr Ile Ala Ser Lys Tyr Val  
65 70 75 80  
Met Ser Pro Pro Ile Arg Pro Val Gly His Gly Lys Ala Leu Gln Asp  
85 90 95  
Ala Leu Ser Thr Gly Ile Leu Gln Leu Val Gly Thr Asp His Cys Thr  
100 105 110  
Phe Asn Ser Thr Gln Lys Ala Leu Gly Leu Asp Asp Phe Arg Lys Ile  
115 120 125  
Pro Asn Gly Val Asn Gly Leu Glu Glu Arg Met His Leu Ile Trp Asp  
130 135 140  
Thr Met Val Glu Ser Gly Gln Leu Ser Ala Thr Asp Tyr Val Arg Ile  
145 150 155 160  
Thr Ser Thr Glu Cys Ala Arg Ile Phe Asn Ile Tyr Pro Arg Lys Gly  
165 170 175  
Ala Ile Leu Ala Gly Ser Asp Ala Asp Ile Ile Ile Leu Asn Pro Asn  
180 185 190  
Ser Ser Tyr Glu Ile Ser Ser Lys Ser His His Ser Arg Ser Asp Thr  
195 200 205  
Asn Val Tyr Glu Gly Arg Arg Gly Lys Gly Lys Val Glu Val Thr Ile  
210 215 220  
Ala Gly Gly Arg Ile Val Trp Glu Asn Glu Glu Leu Lys Val Val Pro  
225 230 235 240  
Arg Ser Gly Lys Tyr Ile Glu Met Pro Pro Phe Ser Tyr Leu Phe Asp  
245 250 255  
Gly Ile Glu Lys Ser Asp Ala Asn Tyr Leu Ser Ser Leu Arg Ala Pro

260 265 270  
Val Lys Arg Val Arg Thr Glu Ala Thr  
275 280

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```
atcacttact taacatacta agagagttat tagaacttgc aaaaaatggc ttccaaggct 60
ttgattctgt taggtctctt ctacagttct ctcgtcgtct ccgaagtgtc tgccgcaagg 120
maatcgggca tgggtgaagcc agagagtgtg gaaactgtgc aacctgaagg ttatggcggt 180
ggccacggag gacatgggtg tcacggaggg ggaggaggcc acggacatgg aggacacaac 240
ggaggagggg gccacggact tgacggatac rgaggagggt gagggcacta tggaggagggt 300
ggaggacact acggagggtg tggaggagga tacggagggt gaggaggaca ccacggaagg 360
gcggaagca ctcccctaaa gccccctaagc taccagttcc tccggtgacc gtcccctaagc 420
taccagttcc tccggtgacc gtcccctaagc taccagttcc taagctaccc gttcccccg 480
taactgtacc taagctaccc gttcctccag tgaccgtccc taagctaccc cttcctccga 540
tttcagggtc acccatacct ccagtggtag gtcccaatct gccattgcca cctttgccaa 600
ttgtagggtc tattcttcca ccgggaacaa ccccaccagc cacaggaggg aaggactgtc 660
ctccaccgcc agggagcgta aagccaccat cagggggcgg gaaggcgaca tgtccaatag 720
acacgtgaa gttagggtgt tgctgcgtac tgttgggagg tttagtaaag atagggcttg 780
gggatccagc agttaacaaa tgttgtccgt tacttaaagg cctcgttgaa atcgaagccg 840
cggtctgtct ctgcactacc ctcaagctca aagctcttga cctcaatctt tatgtccctg 900
tgctcttca gcttctcctt acctgtggca aaaatccacc tccgggctac acttgttcca 960
tatgataaac tcaactccact tataaaggat gctttggaaa aaaaagtgtg aagagaatgg 1020
cagagctcca atctttcctg tcttggttta ccaaatacat catatcaaat cctatccctt 1080
tgattctttc ctctatcggt cccttatgct tgtatcatta attaatgtgt gcttttttaga 1140
ttaatgattc ttctcttgta ttaaagtatg atttgaaatc cttttttttt ctc
```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu
1 5 10 15
Val Val Ser Glu Val Ser Ala Ala Arg Xaa Ser Gly Met Val Lys Pro
20 25 30
Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly Gly His Gly
35 40 45
Gly His Gly Gly His Gly Gly Gly Gly His Gly His Gly Gly His
50 55 60
Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Xaa Gly Gly Gly Gly
65 70 75 80
His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr
85 90 95
Gly Gly Gly Gly Gly His His Gly Arg Ala Glu Ser Thr Pro Leu Lys
100 105 110
```

Pro Leu Ser Tyr Gln Phe Leu Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

```
Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly
1      5      10      15
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly
20      25      30
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Xaa
35      40      45
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly
50      55      60
Gly Gly Gly Tyr Gly Gly Gly Gly Gly His His Gly Arg Ala Glu Ser
65      70      75      80
Thr Pro Leu Lys Pro Leu Ser Tyr Gln Phe Leu Arg
85      90
```

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

```
Met Ala Val Ala Thr Glu Asp Met Val Val Thr Glu Gly Glu Glu Ala
1      5      10      15
Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp
20      25      30
Xaa Glu Glu Val Glu Gly Thr Met Glu Glu Val Glu Asp Thr Thr Glu
35      40      45
Val Val Glu Glu Asp Thr Glu Val Glu Glu Asp Thr Thr Glu Gly Arg
50      55      60
Lys Ala Leu Pro
65
```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1669
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

accgtgatta ctgattactg tgtaattat ttttattctg cgtacgttac gtaagagaga

```
tattgaggaa tggctgcgaa gaagggttttt ggatcggcgag aagcgagtaa tttggtgacg      120
gagcttcgctc ggagtttttga tgatgggtgtg acacgtgggtt atgaatggag agtgactcag      180
cttaagaaac tgatgattat ttgtgataat catgagcctg agatcgctgc ggctcttcgc      240
gatgatcttg gtaagcctga gcttgaatct tctgtttatg aggtatctct actgagaaac      300
tctatcaagt tggctcttaa gcagctaaag aactggatgg ctccggagaa ggcaaagact      360
tctctaacia cgtttcctgc atccgcggag attgtgtctg agcctcttg tgttgtgcta      420
gtgatctcgg cttggaacta tccttttctg ttgtctattg atcctgttat tgggtgcaatt      480
tctgctggga atgctgttgt tttaaagcca tcagaattgg ctccagcttc gtcagctctg      540
ctcactaagt tactggaaca gtatcttgat ccttctgcgg tgcgagttgt cgaaggagct      600
gttaccgaaa caagtgtctc gctagagcag aagtgggaca agatattcta cacaggtagt      660
tcaaaaatcg gacgtgtcat aatggcggca gctgcgaagc atctcacacc ggttggtcta      720
gagcttggag gaaaatctcc tgtcgttgta gactcggata ccgatttgaa agttaccgtc      780
aggcggataa tcgtaggcaa atgggggttg aacaacggac aggcgtgcgt ttcgccggac      840
tatatcttga cgacaaaaga atatgtcctt aaattgattg atgccatgaa gcttgaattg      900
gagaaatttt atgggaagaa ccctatagag tcgaaagata tgtcacgtat cgtaaactcg      960
aatcactttg atcgcttgtc taagttgita gacgagaagg aagtttctga caaaattgtc     1020
tatggtgggtg aaaaggacag agaaaacttg aaaattgtct cgacaatctt gctcgatgta     1080
ccattagatt ctctgatcat gagtgaagaa atatttggcc ctctccttcc aatcctcacg     1140
cttaacaact tggaagagag ctttgacgtg attcgttctc gacctaagcc acttgcggca     1200
tacttgttta cacataacia gaagttgaaa gagagattca cagcgacagt ctccgctgga     1260
ggcattagtag tcaatgacat agctgttcat cttgcacttc acacattgcc attcggagga     1320
gttggtgaaa gtggaatggg tgcttaccat ggtaaattct catttgatgc ttttagtcac     1380
aagaaggcgg ttctctacag aagccttttc ggtgattcag ccgtcaggta tccgccatac     1440
tcgagaggaa agcttagatt gttaaaagcc cttgtcgaca gcaatatatt cgatttattc     1500
aaagtccttc tcggttttagc ttaaaccgga aaaagaccga ggacacttcc ctttgtacct     1560
tatttacttg ttttattttt caaacatgga cttagttggg taatatgttt tggtttggtg     1620
ttgattctat gaattattgaa gttgataaat aaaagatttt cggttggtt
```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..484
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```
Met Ala Ala Lys Lys Val Phe Gly Ser Ala Glu Ala Ser Asn Leu Val
1           5           10           15
Thr Glu Leu Arg Arg Ser Phe Asp Asp Gly Val Thr Arg Gly Tyr Glu
20           25           30
Trp Arg Val Thr Gln Leu Lys Lys Leu Met Ile Ile Cys Asp Asn His
35           40           45
Glu Pro Glu Ile Val Ala Ala Leu Arg Asp Asp Leu Gly Lys Pro Glu
50           55           60
Leu Glu Ser Ser Val Tyr Glu Val Ser Leu Leu Arg Asn Ser Ile Lys
65           70           75           80
Leu Ala Leu Lys Gln Leu Lys Asn Trp Met Ala Pro Glu Lys Ala Lys
85           90           95
Thr Ser Leu Thr Thr Phe Pro Ala Ser Ala Glu Ile Val Ser Glu Pro
100          105          110
Leu Gly Val Val Leu Val Ile Ser Ala Trp Asn Tyr Pro Phe Leu Leu
115          120          125
Ser Ile Asp Pro Val Ile Gly Ala Ile Ser Ala Gly Asn Ala Val Val
130          135          140
Leu Lys Pro Ser Glu Leu Ala Pro Ala Ser Ser Ala Leu Leu Thr Lys
145          150          155          160
Leu Leu Glu Gln Tyr Leu Asp Pro Ser Ala Val Arg Val Val Glu Gly
165          170          175
```

```

Ala Val Thr Glu Thr Ser Ala Leu Leu Glu Gln Lys Trp Asp Lys Ile
      180      185      190
Phe Tyr Thr Gly Ser Ser Lys Ile Gly Arg Val Ile Met Ala Ala Ala
      195      200      205
Ala Lys His Leu Thr Pro Val Val Leu Glu Leu Gly Gly Lys Ser Pro
      210      215      220
Val Val Val Asp Ser Asp Thr Asp Leu Lys Val Thr Val Arg Arg Ile
      225      230      235      240
Ile Val Gly Lys Trp Gly Cys Asn Asn Gly Gln Ala Cys Val Ser Pro
      245      250      255
Asp Tyr Ile Leu Thr Thr Lys Glu Tyr Ala Pro Lys Leu Ile Asp Ala
      260      265      270
Met Lys Leu Glu Leu Glu Lys Phe Tyr Gly Lys Asn Pro Ile Glu Ser
      275      280      285
Lys Asp Met Ser Arg Ile Val Asn Ser Asn His Phe Asp Arg Leu Ser
      290      295      300
Lys Leu Leu Asp Glu Lys Glu Val Ser Asp Lys Ile Val Tyr Gly Gly
      305      310      315      320
Glu Lys Asp Arg Glu Asn Leu Lys Ile Ala Pro Thr Ile Leu Leu Asp
      325      330      335
Val Pro Leu Asp Ser Leu Ile Met Ser Glu Glu Ile Phe Gly Pro Leu
      340      345      350
Leu Pro Ile Leu Thr Leu Asn Asn Leu Glu Glu Ser Phe Asp Val Ile
      355      360      365
Arg Ser Arg Pro Lys Pro Leu Ala Ala Tyr Leu Phe Thr His Asn Lys
      370      375      380
Lys Leu Lys Glu Arg Phe Thr Ala Thr Val Ser Ala Gly Gly Ile Val
      385      390      395      400
Val Asn Asp Ile Ala Val His Leu Ala Leu His Thr Leu Pro Phe Gly
      405      410      415
Gly Val Gly Glu Ser Gly Met Gly Ala Tyr His Gly Lys Phe Ser Phe
      420      425      430
Asp Ala Phe Ser His Lys Lys Ala Val Leu Tyr Arg Ser Leu Phe Gly
      435      440      445
Asp Ser Ala Val Arg Tyr Pro Pro Tyr Ser Arg Gly Lys Leu Arg Leu
      450      455      460
Leu Lys Ala Leu Val Asp Ser Asn Ile Phe Asp Leu Phe Lys Val Leu
      465      470      475      480
Leu Gly Leu Ala

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1498536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```

Met Ile Ile Cys Asp Asn His Glu Pro Glu Ile Val Ala Ala Leu Arg
 1      5      10      15
Asp Asp Leu Gly Lys Pro Glu Leu Glu Ser Ser Val Tyr Glu Val Ser
      20      25      30
Leu Leu Arg Asn Ser Ile Lys Leu Ala Leu Lys Gln Leu Lys Asn Trp
      35      40      45
Met Ala Pro Glu Lys Ala Lys Thr Ser Leu Thr Thr Phe Pro Ala Ser
      50      55      60
Ala Glu Ile Val Ser Glu Pro Leu Gly Val Val Leu Val Ile Ser Ala

```

65					70					75				80
Trp	Asn	Tyr	Pro	Phe	Leu	Leu	Ser	Ile	Asp	Pro	Val	Ile	Gly	Ala
				85					90					95
Ser	Ala	Gly	Asn	Ala	Val	Val	Leu	Lys	Pro	Ser	Glu	Leu	Ala	Pro
			100					105					110	
Ser	Ser	Ala	Leu	Leu	Thr	Lys	Leu	Leu	Glu	Gln	Tyr	Leu	Asp	Pro
		115				120						125		Ser
Ala	Val	Arg	Val	Val	Glu	Gly	Ala	Val	Thr	Glu	Thr	Ser	Ala	Leu
	130					135					140			Leu
Glu	Gln	Lys	Trp	Asp	Lys	Ile	Phe	Tyr	Thr	Gly	Ser	Ser	Lys	Ile
145					150					155				160
Arg	Val	Ile	Met	Ala	Ala	Ala	Ala	Lys	His	Leu	Thr	Pro	Val	Val
			165						170					175
Glu	Leu	Gly	Gly	Lys	Ser	Pro	Val	Val	Val	Asp	Ser	Asp	Thr	Asp
			180					185					190	Leu
Lys	Val	Thr	Val	Arg	Arg	Ile	Ile	Val	Gly	Lys	Trp	Gly	Cys	Asn
	195					200						205		Asn
Gly	Gln	Ala	Cys	Val	Ser	Pro	Asp	Tyr	Ile	Leu	Thr	Thr	Lys	Glu
210						215					220			Tyr
Ala	Pro	Lys	Leu	Ile	Asp	Ala	Met	Lys	Leu	Glu	Leu	Glu	Lys	Phe
225					230					235				240
Gly	Lys	Asn	Pro	Ile	Glu	Ser	Lys	Asp	Met	Ser	Arg	Ile	Val	Asn
			245						250					255
Asn	His	Phe	Asp	Arg	Leu	Ser	Lys	Leu	Leu	Asp	Glu	Lys	Glu	Val
		260						265					270	Ser
Asp	Lys	Ile	Val	Tyr	Gly	Gly	Glu	Lys	Asp	Arg	Glu	Asn	Leu	Lys
	275					280					285			Ile
Ala	Pro	Thr	Ile	Leu	Leu	Asp	Val	Pro	Leu	Asp	Ser	Leu	Ile	Met
290					295						300			Ser
Glu	Glu	Ile	Phe	Gly	Pro	Leu	Leu	Pro	Ile	Leu	Thr	Leu	Asn	Asn
305				310					315					320
Glu	Glu	Ser	Phe	Asp	Val	Ile	Arg	Ser	Arg	Pro	Lys	Pro	Leu	Ala
			325						330					335
Tyr	Leu	Phe	Thr	His	Asn	Lys	Lys	Leu	Lys	Glu	Arg	Phe	Thr	Ala
		340						345				350		Thr
Val	Ser	Ala	Gly	Gly	Ile	Val	Val	Asn	Asp	Ile	Ala	Val	His	Leu
	355						360					365		Ala
Leu	His	Thr	Leu	Pro	Phe	Gly	Gly	Val	Gly	Glu	Ser	Gly	Met	Gly
	370				375					380				Ala
Tyr	His	Gly	Lys	Phe	Ser	Phe	Asp	Ala	Phe	Ser	His	Lys	Lys	Ala
385					390				395					400
Leu	Tyr	Arg	Ser	Leu	Phe	Gly	Asp	Ser	Ala	Val	Arg	Tyr	Pro	Pro
			405					410					415	Tyr
Ser	Arg	Gly	Lys	Leu	Arg	Leu	Leu	Lys	Ala	Leu	Val	Asp	Ser	Asn
		420					425					430		Ile
Phe	Asp	Leu	Phe	Lys	Val	Leu	Leu	Gly	Leu	Ala				
	435					440								

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met	Ala	Pro	Glu	Lys	Ala	Lys	Thr	Ser	Leu	Thr	Thr	Phe	Pro	Ala	Ser
1				5					10					15	

Ala Glu Ile Val Ser Glu Pro Leu Gly Val Val Leu Val Ile Ser Ala  
20 25 30  
Trp Asn Tyr Pro Phe Leu Leu Ser Ile Asp Pro Val Ile Gly Ala Ile  
35 40 45  
Ser Ala Gly Asn Ala Val Val Leu Lys Pro Ser Glu Leu Ala Pro Ala  
50 55 60  
Ser Ser Ala Leu Leu Thr Lys Leu Leu Glu Gln Tyr Leu Asp Pro Ser  
65 70 75 80  
Ala Val Arg Val Val Glu Gly Ala Val Thr Glu Thr Ser Ala Leu Leu  
85 90 95  
Glu Gln Lys Trp Asp Lys Ile Phe Tyr Thr Gly Ser Ser Lys Ile Gly  
100 105 110  
Arg Val Ile Met Ala Ala Ala Lys His Leu Thr Pro Val Val Leu  
115 120 125  
Glu Leu Gly Gly Lys Ser Pro Val Val Val Asp Ser Asp Thr Asp Leu  
130 135 140  
Lys Val Thr Val Arg Arg Ile Ile Val Gly Lys Trp Gly Cys Asn Asn  
145 150 155 160  
Gly Gln Ala Cys Val Ser Pro Asp Tyr Ile Leu Thr Thr Lys Glu Tyr  
165 170 175  
Ala Pro Lys Leu Ile Asp Ala Met Lys Leu Glu Leu Glu Lys Phe Tyr  
180 185 190  
Gly Lys Asn Pro Ile Glu Ser Lys Asp Met Ser Arg Ile Val Asn Ser  
195 200 205  
Asn His Phe Asp Arg Leu Ser Lys Leu Leu Asp Glu Lys Glu Val Ser  
210 215 220  
Asp Lys Ile Val Tyr Gly Gly Glu Lys Asp Arg Glu Asn Leu Lys Ile  
225 230 235 240  
Ala Pro Thr Ile Leu Leu Asp Val Pro Leu Asp Ser Leu Ile Met Ser  
245 250 255  
Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Leu Thr Leu Asn Asn Leu  
260 265 270  
Glu Glu Ser Phe Asp Val Ile Arg Ser Arg Pro Lys Pro Leu Ala Ala  
275 280 285  
Tyr Leu Phe Thr His Asn Lys Lys Leu Lys Glu Arg Phe Thr Ala Thr  
290 295 300  
Val Ser Ala Gly Gly Ile Val Val Asn Asp Ile Ala Val His Leu Ala  
305 310 315 320  
Leu His Thr Leu Pro Phe Gly Gly Val Gly Glu Ser Gly Met Gly Ala  
325 330 335  
Tyr His Gly Lys Phe Ser Phe Asp Ala Phe Ser His Lys Lys Ala Val  
340 345 350  
Leu Tyr Arg Ser Leu Phe Gly Asp Ser Ala Val Arg Tyr Pro Pro Tyr  
355 360 365  
Ser Arg Gly Lys Leu Arg Leu Leu Lys Ala Leu Val Asp Ser Asn Ile  
370 375 380  
Phe Asp Leu Phe Lys Val Leu Leu Gly Leu Ala  
385 390 395

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

aggaattcgc acaagaccat tacystagaa catcmtaatc acaaaaatca aatccatctc

```
ccactcttct agcatcttga agcttaaatc tcagccgtcc gatcatgccg atcagaaaaca 120
tcgccattgg ccgtccagat gaagcaaccc gtcccgatgc cttaaaggcg gcgttggtcg 180
agttcatttc aactttgatc tttgtcgtcg ccggttcagg ctctggcatg gctttcaaca 240
agctcactga aaacggagcc accactcctt ctggtctcgt agctgctgca ctggctcatg 300
cctttggact cttcgtcgtc gtctcagttg gtgccaacat ctctggtgga cacgttaacc 360
ctgccgtcac tttcggtgct ttcattggtg gtaacatcac tctctccgtt ggtatcctct 420
actggattgc tcagcttctc ggctccgtcg tcgcttgccct catccttaaa ttcgccaccg 480
gtggcttggc tgtgccggct tttggtctct ctgctggagt aggagtgttg aacgctttcg 540
ttttcgagat cgtgatgaca ttcgggcttg tttacaccgt ctacgtaca gccattgacc 600
ctggaacat taccttgctg ctacaagacc aagtcggtgg attacaagcc acacgtgaca 660
atggcaagac ctggattacg gttcagcctg ttgaaggagc gtttgtcgtc aatctcggcg 720
accacggcca ttttttgagc aatgggaggt tcaagaatgc tgatcatcag gccgtggtga 780
actctaactc gagcagatta tccatagcca cgttccagaa ccccgcgccg gatgccacag 840
tgtatccact gaaagtaaga gaaggagaga aggcaatatt ggaggagcca atcacgtttg 900
ccgagatgta taagagaaaag atgggaagag atttggagct tgctcgctc aagaagctgg 960
ctaaagagga gcgtgaccac aaagaagttg ccaagcctgt cgaccaaata ttcgcttaga 1020
atctctgtgt tcttgcttac ttgttgttgc gttggttctg ttttgtacgt tggtagttaa 1080
aattatgcta ggctcgggtg gttttgtgtt c
```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1498543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```
Met Pro Ile Arg Asn Ile Ala Ile Gly Arg Pro Asp Glu Ala Thr Arg
1           5           10           15
Pro Asp Ala Leu Lys Ala Ala Leu Ala Glu Phe Ile Ser Thr Leu Ile
20           25           30
Phe Val Val Ala Gly Ser Gly Ser Gly Met Ala Phe Asn Lys Leu Thr
35           40           45
Glu Asn Gly Ala Thr Thr Pro Ser Gly Leu Val Ala Ala Leu Ala
50           55           60
His Ala Phe Gly Leu Phe Val Ala Val Ser Val Gly Ala Asn Ile Ser
65           70           75           80
Gly Gly His Val Asn Pro Ala Val Thr Phe Gly Ala Phe Ile Gly Gly
85           90           95
Asn Ile Thr Leu Leu Arg Gly Ile Leu Tyr Trp Ile Ala Gln Leu Leu
100          105          110
Gly Ser Val Val Ala Cys Leu Ile Leu Lys Phe Ala Thr Gly Gly Leu
115          120          125
Ala Val Pro Ala Phe Gly Leu Ser Ala Gly Val Gly Val Leu Asn Ala
130          135          140
Phe Val Phe Glu Ile Val Met Thr Phe Gly Leu Val Tyr Thr Val Tyr
145          150          155          160
Ala Thr Ala Ile Asp Pro Gly Thr Ile Thr Leu Leu Leu Gln Asp Gln
165          170          175
Val Gly Gly Leu Gln Ala Thr Arg Asp Asn Gly Lys Thr Trp Ile Thr
180          185          190
Val Gln Pro Val Glu Gly Ala Phe Val Val Asn Leu Gly Asp His Gly
195          200          205
His Phe Leu Ser Asn Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val
210          215          220
Val Asn Ser Asn Ser Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro
225          230          235          240
Ala Pro Asp Ala Thr Val Tyr Pro Leu Lys Val Arg Glu Gly Glu Lys
```



	245		250		255										
Ala	Ile	Leu	Glu	Pro	Ile	Thr	Phe	Ala	Glu	Met	Tyr	Lys	Arg	Lys	
	260		265		270										
Met	Gly	Arg	Asp	Leu	Glu	Leu	Ala	Arg	Leu	Lys	Lys	Leu	Ala	Lys	Glu
	275		280		285										
Glu	Arg	Asp	His	Lys	Glu	Val	Ala	Lys	Pro	Val	Asp	Gln	Ile	Phe	Ala
	290		295		300										

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1498544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Met	Ala	Phe	Asn	Lys	Leu	Thr	Glu	Asn	Gly	Ala	Thr	Thr	Pro	Ser	Gly
1			5						10					15	
Leu	Val	Ala	Ala	Ala	Leu	Ala	His	Ala	Phe	Gly	Leu	Phe	Val	Ala	Val
		20						25					30		
Ser	Val	Gly	Ala	Asn	Ile	Ser	Gly	Gly	His	Val	Asn	Pro	Ala	Val	Thr
		35					40					45			
Phe	Gly	Ala	Phe	Ile	Gly	Gly	Asn	Ile	Thr	Leu	Leu	Arg	Gly	Ile	Leu
	50					55				60					
Tyr	Trp	Ile	Ala	Gln	Leu	Leu	Gly	Ser	Val	Val	Ala	Cys	Leu	Ile	Leu
65				70					75					80	
Lys	Phe	Ala	Thr	Gly	Gly	Leu	Ala	Val	Pro	Ala	Phe	Gly	Leu	Ser	Ala
			85						90					95	
Gly	Val	Gly	Val	Leu	Asn	Ala	Phe	Val	Phe	Glu	Ile	Val	Met	Thr	Phe
		100						105					110		
Gly	Leu	Val	Tyr	Thr	Val	Tyr	Ala	Thr	Ala	Ile	Asp	Pro	Gly	Thr	Ile
	115						120					125			
Thr	Leu	Leu	Gln	Asp	Gln	Val	Gly	Gly	Leu	Gln	Ala	Thr	Arg	Asp	
	130				135					140					
Asn	Gly	Lys	Thr	Trp	Ile	Thr	Val	Gln	Pro	Val	Glu	Gly	Ala	Phe	Val
145				150						155				160	
Val	Asn	Leu	Gly	Asp	His	Gly	His	Phe	Leu	Ser	Asn	Gly	Arg	Phe	Lys
			165					170						175	
Asn	Ala	Asp	His	Gln	Ala	Val	Val	Asn	Ser	Asn	Ser	Ser	Arg	Leu	Ser
		180						185					190		
Ile	Ala	Thr	Phe	Gln	Asn	Pro	Ala	Pro	Asp	Ala	Thr	Val	Tyr	Pro	Leu
	195					200						205			
Lys	Val	Arg	Glu	Gly	Glu	Lys	Ala	Ile	Leu	Glu	Glu	Pro	Ile	Thr	Phe
	210					215					220				
Ala	Glu	Met	Tyr	Lys	Arg	Lys	Met	Gly	Arg	Asp	Leu	Glu	Leu	Ala	Arg
225				230						235				240	
Leu	Lys	Lys	Leu	Ala	Lys	Glu	Glu	Arg	Asp	His	Lys	Glu	Val	Ala	Lys
			245					250						255	
Pro	Val	Asp	Gln	Ile	Phe	Ala									
			260												

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..154  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498545  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:  
Met Thr Phe Gly Leu Val Tyr Thr Val Tyr Ala Thr Ala Ile Asp Pro  
1                  5                  10                  15  
Gly Thr Ile Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala  
                  20                  25                  30  
Thr Arg Asp Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly  
                  35                  40                  45  
Ala Phe Val Val Asn Leu Gly Asp His Gly His Phe Leu Ser Asn Gly  
                  50                  55                  60  
Arg Phe Lys Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Ser Ser  
65                  70                  75                  80  
Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val  
                  85                  90                  95  
Tyr Pro Leu Lys Val Arg Glu Gly Glu Lys Ala Ile Leu Glu Glu Pro  
                  100                  105                  110  
Ile Thr Phe Ala Glu Met Tyr Lys Arg Lys Met Gly Arg Asp Leu Glu  
                  115                  120                  125  
Leu Ala Arg Leu Lys Lys Leu Ala Lys Glu Glu Arg Asp His Lys Glu  
                  130                  135                  140  
Val Ala Lys Pro Val Asp Gln Ile Phe Ala  
145                  150

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..382
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

aaacacaaac	aaaactcata	ttttcaatct	ccaggtgctt	tacaccaaca	gagtcgcaag	60
aaaacaaaaa	ccaaactcgg	atttagtttg	acagaagaag	gaatcgagag	tcgggtatgc	120
attatcctaa	caacagaacc	gaattcgtcg	gagctccagc	cccaaccg	tatcaaaagg	180
agcagttgtc	accggagcaa	gagctttcag	ttattgtctc	tgctttgcaa	cacgtgatct	240
caggggaaaa	cgaaacggcg	csgtgtcagg	gtttttccag	tgacagcaca	gtgataagcg	300
cggaatgcs	tcggttgat	tcagacactt	gtcaagtctg	taggatcgaa	ggatgtctcg	360
gctgtaacta ctttttcgcg cc						

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Lys His Lys	Gln Asn Ser	Tyr Phe Gln	Ser Pro Gly	Ala Leu His	Gln
1          5			10		15
Gln Ser Arg	Lys Lys Thr	Lys Thr Lys	Leu Gly Phe	Ser Leu Thr	Glu
20			25		30

Glu Gly Ile Glu Ser Arg Val Cys Ile Ile Leu Thr Thr Glu Pro Asn  
35 40 45  
Ser Ser Glu Leu Gln Pro Gln Pro Gly Ile Lys Arg Ser Ser Cys His  
50 55 60  
Arg Ser Lys Ser Phe Gln Leu Leu Ser Leu Leu Cys Asn Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1498552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Met His Tyr Pro Asn Asn Arg Thr Glu Phe Val Gly Ala Pro Ala Pro  
1 5 10 15  
Thr Arg Tyr Gln Lys Glu Gln Leu Ser Pro Glu Gln Glu Leu Ser Val  
20 25 30  
Ile Val Ser Ala Leu Gln His Val Ile Ser Gly Glu Asn Glu Thr Ala  
35 40 45  
Xaa Cys Gln Gly Phe Ser Ser Asp Ser Thr Val Ile Ser Ala Gly Met  
50 55 60  
Xaa Arg Leu Asp Ser Asp Thr Cys Gln Val Cys Arg Ile Glu Gly Cys  
65 70 75 80  
Leu Gly Cys Asn Tyr Phe Phe Ala  
85

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1396

(D) OTHER INFORMATION: / Ceres Seq. ID 1498553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

attattattt ccagagaagc ttctcttttg attctctcgc tctctctttc ttcacgcgct	60
cttcgagctt cgatgggttg gaattattctg gtgaccgggtg gtgctgggta catcggaagt	120
cacacggttc ttcagcttct tctcggaggc tataacaccg tcgttataga caacctcgac	180
aattcctctc tcgtttcgat ccaacgcgtc aaggatctcg ccggagatca tggacaaaat	240
ctcaccgtcc accagggtga ccttcgcgat aaaccgcac ttgagaaggt tttctccgaa	300
acaaagtttg atgcagtaat gcattttgct ggattgaaag cagttggtga gagcgtggcg	360
aaaccacttc tgtattataa caataacttg attgcgacta ttacactttt ggaagtaatg	420
gctgcacacg gatgtaaaaa gcttgtattt tcttcgtccg ctactgtgta tggctggcca	480
aaggaggttc cttgtacaga agagtctccc ctgtctggaa tgagtcctta tggacggaca	540
aagctgttca tagaggacat ttgccgtgat gtacaacgtg gtgaccccta atggagaatc	600
ataatgctga ggtactttta ccctgtggga gctcacccta gcggtcgcat tgggtaggat	660
ccttgtggga ctccaaataa tctcatgcct tatgtccagc aagtcgttgt tgggaggcta	720
cctaacctaa aaatttatgg aactgactat accactaaag atggcactgg tgtacgagac	780
tatattcatg ttgttgatct agcagatggc catatatattg cgcttcaaaa gctagacgat	840
actgaaatag gttgtgaggt atacaacctg ggaaccggaa aaggaacaac agtgttgagg	900
atgggttgatg catttgagaa agcttctgga atgaaaatcc cactggtgaa ggttggaagg	960
agaccaggtg atgcagaaac cgtctatgcy tcaacagaaa aagctgaacg cgaactaaac	1020
tgggaaggcaa attttggaat cgaagaaatg ttagggatc agtggaactg ggcaagcaac	1080
aatcctttcg gttacggttc ttcaccaaac tcaacataac gaagctaacg tatccaacac	1140

```
tccattcttt ttcttttggg tcgtcggctg ttatctttat gttacacact caggtttttag 1200
ctttaaagcc taaacacagt gagggagaag ttacttctct attcatatat ctgctttctc 1260
cttttgtaat ttatatatat ctatatatag cataggttta acttaagcgg atccttttgt 1320
tttttgatt tgtataatct ctcttaggaa attaattgtc atgggattat atttgatta 1380
aatagaaact gaattc
```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

Ile	Ile	Ile	Ser	Arg	Glu	Ala	Ser	Leu	Leu	Ile	Leu	Ser	Leu	Ser	Leu
1			5						10				15		
Ser	Ser	Ser	Pro	Leu	Arg	Ala	Ser	Met	Val	Gly	Asn	Ile	Leu	Val	Thr
			20					25				30			
Gly	Gly	Ala	Gly	Tyr	Ile	Gly	Ser	His	Thr	Val	Leu	Gln	Leu	Leu	Leu
		35					40					45			
Gly	Gly	Tyr	Asn	Thr	Val	Val	Ile	Asp	Asn	Leu	Asp	Asn	Ser	Ser	Leu
	50					55				60					
Val	Ser	Ile	Gln	Arg	Val	Lys	Asp	Leu	Ala	Gly	Asp	His	Gly	Gln	Asn
65					70				75					80	
Leu	Thr	Val	His	Gln	Val	Asp	Leu	Arg	Asp	Lys	Pro	Ala	Leu	Glu	Lys
			85						90					95	
Val	Phe	Ser	Glu	Thr	Lys	Phe	Asp	Ala	Val	Met	His	Phe	Ala	Gly	Leu
			100					105					110		
Lys	Ala	Val	Gly	Glu	Ser	Val	Ala	Lys	Pro	Leu	Leu	Tyr	Tyr	Asn	Asn
		115					120					125			
Asn	Leu	Ile	Ala	Thr	Ile	Thr	Leu	Leu	Glu	Val	Met	Ala	Ala	His	Gly
	130					135					140				
Cys	Lys	Lys	Leu	Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Trp	Pro
145					150				155					160	
Lys	Glu	Val	Pro	Cys	Thr	Glu	Glu	Ser	Pro	Leu	Ser	Gly	Met	Ser	Pro
			165						170					175	
Tyr	Gly	Arg	Thr	Lys	Leu	Phe	Ile	Glu	Asp	Ile	Cys	Arg	Asp	Val	Gln
			180					185					190		
Arg	Gly	Asp	Pro	Glu	Trp	Arg	Ile	Ile	Met	Leu	Arg	Tyr	Phe	Asn	Pro
		195					200					205			
Val	Gly	Ala	His	Pro	Ser	Gly	Arg	Ile	Gly	Glu	Asp	Pro	Cys	Gly	Thr
	210					215					220				
Pro	Asn	Asn	Leu	Met	Pro	Tyr	Val	Gln	Gln	Val	Val	Val	Gly	Arg	Leu
225					230				235					240	
Pro	Asn	Leu	Lys	Ile	Tyr	Gly	Thr	Asp	Tyr	Thr	Thr	Lys	Asp	Gly	Thr
			245						250					255	
Gly	Val	Arg	Asp	Tyr	Ile	His	Val	Val	Asp	Leu	Ala	Asp	Gly	His	Ile
		260					265						270		
Phe	Ala	Leu	Gln	Lys	Leu	Asp	Asp	Thr	Glu	Ile	Gly	Cys	Glu	Val	Tyr
		275					280					285			
Asn	Leu	Gly	Thr	Gly	Lys	Gly	Thr	Thr	Val	Leu	Glu	Met	Val	Asp	Ala
	290					295					300				
Phe	Glu	Lys	Ala	Ser	Gly	Met	Lys	Ile	Pro	Leu	Val	Lys	Val	Gly	Arg
305					310					315				320	
Arg	Pro	Gly	Asp	Ala	Glu	Thr	Val	Tyr	Ala	Ser	Thr	Glu	Lys	Ala	Glu
			325						330					335	
Arg	Glu	Leu	Asn	Trp	Lys	Ala	Asn	Phe	Gly	Ile	Glu	Glu	Met	Cys	Arg
		340						345					350		

Asp Gln Trp Asn Trp Ala Ser Asn Asn Pro Phe Gly Tyr Gly Ser Ser  
355 360 365  
Pro Asn Ser Thr  
370

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

Met Val Gly Asn Ile Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly Ser  
1 5 10 15  
His Thr Val Leu Gln Leu Leu Leu Gly Gly Tyr Asn Thr Val Val Ile  
20 25 30  
Asp Asn Leu Asp Asn Ser Ser Leu Val Ser Ile Gln Arg Val Lys Asp  
35 40 45  
Leu Ala Gly Asp His Gly Gln Asn Leu Thr Val His Gln Val Asp Leu  
50 55 60  
Arg Asp Lys Pro Ala Leu Glu Lys Val Phe Ser Glu Thr Lys Phe Asp  
65 70 75 80  
Ala Val Met His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala  
85 90 95  
Lys Pro Leu Leu Tyr Tyr Asn Asn Asn Leu Ile Ala Thr Ile Thr Leu  
100 105 110  
Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser Ser  
115 120 125  
Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro Cys Thr Glu Glu  
130 135 140  
Ser Pro Leu Ser Gly Met Ser Pro Tyr Gly Arg Thr Lys Leu Phe Ile  
145 150 155 160  
Glu Asp Ile Cys Arg Asp Val Gln Arg Gly Asp Pro Glu Trp Arg Ile  
165 170 175  
Ile Met Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly Arg  
180 185 190  
Ile Gly Glu Asp Pro Cys Gly Thr Pro Asn Asn Leu Met Pro Tyr Val  
195 200 205  
Gln Gln Val Val Val Gly Arg Leu Pro Asn Leu Lys Ile Tyr Gly Thr  
210 215 220  
Asp Tyr Thr Thr Lys Asp Gly Thr Gly Val Arg Asp Tyr Ile His Val  
225 230 235 240  
Val Asp Leu Ala Asp Gly His Ile Phe Ala Leu Gln Lys Leu Asp Asp  
245 250 255  
Thr Glu Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly Thr  
260 265 270  
Thr Val Leu Glu Met Val Asp Ala Phe Glu Lys Ala Ser Gly Met Lys  
275 280 285  
Ile Pro Leu Val Lys Val Gly Arg Arg Pro Gly Asp Ala Glu Thr Val  
290 295 300  
Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Asn Trp Lys Ala Asn  
305 310 315 320  
Phe Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser Asn  
325 330 335  
Asn Pro Phe Gly Tyr Gly Ser Ser Pro Asn Ser Thr  
340 345

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

Met	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	Gly	Glu	Ser	Val	Ala	Lys	Pro
1			5						10					15	
Leu	Leu	Tyr	Tyr	Asn	Asn	Asn	Leu	Ile	Ala	Thr	Ile	Thr	Leu	Leu	Glu
			20					25					30		
Val	Met	Ala	Ala	His	Gly	Cys	Lys	Lys	Leu	Val	Phe	Ser	Ser	Ser	Ala
			35				40					45			
Thr	Val	Tyr	Gly	Trp	Pro	Lys	Glu	Val	Pro	Cys	Thr	Glu	Glu	Ser	Pro
	50					55					60				
Leu	Ser	Gly	Met	Ser	Pro	Tyr	Gly	Arg	Thr	Lys	Leu	Phe	Ile	Glu	Asp
65					70					75				80	
Ile	Cys	Arg	Asp	Val	Gln	Arg	Gly	Asp	Pro	Glu	Trp	Arg	Ile	Ile	Met
			85					90					95		
Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	His	Pro	Ser	Gly	Arg	Ile	Gly
			100					105					110		
Glu	Asp	Pro	Cys	Gly	Thr	Pro	Asn	Asn	Leu	Met	Pro	Tyr	Val	Gln	Gln
	115					120					125				
Val	Val	Val	Gly	Arg	Leu	Pro	Asn	Leu	Lys	Ile	Tyr	Gly	Thr	Asp	Tyr
	130					135					140				
Thr	Thr	Lys	Asp	Gly	Thr	Gly	Val	Arg	Asp	Tyr	Ile	His	Val	Val	Asp
145					150					155				160	
Leu	Ala	Asp	Gly	His	Ile	Phe	Ala	Leu	Gln	Lys	Leu	Asp	Asp	Thr	Glu
			165					170						175	
Ile	Gly	Cys	Glu	Val	Tyr	Asn	Leu	Gly	Thr	Gly	Lys	Gly	Thr	Thr	Val
		180					185					190			
Leu	Glu	Met	Val	Asp	Ala	Phe	Glu	Lys	Ala	Ser	Gly	Met	Lys	Ile	Pro
	195						200					205			
Leu	Val	Lys	Val	Gly	Arg	Arg	Pro	Gly	Asp	Ala	Glu	Thr	Val	Tyr	Ala
	210				215						220				
Ser	Thr	Glu	Lys	Ala	Glu	Arg	Glu	Leu	Asn	Trp	Lys	Ala	Asn	Phe	Gly
225				230						235				240	
Ile	Glu	Glu	Met	Cys	Arg	Asp	Gln	Trp	Asn	Trp	Ala	Ser	Asn	Asn	Pro
			245					250						255	
Phe	Gly	Tyr	Gly	Ser	Ser	Pro	Asn	Ser	Thr						
			260					265							

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..558
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

rysgtcgctt	attgccggga	gattaccggg	aagaacagat	aacgagataa	agaactattg	60
gaacacacat	atacgaagaa	agcttataaa	cagagggatt	gatccaacga	gtcacagacc	120
aatccaagaa	tcatacagctt	ctcaagattc	taaacctaca	caactagaac	cagttacgag	180
taacaccatt	aatatctcat	tcacttctgc	tccaaaggtc	gaaacgttcc	atgaaagtat	240

```
aagctttccg ggaaaatcag aaaaaatctc aatgcttacg ttcaaagaag aaaaagatga 300
gtgtccagtt caagaaaagt tcccagatgt gaatcttgag ctcaaatca gtcttcctga 360
tgatgttgat cgtcttcaag gacatggaaa gtcaacaacg ccacgttggt tcaagtgcag 420
cttagggatg ataaacggca tggagtgcag atgcggaaga atgagatgcg atgtagtcgg 480
aggtagcagc aaggggagtg acatgagcaa tggatttgat tttttagggt tggcaaagaa 540
agagaccact tctctttt
```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1498562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```
Xaa Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
1      5      10      15
Lys Asn Tyr Trp Asn Thr His Ile Arg Lys Leu Ile Asn Arg Gly
20     25     30
Ile Asp Pro Thr Ser His Arg Pro Ile Gln Glu Ser Ser Ala Ser Gln
35     40     45
Asp Ser Lys Pro Thr Gln Leu Glu Pro Val Thr Ser Asn Thr Ile Asn
50     55     60
Ile Ser Phe Thr Ser Ala Pro Lys Val Glu Thr Phe His Glu Ser Ile
65     70     75     80
Ser Phe Pro Gly Lys Ser Glu Lys Ile Ser Met Leu Thr Phe Lys Glu
85     90     95
Glu Lys Asp Glu Cys Pro Val Gln Glu Lys Phe Pro Asp Leu Asn Leu
100    105    110
Glu Leu Arg Ile Ser Leu Pro Asp Asp Val Asp Arg Leu Gln Gly His
115    120    125
Gly Lys Ser Thr Thr Pro Arg Cys Phe Lys Cys Ser Leu Gly Met Ile
130    135    140
Asn Gly Met Glu Cys Arg Cys Gly Arg Met Arg Cys Asp Val Val Gly
145    150    155    160
Gly Ser Ser Lys Gly Ser Asp Met Ser Asn Gly Phe Asp Phe Leu Gly
165    170    175
Leu Ala Lys Lys Glu Thr Thr Ser Leu
180    185
```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```
Met Leu Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln Glu Lys
1      5      10      15
Phe Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp Asp Val
20     25     30
Asp Arg Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys Phe Lys
35     40     45
Cys Ser Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly Arg Met
```

50	55	60
Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met Ser Asn		
65	70	75
Gly Phe Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser Leu		
85	90	95

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..802
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

aacacatttc aagcatttga ttaatcaaag acaaagaaaa cgaaaatggt ggcaatat	60
cagaaagctt ttgctcacc accggaagaa ctcaacagtc cggttctca tttctccggc	120
aaaactccta aacttcccgg cgaaactctc tccgacttcc tctctcatca ccaaaacaat	180
gctttctcta tgaacttcgg cgactccgcc gtcttagctt acgctcgcca agaaacctct	240
cttcgtcaaa ggttggttctg tggactagat gggatctact gtatgtttct agggagattg	300
aataatctct gtacattgaa tcgacaatac gggttatctg ggaagaagat tgagaaggag	360
cccaagttct tgaagaatgg tgatgctggt atggtgaaga tgactccaac caagcccatg	420
gttggtgaga ctttctctga gtaccacca cttggacgtt tcgctgtgca gggacatgag	480
gcagactggt gcagtcggtg ttatcaagag tgttgacaag aaggacccaa ccggagccaa	540
ggttaccaag gctgccgtca agaagggtgc gaagtgaacc atcctcaaaa ctctatctgc	600
cgcaggtgaa tcaaaggaca gtgttagttt tattacaata gtttggtatt tggtcgcgtg	660
tctgtgttct tgtttcgttt tctccccgtc agagcgttgt tctcgtaatt gggttcttga	720
tcggaggtgg cggatctaca cacacattct tcctgttttt tgctttttat ttgttttctc	780
attttgaact gtttaaatg ag	

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Met Leu Ala Ile Phe Gln Lys Ala Phe Ala His Pro Pro Glu Glu Leu	
1	5
Asn Ser Pro Ala Ser His Phe Ser Gly Lys Thr Pro Lys Leu Pro Gly	10
20	25
Glu Thr Leu Ser Asp Phe Leu Ser His His Gln Asn Asn Ala Phe Ser	30
35	40
Met Asn Phe Gly Asp Ser Ala Val Leu Ala Tyr Ala Arg Gln Glu Thr	45
50	55
Ser Leu Arg Gln Arg Leu Phe Cys Gly Leu Asp Gly Ile Tyr Cys Met	60
65	70
Phe Leu Gly Arg Leu Asn Asn Leu Cys Thr Leu Asn Arg Gln Tyr Gly	75
85	90
Leu Ser Gly Lys Lys Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly	95
100	105
Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu	110
115	120
Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Gln Gly His	125
130	135
	140



Glu Ala Asp Cys Cys Ser Arg Cys Tyr Gln Glu Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Asn Phe Gly Asp Ser Ala Val Leu Ala Tyr Ala Arg Gln Glu Thr  
1 5 10 15  
Ser Leu Arg Gln Arg Leu Phe Cys Gly Leu Asp Gly Ile Tyr Cys Met  
20 25 30  
Phe Leu Gly Arg Leu Asn Asn Leu Cys Thr Leu Asn Arg Gln Tyr Gly  
35 40 45  
Leu Ser Gly Lys Lys Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly  
50 55 60  
Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu  
65 70 75 80  
Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Gln Gly His  
85 90 95  
Glu Ala Asp Cys Cys Ser Arg Cys Tyr Gln Glu Cys  
100 105

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

aaaccaagtt ttcttctaag ctgtatttga aagggtatat atttcacaca ccaaacagat 60  
cagaagcnaa aaggtataata tataatggcg gatttgaggg acgaaaaagg taaccaaatc 120  
catctaaccg acacacaggg aaaccaatt gtcgacctga ctgatgagca cggttaacccc 180  
atgtacctaa cgggtgttgt tagctccact cctcagcagt aaggagagna ctaccagcga 240  
cattgcagag caccctacta gcaccgttgg agaaacacat ccggcagctg ctccagctgg 300  
tgctggtgct gccaccgctg ccaactgcgac aggagtctct gctggtactg gagcaaccac 360  
cacagggcag caacaccatg ggtcgcttga agagcatctt cgtcgggtctg gaagttcatc 420  
tagctctagc tcggaggatg acgggcaagg agggaggagg aagaagagca taaaggagaa 480  
aattaaagag aagctcaaag cgcacaacga attccaagaa actgattgtt ggat

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Ala Asp Leu Arg Asp Glu Lys Gly Asn Pro Ile His Leu Thr Asp  
1 5 10 15  
Thr Gln Gly Asn Pro Ile Val Asp Leu Thr Asp Glu His Gly Asn Pro  
20 25 30  
Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln Gln  
35 40 45

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1498569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

Met Gly Arg Leu Lys Ser Ile Phe Val Gly Leu Glu Val His Leu Ala  
1 5 10 15  
Leu Ala Arg Arg Met Thr Gly Lys Glu Gly Gly Arg Arg Ala  
20 25 30

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1548

(D) OTHER INFORMATION: / Ceres Seq. ID 1498574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

aaaattagg	ctttatctta	tcttcgcgat	tctctcatct	cctccctcta	aaattctccg	60
jcgacacagt	tcaccgaaa	tcgtagacga	aatcagattc	tttctcttta	gtatgaaaca	120
atgaatttga	tctcaagaac	attgacaaga	gcagtgtctt	cgctactata	ccactcaaaa	180
gcagcgaagc	tccccactca	aaaatggata	atctcgcagc	aaatccgtgt	tttctccgcc	240
acagtcata	gcggtggagg	aaagaaacct	ctggcaaaaag	tatccgtgaa	accaccgcta	300
aatgtagcga	cggagaaaaga	atcgactccg	ccgaagacaa	ttgagtacaa	accggaaatt	360
tcaaaactgga	tcaacctaat	cggattcggt	gaacaaccag	ttcaattcgg	tccttgctcc	420
gatggaaaat	tctgggctgg	aacagttatt	tctcagcggt	ctgggtcaaa	atcatctaatt	480
ttctggattc	cgattatatt	cgaaggagat	ttagctaaaa	ttgcagttca	acatgtaaaag	540
aaagaagatc	ggattcatgt	ttccgggaag	ctgtttattg	attcgccctcc	tccaaatgtg	600
acatattctc	aatccaatgt	tcaggttatg	gttcagaatc	ttaacttcgt	acaagctgct	660
acttctacga	ctaagacgat	ctcaccacct	gaaaaagaag	ttaccagcat	caagaaaaag	720
cccgaagat	ccaaaaagggt	taaagtcata	gatgaagaaa	cctctaattc	ttggaagcat	780
cttattgaaa	atcctaaaaga	gtggttgat	caccgtggga	ataaagctaa	cggattggta	840
aagccaggac	atcccgattt	caagatgaag	gttggtgggt	tgtccctgtg	gctcagcaca	900
gctcctgatt	gggctttgct	aaaactcgaa	gagcttaagt	ttgatgtctt	agtcctaaa	960
ggaaacatca	aactgaatca	acttaaagga	gaggaatctt	ggaaggattt	ggttcagaac	1020
ccagacaaat	ggtagacaa	cagatcagat	aagacaaacg	tgaaataccc	tgacttcaag	1080
cataaagaga	ctggtgaagc	actgtggatg	accaattctc	ctatttgggt	actgtcaaag	1140
ttaccacctc	taaagaagaa	ccaagaaaga	cctctcatgt	ctaataaagt	ctcgcagctt	1200
gagcttgacg	ttgaagtacc	taaaggaaat	ctgaaacagc	ttaaaagaga	ggaaatttgg	1260
aagaacttgg	ttgagaaccc	cagtaaatgg	tgggataaca	gattagacaa	gagaaacctt	1320
aaaggccctg	actttaagca	taaggagacc	gggtgaagcac	tgtggatagg	tgattctccg	1380
acttgggcgc	tgtcaaagtt	accacctcta	aagaaaaacc	aagaaagacc	tgtcatggcc	1440
taagcttctc	tagcagcctt	atgttaattt	tggcccccac	tatgtaaaaa	ggccctatga	1500
ctttattatc	cagtcttata	caaagagaat	tgctatagta	tcagtgcc		

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 440 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..440  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498575  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Met	Asn	Leu	Ile	Ser	Arg	Thr	Leu	Thr	Arg	Ala	Val	Ser	Ser	Ser	Leu
1			5					10					15		
Tyr	His	Ser	Lys	Ala	Ala	Lys	Leu	Pro	Thr	Gln	Lys	Trp	Ile	Ile	Ser
			20					25					30		
Gln	Gln	Ile	Arg	Val	Phe	Ser	Ala	Thr	Val	Ile	Ser	Gly	Gly	Gly	Lys
			35					40					45		
Lys	Pro	Leu	Ala	Lys	Val	Ser	Val	Lys	Pro	Pro	Leu	Asn	Val	Ala	Thr
	50					55					60				
Glu	Lys	Glu	Ser	Thr	Pro	Lys	Thr	Ile	Glu	Tyr	Lys	Pro	Glu	Ile	
65					70				75					80	
Ser	Asn	Trp	Ile	Asn	Leu	Ile	Gly	Phe	Val	Glu	Gln	Pro	Val	Gln	Phe
				85					90					95	
Gly	Pro	Cys	Ser	Asp	Gly	Lys	Phe	Trp	Ala	Gly	Thr	Val	Ile	Ser	Gln
			100					105					110		
Arg	Ser	Gly	Ser	Lys	Ser	Ser	Asn	Phe	Trp	Ile	Pro	Ile	Ile	Phe	Glu
			115				120					125			
Gly	Asp	Leu	Ala	Lys	Ile	Ala	Val	Gln	His	Val	Lys	Lys	Glu	Asp	Arg
	130					135					140				
Ile	His	Val	Ser	Gly	Lys	Leu	Phe	Ile	Asp	Ser	Pro	Pro	Pro	Asn	Val
145					150					155				160	
Thr	Tyr	Ser	Gln	Ser	Asn	Val	Gln	Val	Met	Val	Gln	Asn	Leu	Asn	Phe
				165					170					175	
Val	Gln	Ala	Ala	Thr	Ser	Thr	Thr	Lys	Thr	Ile	Ser	Pro	Pro	Glu	Lys
			180					185					190		
Glu	Val	Thr	Ser	Ile	Lys	Lys	Lys	Pro	Ala	Arg	Ser	Lys	Lys	Val	Lys
		195					200					205			
Val	Ile	Asp	Glu	Glu	Thr	Ser	Asn	Ser	Trp	Lys	His	Leu	Ile	Glu	Asn
	210					215					220				
Pro	Lys	Glu	Trp	Leu	Asp	His	Arg	Gly	Asn	Lys	Ala	Asn	Gly	Leu	Val
225					230					235				240	
Lys	Pro	Gly	His	Pro	Asp	Phe	Lys	Met	Lys	Val	Gly	Gly	Leu	Ser	Leu
			245						250					255	
Trp	Leu	Ser	Thr	Ala	Pro	Asp	Trp	Ala	Leu	Leu	Lys	Leu	Glu	Glu	Leu
			260					265					270		
Lys	Phe	Asp	Val	Leu	Val	Pro	Lys	Gly	Asn	Ile	Lys	Leu	Asn	Gln	Leu
		275					280					285			
Lys	Gly	Glu	Glu	Ser	Trp	Lys	Asp	Leu	Val	Gln	Asn	Pro	Asp	Lys	Trp
	290					295					300				
Leu	Asp	Asn	Arg	Ser	Asp	Lys	Thr	Asn	Val	Lys	Tyr	Pro	Asp	Phe	Lys
305					310					315				320	
His	Lys	Glu	Thr	Gly	Glu	Ala	Leu	Trp	Met	Thr	Asn	Ser	Pro	Ile	Trp
			325						330					335	
Val	Leu	Ser	Lys	Leu	Pro	Pro	Leu	Lys	Lys	Asn	Gln	Glu	Arg	Pro	Leu
			340					345					350		
Met	Ser	Asn	Lys	Val	Ser	Gln	Leu	Glu	Leu	Asp	Val	Glu	Val	Pro	Lys
		355					360					365			
Gly	Asn	Leu	Lys	Gln	Leu	Lys	Arg	Glu	Glu	Ile	Trp	Lys	Asn	Leu	Val
	370					375					380				
Glu	Asn	Pro	Ser	Lys	Trp	Trp	Asp	Asn	Arg	Leu	Asp	Lys	Arg	Asn	Pro
385					390					395					400

Lys Gly Pro Asp Phe Lys His Lys Glu Thr Gly Glu Ala Leu Trp Ile  
405 410 415  
Gly Asp Ser Pro Thr Trp Ala Leu Ser Lys Leu Pro Pro Leu Lys Lys  
420 425 430  
Asn Gln Glu Arg Pro Val Met Ala  
435 440

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1498576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Val Gln Asn Leu Asn Phe Val Gln Ala Ala Thr Ser Thr Lys  
1 5 10 15  
Thr Ile Ser Pro Glu Lys Glu Val Thr Ser Ile Lys Lys Lys Pro  
20 25 30  
Ala Arg Ser Lys Lys Val Lys Val Ile Asp Glu Glu Thr Ser Asn Ser  
35 40 45  
Trp Lys His Leu Ile Glu Asn Pro Lys Glu Trp Leu Asp His Arg Gly  
50 55 60  
Asn Lys Ala Asn Gly Leu Val Lys Pro Gly His Pro Asp Phe Lys Met  
65 70 75 80  
Lys Val Gly Gly Leu Ser Leu Trp Leu Ser Thr Ala Pro Asp Trp Ala  
85 90 95  
Leu Leu Lys Leu Glu Glu Leu Lys Phe Asp Val Leu Val Pro Lys Gly  
100 105 110  
Asn Ile Lys Leu Asn Gln Leu Lys Gly Glu Glu Ser Trp Lys Asp Leu  
115 120 125  
Val Gln Asn Pro Asp Lys Trp Leu Asp Asn Arg Ser Asp Lys Thr Asn  
130 135 140  
Val Lys Tyr Pro Asp Phe Lys His Lys Glu Thr Gly Glu Ala Leu Trp  
145 150 155 160  
Met Thr Asn Ser Pro Ile Trp Val Leu Ser Lys Leu Pro Pro Leu Lys  
165 170 175  
Lys Asn Gln Glu Arg Pro Leu Met Ser Asn Lys Val Ser Gln Leu Glu  
180 185 190  
Leu Asp Val Glu Val Pro Lys Gly Asn Leu Lys Gln Leu Lys Arg Glu  
195 200 205  
Glu Ile Trp Lys Asn Leu Val Glu Asn Pro Ser Lys Trp Trp Asp Asn  
210 215 220  
Arg Leu Asp Lys Arg Asn Pro Lys Gly Pro Asp Phe Lys His Lys Glu  
225 230 235 240  
Thr Gly Glu Ala Leu Trp Ile Gly Asp Ser Pro Thr Trp Ala Leu Ser  
245 250 255  
Lys Leu Pro Pro Leu Lys Lys Asn Gln Glu Arg Pro Val Met Ala  
260 265 270

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1498577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

atcaacttca gatactttca ccagcaacac aagttatttt caaaagatga tgccaaattc	60
tagatcggcg acaataactc cgacgacaga atcaaccacc acgacaacaa caacaacaac	120
gactctaacg acgtcgtatt ggtgttacag ttgtacacga ttcacacagc tttgggaaga	180
tcaagacgca aacgctggag tcttatgtcc ttattgcaac ggtggattca tcgaagagat	240
tgaagattct tctaattcca ccgtcgcggc gattccggct tcgactccgg aagttagatc	300
ggttgaggaa acacatagat ctataattag acgtcgtaga tctaatacgcc ggacgtcctt	360
taatccggta atcgtcttac acggcggagg aggaggagga gccggtgaga gagttgagaa	420
cgaagaaggt gacggagcta ctagagaacg acgagcttat gagtyttatt acgatgatgg	480
atctggttca ggtctaagac ctcttcctga ttctgtatct gagatcttga ttggatctgg	540
attcgaacgg ttacttgaac aattgagtca gatcgaagcg tcaggtaacg gaatcggtag	600
atctggg	

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1498578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Ser	Thr	Ser	Asp	Pro	Phe	Thr	Ser	Asn	Thr	Ser	Tyr	Phe	Gln	Lys	Met
1				5				10						15	
Met	Pro	Asn	Ser	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Thr	Thr	Glu	Ser	Thr
				20				25					30		
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Thr	Ser	Tyr	Trp	Cys	
				35			40					45			
Tyr	Ser	Cys	Thr	Arg	Phe	Ile	Ser	Val	Trp	Glu	Asp	Gln	Asp	Ala	Asn
						55				60					
Ala	Gly	Val	Leu	Cys	Pro	Tyr	Cys	Asn	Gly	Gly	Phe	Ile	Glu	Glu	Ile
65					70				75						80
Glu	Asp	Ser	Ser	Asn	Ser	Thr	Val	Ala	Ala	Ile	Pro	Ala	Ser	Thr	Pro
				85					90					95	
Glu	Val	Arg	Ser	Val	Glu	Glu	Thr	His	Arg	Ser	Ile	Ile	Arg	Arg	Arg
				100				105					110		
Arg	Ser	Asn	Arg	Arg	Thr	Ser	Phe	Asn	Pro	Val	Ile	Val	Leu	His	Gly
				115				120					125		
Gly	Gly	Gly	Gly	Gly	Ala	Gly	Glu	Arg	Val	Glu	Asn	Glu	Glu	Gly	Asp
				130				135				140			
Gly	Ala	Thr	Arg	Glu	Arg	Arg	Ala	Tyr	Glu	Xaa	Tyr	Tyr	Asp	Asp	Gly
145					150					155					160
Ser	Gly	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Asp	Ser	Val	Ser	Glu	Ile	Leu
				165					170					175	
Ile	Gly	Ser	Gly	Phe	Glu	Arg	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Ile	Glu
				180					185					190	
Ala	Ser	Gly	Asn	Gly	Ile	Gly	Arg	Ser	Gly						
				195				200							

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1498579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met	Pro	Asn	Ser	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Thr	Thr	Glu	Ser
1		5						10					15	
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Thr	Ser	Tyr
		20						25				30		Trp
Cys	Tyr	Ser	Cys	Thr	Arg	Phe	Ile	Ser	Val	Trp	Glu	Asp	Gln	Asp
		35					40				45			Ala
Asn	Ala	Gly	Val	Leu	Cys	Pro	Tyr	Cys	Asn	Gly	Gly	Phe	Ile	Glu
	50					55					60			Glu
Ile	Glu	Asp	Ser	Ser	Asn	Ser	Thr	Val	Ala	Ala	Ile	Pro	Ala	Ser
65					70					75				80
Pro	Glu	Val	Arg	Ser	Val	Glu	Glu	Thr	His	Arg	Ser	Ile	Ile	Arg
			85						90					95
Arg	Arg	Ser	Asn	Arg	Arg	Thr	Ser	Phe	Asn	Pro	Val	Ile	Val	Leu
			100					105					110	His
Gly	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Glu	Arg	Val	Glu	Asn	Glu	Glu
		115					120					125		Gly
Asp	Gly	Ala	Thr	Arg	Glu	Arg	Arg	Ala	Tyr	Glu	Xaa	Tyr	Tyr	Asp
	130					135					140			Asp
Gly	Ser	Gly	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Asp	Ser	Val	Ser	Glu
145					150					155				160
Leu	Ile	Gly	Ser	Gly	Phe	Glu	Arg	Leu	Leu	Glu	Gln	Leu	Ser	Gln
				165				170						175
Glu	Ala	Ser	Gly	Asn	Gly	Ile	Gly	Arg	Ser	Gly				
				180				185						

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Met	Pro	Asn	Ser	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Thr	Thr	Glu	Ser	Thr
1		5						10					15		
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Thr	Ser	Tyr	Trp	Cys
		20						25				30			
Tyr	Ser	Cys	Thr	Arg	Phe	Ile	Ser	Val	Trp	Glu	Asp	Gln	Asp	Ala	Asn
		35					40				45				
Ala	Gly	Val	Leu	Cys	Pro	Tyr	Cys	Asn	Gly	Gly	Phe	Ile	Glu	Glu	Ile
	50					55					60				
Glu	Asp	Ser	Ser	Asn	Ser	Thr	Val	Ala	Ala	Ile	Pro	Ala	Ser	Thr	Pro
65				70						75					80
Glu	Val	Arg	Ser	Val	Glu	Glu	Thr	His	Arg	Ser	Ile	Ile	Arg	Arg	Arg
			85					90						95	
Arg	Ser	Asn	Arg	Arg	Thr	Ser	Phe	Asn	Pro	Val	Ile	Val	Leu	His	Gly
		100						105					110		
Gly	Gly	Gly	Gly	Gly	Ala	Gly	Glu	Arg	Val	Glu	Asn	Glu	Glu	Gly	Asp
		115					120					125			
Gly	Ala	Thr	Arg	Glu	Arg	Arg	Ala	Tyr	Glu	Xaa	Tyr	Tyr	Asp	Asp	Gly
	130					135					140				
Ser	Gly	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Asp	Ser	Val	Ser	Glu	Ile	Leu
145				150						155					160
Ile	Gly	Ser	Gly	Phe	Glu	Arg	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Ile	Glu
				165				170						175	

Ala Ser Gly Asn Gly Ile Gly Arg Ser Gly  
180 185

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

```
aaagctcaga tatctgaata actcgcttgc gtgcctctct ctctctaaaa gcccatctct 60
ttctcctcct cctcctccat tgaagaagaa acctaccttc gtaatatatt ctcaattacg 120
atcatggtga atgttaaagg gtcaacccaaa aaatcgaatc ttgatcgatt ccttcattgc 180
ataacaccct tagtgccacc ccaatctctc cccaagacgg agattagaac cctaaatcga 240
ttgtggcatc catgggagag acaaaagggt gagtttttca ggttgagtga tttgtgggat 300
tgttatgatg aatggagcgc ttatggagct agcggttccta ttcatgttac caacggagaa 360
tctcttggtc aatactatgt tccttatctc tctgccatcc agattttcac ctctcattcc 420
tccttgatcc gcttaaggga agagtctgaa gatggggaat gtgagggtag agatccggtt 480
agcgattcag gtagcgatga gagtgctctc gaggaaggac ttgagaacaa cacgctcttg 540
catccaagtg atcgtttggg ttatctttat ctccaatact ttgagagatc agctccttat 600
accagagttc ctctgatgga taagatcaat gaattggctc aaagataccc gggattgatg 660
tcgttgagaa gcgttgatct ttctccagct agttggatgt cagtagcatg gtacccgatt 720
taccatatac caatgggaag aaccattaaa gacttatcca cgtgtttcct cacttatcac 780
actctttcct cttcttttca agatatggaa ccggaagaaa atggtgggga caaggagaga 840
gtgcggaggg aagggaaga tataactctg ctcccatttg ggatggctac ttacaagatg 900
caaggcgatg tttggctttc gcaggaccac gatgatcaag agagattggc ttcgctttac 960
agtgttgceg attcttggct taaacagctc aggtccaac atcatgactt caactacttc 1020
tgcaatatgt caatgactca tcgtggctaa acctcggttg gatgacacca tgatgtttgc 1080
ttgtttcctc atatatagtc taattcttgc tttgttctgg aaccgcttgc gttttgtaaa 1140
acgcaatgga gcgattcgct ttgcagtgtt ttgggttagaa tagcgttttg agtcttctaa 1200
cctttgagag agtatatgtc gtatatagag ttttgttgct tgttgaaaca gagtacaatt 1260
gttgttgctt gttaaaaaca gagtgattgt ttcttataag ttg
```

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

```
Met Val Asn Val Lys Gly Ser Thr Lys Lys Ser Asn Leu Asp Arg Phe
1      5      10      15
Leu His Cys Ile Thr Pro Leu Val Pro Pro Gln Ser Leu Pro Lys Thr
20      25      30
Glu Ile Arg Thr Leu Asn Arg Leu Trp His Pro Trp Glu Arg Gln Lys
35      40      45
Val Glu Phe Phe Arg Leu Ser Asp Leu Trp Asp Cys Tyr Asp Glu Trp
50      55      60
Ser Ala Tyr Gly Ala Ser Val Pro Ile His Val Thr Asn Gly Glu Ser
65      70      75      80
Leu Val Gln Tyr Tyr Val Pro Tyr Leu Ser Ala Ile Gln Ile Phe Thr
85      90      95
Ser His Ser Ser Leu Ile Arg Leu Arg Glu Glu Ser Glu Asp Gly Glu
```

Val Arg Val Thr Met Ser Gln Leu Gly Asp Leu Leu Arg Glu Ser Glu



1				5					10					15
Asp	Gly	Thr	Arg	Ser	Glu	Arg	Thr	Met	Met	Ser	Leu	Leu	Glu	Glu
			20					25				30		
Asp	Gln	Ile	Asn	Gly	Gly	Asp	Arg	Thr	Met	Ser	Lys	Trp	Thr	Thr
		35					40					45		
Lys	Gln	Arg	Leu	Arg	Phe	Asp	Trp	Val	Gly	Cys	Xaa	Gly	Lys	Pro
	50					55					60			
Thr	Leu	Arg	Leu	Arg	Gln	Ala	Glu	Thr	Pro	Ile	Val	Val	Asp	Asp
65					70					75				80
Asp	Asp	Glu	Glu	Glu	Ser	Gln	Asn	Gln	Val	Val	Asp	Phe	Ser	Asp
				85					90					95
Gly	Thr	Gly	Thr	Glu	Leu	Asp	Cys	Leu	Arg	Arg	Arg	Val	Arg	Gly
			100					105					110	
Pro	Gln	Gln	Pro	Thr	Gln	Ser	Asn	Leu	Ser	Arg	Cys	Phe	Asn	Val
		115					120					125		
Leu	Trp	Trp	Phe	Met	Phe	Trp	Gly	His	Val	Gln	Pro	Leu	Ile	Asn
	130						135					140		

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met	Ser	Gln	Leu	Gly	Asp	Leu	Leu	Arg	Glu	Ser	Glu	Asp	Gly	Thr	Arg
1				5					10					15	
Ser	Glu	Arg	Thr	Met	Met	Met	Ser	Leu	Leu	Glu	Glu	Asp	Gln	Ile	Asn
			20					25					30		
Gly	Gly	Asp	Arg	Thr	Met	Ser	Lys	Trp	Thr	Thr	Leu	Lys	Gln	Arg	Leu
		35					40					45			
Arg	Phe	Asp	Trp	Val	Gly	Cys	Xaa	Gly	Lys	Pro	Leu	Thr	Leu	Arg	Leu
	50					55					60				
Arg	Gln	Ala	Glu	Thr	Pro	Ile	Val	Val	Asp	Asp	Asp	Asp	Asp	Glu	Glu
65					70					75					80
Glu	Ser	Gln	Asn	Gln	Val	Val	Asp	Phe	Ser	Asp	Pro	Gly	Thr	Gly	Thr
			85						90					95	
Glu	Leu	Asp	Cys	Leu	Arg	Arg	Arg	Val	Arg	Gly	Leu	Pro	Gln	Gln	Pro
			100					105					110		
Thr	Gln	Ser	Asn	Leu	Ser	Arg	Cys	Phe	Asn	Val	Val	Leu	Trp	Trp	Phe
		115					120					125			
Met	Phe	Trp	Gly	His	Val	Gln	Pro	Leu	Ile	Asn	Asn				
	130						135					140			

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Met Met Met Ser Leu Leu Glu Glu Asp Gln Ile Asn Gly Gly Asp Arg  
1 5 10 15  
Thr Met Ser Lys Trp Thr Thr Leu Lys Gln Arg Leu Arg Phe Asp Trp  
20 25 30  
Val Gly Cys Xaa Gly Lys Pro Leu Thr Leu Arg Leu Arg Gln Ala Glu  
35 40 45  
Thr Pro Ile Val Val Asp Asp Asp Asp Asp Glu Glu Glu Ser Gln Asn  
50 55 60  
Gln Val Val Asp Phe Ser Asp Pro Gly Thr Gly Thr Glu Leu Asp Cys  
65 70 75 80  
Leu Arg Arg Arg Val Arg Gly Leu Pro Gln Gln Pro Thr Gln Ser Asn  
85 90 95  
Leu Ser Arg Cys Phe Asn Val Val Leu Trp Trp Phe Met Phe Trp Gly  
100 105 110  
His Val Gln Pro Leu Ile Asn Asn  
115 120

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

cattaagagc	aaaaactagt	tttgctttca	tttttttttg	gtaggaaagg	gttaattata	60
cgtaacacag	aaacaaaaac	aattctcttt	tcctctagaa	aaagagatta	aaaaaaaaat	120
ggaggggagg	ttattgacgg	tggttggtctg	cctcgtctct	acggtggcga	tcgtgaacgc	180
cggtgacctt	tacttcttcc	atacatggaa	cgtgacttac	ggaactgcct	cacctctcgg	240
tgttcctcaa	aaggtgattc	tcatcaacgg	tcaattccct	ggtcctaacc	ttactcaaac	300
ctctaacaac	aacgtcgtca	tcaatgtctt	caaccaccta	gacgaacctt	tcctcttgac	360
ctggagtggg	attcagcatc	ggaagaactg	ctggcaagat	ggtgtggctg	gaacttcatg	420
ccccatccca	gctggacaga	actttactta	ccatttccaa	cctaaggacc	agattggttc	480
ctacttctat	tacccaacca	cttctctcca	ccgctttgct	ggtggttttg	gtggtctccg	540
tgtaacacag	cgtctcctaa	ttcccgttcc	ttatgctgat	cctgaagatg	actacactgt	600
ccttctcggg	gactggtaca	cagctggcca	cactgctctc	aagaacttcc	ttgacagttg	660
acgcaccctt	ggattgccta	acggtgtttt	gatcaatgga	aagtctggaa	aggttgaggg	720
aaagaacgag	cctttgttca	caatgaagcc	tggaagact	tacaagtaca	ggctctgcaa	780
tggttggttc	aagtctacac	ttactttcag	gatccagaac	cacaagatga	agctcgtgga	840
gatggaagga	tcccatgtta	ttcagaacga	ctatgactct	ctcgatgtcc	atgttgacca	900
gtgcttttca	gttcttggtg	ctgctaacca	agcagctaag	gattactaca	tggttgcatc	960
gactagggtc	ctcaagaagg	agttgagcac	cgtgggtgtg	atccggtatg	agggagacaa	1020
cgttcagggt	tcaactgagc	tacccaaggc	tcctgttgga	tgggcttggt	ctttgaacca	1080
gttcagggtc	ttcaggtgga	accttacctc	taacgctgca	aggcctaacc	cccaaggctc	1140
ataccattac	ggaaagatca	atattaccgc	tagcatcaag	cttgtcaact	ctaaaagtgt	1200
gggtgacggt	aaagtccggt	ttggtttcaa	tggtgtatca	cacgttgaca	ccgagactcc	1260
tttgaagctt	gctgagtact	tccaaatgtc	agagaagggt	ttcaagtaca	atgtgatcaa	1320
ggacgagcct	gcagccaaaa	tcacagcatt	gactgtacaa	cctaattgtt	tcaacatcac	1380
tttccgtacc	tttgtagaga	tcatttttcga	gaaccacgag	aagaccatgc	agtcattcca	1440
tttggttggt	tactccttct	tcgctgtcgc	ttctgagcca	gggaggtgga	cgctgaaaa	1500
gagagagaac	tacaacttgc	tcgatgcggt	tagcagacac	accgtgcaag	tctaccccaa	1560
gtcttggtca	gctactcctt	tgacattcga	caacgccggt	atgtggaaca	tcaggtctga	1620
gaacttgag	aggaaatacc	taggcgagca	attgtatgtc	agtgttctat	caccggagaa	1680
atcgctaagg	gacgagtaca	acatccccct	caacacaaac	ctctgtggca	tcgtcaaggg	1740
cttgccatta	cctgcacact	actoctaaat	caatattcaa	ttactacta	ctctacaaag	1800
tggggtgcaa	tattaaatta	actaattaac	cctttcctag	attttaagt	taatttgtaa	1860
acccttctt	tcataacta	tcattaaacc	ataatcatat	accaagtttt	gctttcatt	

(2) INFORMATION FOR SEQ ID NO:533:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 341 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..341  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498600  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Met	Lys	Pro	Gly	Lys	Thr	Tyr	Lys	Tyr	Arg	Leu	Cys	Asn	Val	Gly	Phe
1				5					10					15	
Lys	Ser	Thr	Leu	Asn	Phe	Arg	Ile	Gln	Asn	His	Lys	Met	Lys	Leu	Val
			20					25					30		
Glu	Met	Glu	Gly	Ser	His	Val	Ile	Gln	Asn	Asp	Tyr	Asp	Ser	Leu	Asp
			35				40					45			
Val	His	Val	Gly	Gln	Cys	Phe	Ser	Val	Leu	Val	Thr	Ala	Asn	Gln	Ala
	50					55					60				
Ala	Lys	Asp	Tyr	Tyr	Met	Val	Ala	Ser	Thr	Arg	Phe	Leu	Lys	Lys	Glu
65					70					75					80
Leu	Ser	Thr	Val	Gly	Val	Ile	Arg	Tyr	Glu	Gly	Ser	Asn	Val	Gln	Ala
				85					90					95	
Ser	Thr	Glu	Leu	Pro	Lys	Ala	Pro	Val	Gly	Trp	Ala	Trp	Ser	Leu	Asn
			100					105					110		
Gln	Phe	Arg	Ser	Phe	Arg	Trp	Asn	Leu	Thr	Ser	Asn	Ala	Ala	Arg	Pro
	115					120						125			
Asn	Pro	Gln	Gly	Ser	Tyr	His	Tyr	Gly	Lys	Ile	Asn	Ile	Thr	Arg	Ser
	130					135					140				
Ile	Lys	Leu	Val	Asn	Ser	Lys	Ser	Val	Val	Asp	Gly	Lys	Val	Arg	Phe
145					150					155					160
Gly	Phe	Asn	Gly	Val	Ser	His	Val	Asp	Thr	Glu	Thr	Pro	Leu	Lys	Leu
			165					170						175	
Ala	Glu	Tyr	Phe	Gln	Met	Ser	Glu	Lys	Val	Phe	Lys	Tyr	Asn	Val	Ile
			180					185					190		
Lys	Asp	Glu	Pro	Ala	Ala	Lys	Ile	Thr	Ala	Leu	Thr	Val	Gln	Pro	Asn
	195					200							205		
Val	Leu	Asn	Ile	Thr	Phe	Arg	Thr	Phe	Val	Glu	Ile	Ile	Phe	Glu	Asn
	210					215					220				
His	Glu	Lys	Thr	Met	Gln	Ser	Phe	His	Leu	Asp	Gly	Tyr	Ser	Phe	Phe
225					230					235					240
Ala	Val	Ala	Ser	Glu	Pro	Gly	Arg	Trp	Thr	Pro	Glu	Lys	Arg	Glu	Asn
			245						250					255	
Tyr	Asn	Leu	Leu	Asp	Ala	Val	Ser	Arg	His	Thr	Val	Gln	Val	Tyr	Pro
		260						265					270		
Lys	Ser	Trp	Ser	Ala	Ile	Leu	Leu	Thr	Phe	Asp	Asn	Ala	Gly	Met	Trp
	275					280						285			
Asn	Ile	Arg	Ser	Glu	Asn	Leu	Glu	Arg	Lys	Tyr	Leu	Gly	Glu	Gln	Leu
	290					295					300				
Tyr	Val	Ser	Val	Leu	Ser	Pro	Glu	Lys	Ser	Leu	Arg	Asp	Glu	Tyr	Asn
305					310					315					320
Ile	Pro	Leu	Asn	Thr	Asn	Leu	Cys	Gly	Ile	Val	Lys	Gly	Leu	Pro	Leu
			325						330					335	
Pro	Ala	His	Tyr	Ser											
			340												

- (2) INFORMATION FOR SEQ ID NO:534:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 313 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1498601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met	Lys	Leu	Val	Glu	Met	Glu	Gly	Ser	His	Val	Ile	Gln	Asn	Asp	Tyr
1				5				10						15	
Asp	Ser	Leu	Asp	Val	His	Val	Gly	Gln	Cys	Phe	Ser	Val	Leu	Val	Thr
			20					25					30		
Ala	Asn	Gln	Ala	Ala	Lys	Asp	Tyr	Met	Val	Ala	Ser	Thr	Arg	Phe	
		35					40				45				
Leu	Lys	Lys	Glu	Leu	Ser	Thr	Val	Gly	Val	Ile	Arg	Tyr	Glu	Gly	Ser
	50					55				60					
Asn	Val	Gln	Ala	Ser	Thr	Glu	Leu	Pro	Lys	Ala	Pro	Val	Gly	Trp	Ala
65					70					75					80
Trp	Ser	Leu	Asn	Gln	Phe	Arg	Ser	Phe	Arg	Trp	Asn	Leu	Thr	Ser	Asn
			85					90					95		
Ala	Ala	Arg	Pro	Asn	Pro	Gln	Gly	Ser	Tyr	His	Tyr	Gly	Lys	Ile	Asn
			100					105					110		
Ile	Thr	Arg	Ser	Ile	Lys	Leu	Val	Asn	Ser	Lys	Ser	Val	Val	Asp	Gly
		115				120						125			
Lys	Val	Arg	Phe	Gly	Phe	Asn	Gly	Val	Ser	His	Val	Asp	Thr	Glu	Thr
	130					135					140				
Pro	Leu	Lys	Leu	Ala	Glu	Tyr	Phe	Gln	Met	Ser	Glu	Lys	Val	Phe	Lys
145				150						155				160	
Tyr	Asn	Val	Ile	Lys	Asp	Glu	Pro	Ala	Ala	Lys	Ile	Thr	Ala	Leu	Thr
			165					170						175	
Val	Gln	Pro	Asn	Val	Leu	Asn	Ile	Thr	Phe	Arg	Thr	Phe	Val	Glu	Ile
		180						185					190		
Ile	Phe	Glu	Asn	His	Glu	Lys	Thr	Met	Gln	Ser	Phe	His	Leu	Asp	Gly
	195					200						205			
Tyr	Ser	Phe	Phe	Ala	Val	Ala	Ser	Glu	Pro	Gly	Arg	Trp	Thr	Pro	Glu
	210					215					220				
Lys	Arg	Glu	Asn	Tyr	Asn	Leu	Leu	Asp	Ala	Val	Ser	Arg	His	Thr	Val
225				230						235				240	
Gln	Val	Tyr	Pro	Lys	Ser	Trp	Ser	Ala	Ile	Leu	Leu	Thr	Phe	Asp	Asn
			245					250						255	
Ala	Gly	Met	Trp	Asn	Ile	Arg	Ser	Glu	Asn	Leu	Glu	Arg	Lys	Tyr	Leu
		260						265					270		
Gly	Glu	Gln	Leu	Tyr	Val	Ser	Val	Leu	Ser	Pro	Glu	Lys	Ser	Leu	Arg
		275						280				285			
Asp	Glu	Tyr	Asn	Ile	Pro	Leu	Asn	Thr	Asn	Leu	Cys	Gly	Ile	Val	Lys
	290					295					300				
Gly	Leu	Pro	Leu	Pro	Ala	His	Tyr	Ser							
305					310										

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Met	Glu	Gly	Ser	His	Val	Ile	Gln	Asn	Asp	Tyr	Asp	Ser	Leu	Asp	Val
1				5				10					15		
His	Val	Gly	Gln	Cys	Phe	Ser	Val	Leu	Val	Thr	Ala	Asn	Gln	Ala	Ala

(A1) SEQUENCE EDITORIAL CHANGES						
aaaatatcaa	aacacgagac	agattttgatt	ccattttttat	tactgttact	atcatccaaa	60
accttggtat	ttgtagccat	gagtccttgtt	tcagatctca	tcaaccttaa	cctctcagac	120
tccactgaca	aaatcattgc	tgaatacata	tgggttggtg	gtcttggaat	ggacatgaga	180
agcaaagcca	ggactctacc	tggaccagct	actgaccctt	cgcagctacc	aaagtggaac	240
tatgatggtt	caagcacagg	acaagctcct	ggtgaagaca	gtgaagtcac	cttatagtta	300
ataatccttc	ttctctgata	tttaataaag	ttctctctca	tgtgtttttt	tttcgattct	360
tgtttactaa	tcttttgtgt	gtttgtatat	ctttgttttag	ccctcaagcc	atattcaaag	420
atccttttccg	tagaggaaac	aacattcttg	tcattgtcga	tgcgtacact	cccgcggtg	480
aaccaatccc	gactaacaaa	agacacgctg	cggctaaggt	ctttagcaac	cctgatgttg	540
cagctgaagt	gccatggtat	ggtattgagc	aagaatacac	tttactccag	aaagatgtga	600
ggtggcctgt	ttggttgcct	attggcggtt	atcccgccc	tcaggaccg	tactattgcg	660
gtattggagc	agacaaatct	tttggcagag	atgttgttga	ttctcactac	aaggcctgtt	720

```
tatacgcctgg aatcaacatt agtggcatca atggagaagt catgccgggt cagtggggagt 780
tccaggtcgg tccagctgtt ggtatctcgg ctgctgatga aatttgggtc gctcgtttaca 840
ttttggagag gatcacagag attgctggtg tagtggtatc ttttgacccg aaaccgattc 900
ccggtgactg gaacggtgct ggtgctcact gcaactacag taccaagtca atgagggaag 960
aaggcggtta cgagatcatc aagaaagcaa tcgataaatt gggactgaga cacaaagarc 1020
rcattgctgc ttacsgtgaa ggcaatgagc gtcgtctcac aggacaccac gagactgctg 1080
acatcaacac tttccttttg ggtgttgcca accgtggagc atcgatccga gtaggacgtg 1140
atacgagaaa agaagggaaa ggatactttg aggacaggag gccagcttcg aacatggatc 1200
cttacattgt tacttccatg attgcagaga ccaccatcct ctggaatcct tgatgatcat 1260
cagatcaaga aaaaatcttg aatgtcactc aaatttgtgt ttcttgcaag attcaaagtt 1320
tgtgttctct atcaagcaat gtcttaggat aagtcaaaga tttgctctgc ttattctgct 1380
ttttatttac ttcacatcct attgaaaaca tttctgtgta ttatttatga ataaacatta 1440
tctt
```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

```
Met Cys Asp Ala Tyr Thr Pro Ala Gly Glu Pro Ile Pro Thr Asn Lys
1          5          10          15
Arg His Ala Ala Lys Val Phe Ser Asn Pro Asp Val Ala Ala Glu
20          25          30
Val Pro Trp Tyr Gly Ile Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp
35          40          45
Val Arg Trp Pro Val Gly Trp Pro Ile Gly Gly Tyr Pro Gly Pro Gln
50          55          60
Gly Pro Tyr Tyr Cys Gly Ile Gly Ala Asp Lys Ser Phe Gly Arg Asp
65          70          75          80
Val Val Asp Ser His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile
85          90          95
Ser Gly Ile Asn Gly Glu Val Met Pro Gly Gln Trp Glu Phe Gln Val
100          105          110
Gly Pro Ala Val Gly Ile Ser Ala Ala Asp Glu Ile Trp Val Ala Arg
115          120          125
Tyr Ile Leu Glu Arg Ile Thr Glu Ile Ala Gly Val Val Val Ser Phe
130          135          140
Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly Ala Gly Ala His Cys
145          150          155          160
Asn Tyr Ser Thr Lys Ser Met Arg Glu Glu Gly Gly Tyr Glu Ile Ile
165          170          175
Lys Lys Ala Ile Asp Lys Leu Gly Leu Arg His Lys Xaa Xaa Ile Ala
180          185          190
Ala Tyr Xaa Glu Gly Asn Glu Arg Arg Leu Thr Gly His His Glu Thr
195          200          205
Ala Asp Ile Asn Thr Phe Leu Trp Gly Val Ala Asn Arg Gly Ala Ser
210          215          220
Ile Arg Val Gly Arg Asp Thr Glu Lys Glu Gly Lys Gly Tyr Phe Glu
225          230          235          240
Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr Ser Met
245          250          255
Ile Ala Glu Thr Thr Ile Leu Trp Asn Pro
260          265
```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..163  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498612  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:  
Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ala Val Gly Ile Ser  
1 5 10 15  
Ala Ala Asp Glu Ile Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile Thr  
20 25 30  
Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro Gly  
35 40 45  
Asp Trp Asn Gly Ala Gly Ala His Cys Asn Tyr Ser Thr Lys Ser Met  
50 55 60  
Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys Leu  
65 70 75 80  
Gly Leu Arg His Lys Xaa Xaa Ile Ala Ala Tyr Xaa Glu Gly Asn Glu  
85 90 95  
Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe Leu  
100 105 110  
Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp Thr  
115 120 125  
Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser Asn  
130 135 140  
Met Asp Pro Tyr Ile Val Thr Ser Met Ile Ala Glu Thr Thr Ile Leu  
145 150 155 160  
Trp Asn Pro

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1772 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1772  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

agcacatgac	cgagtccgcg	tcagaaaaag	gggccaactg	ctccgtagcc	gccaagaatc	60
tcgcagatcc	cgattcctct	tgatcatcgt	cttcttctac	caaaattggt	gcgcgacaat	120
ggagaaatac	aacagtttat	cagattttct	caaggagtgc	tacatcccta	cgtacgtcct	180
ctcggcggaa	acagaagagg	aggaggagga	ggagagtcgt	cctacacctg	cgagccccgt	240
ccttgtcttc	atcaactcca	aaagcggtag	tcagttgggt	ggcgaactca	ttctcaccta	300
ccgatctctt	ctcaatcaca	atcaggtctt	tgatctcgac	caggagactc	cagataaagt	360
gctccgcaga	atctatctta	acctggagag	gctcaaagat	gatgattccg	ctcgtcagat	420
tggggagaaa	ttaaaaatca	ttgttgacag	agggtgatgg	actgctgggt	ggctccttgg	480
agttgtatgt	gaccttaaat	tgatcacatc	tcttccaatt	gccactgtac	ctttgggtac	540
aggaaacaac	cttccctttg	cttttgatg	gggaaagaag	aatccaggaa	cagataggac	600
tgagtgagag	tcgtttttgg	aacaagtgtt	gaaggcaaaa	gtgatgaaga	ttgacaattg	660
gcacatactt	atgaggatga	aaactcccaa	agaaggtggt	tcttgtgatc	ctgttgctcc	720
tcttgagtta	ccacattctc	tacatgcatt	tcaccgtgtt	tctccaactg	atgaactaaa	780
caaggaaggc	tgccacactt	ttcgaggagg	gttctggaat	tacttttagc	tcggaatgga	840
tgctcagatt	tcttatgcgt	ttcattctga	gaggaagctt	caccctgaaa	agtttaagaa	900
tcagctgggt	aatcagagta	cgtatgtaaa	gcttggttgc	acgcaaggat	ggttttgtgc	960
ctctcttttc	caccctgctt	cacggaatat	agctcagctt	gccaaaggta	agattgcaac	1020

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tagaaatggc cagtggcagg acctccacat accacatagc atcaggtcca ttgtatgtct 1080
gaatctgccc agcttttcgg gaggattaaa tccttggggc acaccaaadc ccaggaaaca 1140
acgtgataga ggcttgactc caccatttgt agatgatggc ctcataggagg ttgttgggtt 1200
tagaaatgct tggcatggtc ttgttctgct cgctcccaat ggacatggga cagcacttgc 1260
ccaggcaaat cgtattcgct tcgaatttca caaaggtgca accgaccata cattcatgag 1320
gatggatggg gagccctgga aacagccact gccactggat gatgaaactg tgatggtaga 1380
gatttcacac cttggccaag tgaacatgct tgcaactcat gactgccggt ccagaagtgt 1440
gtttgaccct tcaacacccc gccatcagga tgggtgcagaa gattatgatg ataatgaaga 1500
cgactcantg gctgaaggcg aagaatttag aaagtttggg gctgcggata ccttcaagat 1560
tcctgatgag gttgatattt ctcaacttag ttagacaatt aaccattttc attgttgatt 1620
ctatgcattc ttcttcggga ctccaatttt tttattcact ctttcataaa ggagcaacta 1680
gcagcaactg gtttagattg gtaaccatct ttttctttg cttttgtttg gttgttcacg 1740
tttaatggcc gagataatgt atctggattt at
```

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..530
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

```
Ala His Asp Arg Val Arg Val Arg Lys Arg Gly Gln Leu Leu Arg Ser
1          5          10          15
Arg Gln Glu Ser Arg Arg Ser Arg Phe Leu Leu Ile Ile Val Phe Phe
20          25          30
Tyr Gln Asn Cys Cys Ala Thr Met Glu Lys Tyr Asn Ser Leu Ser Asp
35          40          45
Phe Leu Lys Glu Phe Tyr Ile Pro Thr Tyr Val Leu Ser Ala Glu Thr
50          55          60
Glu Glu Glu Glu Glu Glu Glu Ser Arg Pro Thr Pro Ala Ser Pro Val
65          70          75          80
Leu Val Phe Ile Asn Ser Lys Ser Gly Gly Gln Leu Gly Gly Glu Leu
85          90          95
Ile Leu Thr Tyr Arg Ser Leu Leu Asn His Asn Gln Val Phe Asp Leu
100          105          110
Asp Gln Glu Thr Pro Asp Lys Val Leu Arg Arg Ile Tyr Leu Asn Leu
115          120          125
Glu Arg Leu Lys Asp Asp Asp Ser Ala Arg Gln Ile Gly Glu Lys Leu
130          135          140
Lys Ile Ile Val Ala Gly Gly Asp Gly Thr Ala Gly Trp Leu Leu Gly
145          150          155          160
Val Val Cys Asp Leu Lys Leu Ser His Pro Pro Pro Ile Ala Thr Val
165          170          175
Pro Leu Gly Thr Gly Asn Asn Leu Pro Phe Ala Phe Gly Trp Gly Lys
180          185          190
Lys Asn Pro Gly Thr Asp Arg Thr Ala Val Glu Ser Phe Leu Glu Gln
195          200          205
Val Leu Lys Ala Lys Val Met Lys Ile Asp Asn Trp His Ile Leu Met
210          215          220
Arg Met Lys Thr Pro Lys Glu Gly Gly Ser Cys Asp Pro Val Ala Pro
225          230          235          240
Leu Glu Leu Pro His Ser Leu His Ala Phe His Arg Val Ser Pro Thr
245          250          255
Asp Glu Leu Asn Lys Glu Gly Cys His Thr Phe Arg Gly Gly Phe Trp
260          265          270
Asn Tyr Phe Ser Leu Gly Met Asp Ala Gln Ile Ser Tyr Ala Phe His
275          280          285
```



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Ser Glu Arg Lys Leu His Pro Glu Lys Phe Lys Asn Gln Leu Val Asn
290                295                300
Gln Ser Thr Tyr Val Lys Leu Gly Cys Thr Gln Gly Trp Phe Cys Ala
305                310                315                320
Ser Leu Phe His Pro Ala Ser Arg Asn Ile Ala Gln Leu Ala Lys Val
325                330                335
Lys Ile Ala Thr Arg Asn Gly Gln Trp Gln Asp Leu His Ile Pro His
340                345                350
Ser Ile Arg Ser Ile Val Cys Leu Asn Leu Pro Ser Phe Ser Gly Gly
355                360                365
Leu Asn Pro Trp Gly Thr Pro Asn Pro Arg Lys Gln Arg Asp Arg Gly
370                375                380
Leu Thr Pro Pro Phe Val Asp Asp Gly Leu Ile Glu Val Val Gly Phe
385                390                395                400
Arg Asn Ala Trp His Gly Leu Val Leu Leu Ala Pro Asn Gly His Gly
405                410                415
Thr Arg Leu Ala Gln Ala Asn Arg Ile Arg Phe Glu Phe His Lys Gly
420                425                430
Ala Thr Asp His Thr Phe Met Arg Met Asp Gly Glu Pro Trp Lys Gln
435                440                445
Pro Leu Pro Leu Asp Asp Glu Thr Val Met Val Glu Ile Ser His Leu
450                455                460
Gly Gln Val Asn Met Leu Ala Thr His Asp Cys Arg Ser Arg Ser Val
465                470                475                480
Phe Asp Pro Ser Thr Pro Arg His Gln Asp Gly Ala Glu Asp Tyr Asp
485                490                495
Asp Asn Glu Asp Asp Ser Xaa Ala Glu Gly Glu Glu Phe Arg Lys Phe
500                505                510
Gly Ala Ala Asp Thr Phe Lys Ile Pro Asp Glu Val Asp Ile Ser Gln
515                520                525
Leu Ser
530

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1498618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

```

Met Glu Lys Tyr Asn Ser Leu Ser Asp Phe Leu Lys Glu Phe Tyr Ile
1          5          10          15
Pro Thr Tyr Val Leu Ser Ala Glu Thr Glu Glu Glu Glu Glu Glu
20          25          30
Ser Arg Pro Thr Pro Ala Ser Pro Val Leu Val Phe Ile Asn Ser Lys
35          40          45
Ser Gly Gly Gln Leu Gly Gly Glu Leu Ile Leu Thr Tyr Arg Ser Leu
50          55          60
Leu Asn His Asn Gln Val Phe Asp Leu Asp Gln Glu Thr Pro Asp Lys
65          70          75          80
Val Leu Arg Arg Ile Tyr Leu Asn Leu Glu Arg Leu Lys Asp Asp Asp
85          90          95
Ser Ala Arg Gln Ile Gly Glu Lys Leu Lys Ile Ile Val Ala Gly Gly
100         105         110
Asp Gly Thr Ala Gly Trp Leu Leu Gly Val Val Cys Asp Leu Lys Leu
115        120        125
Ser His Pro Pro Pro Ile Ala Thr Val Pro Leu Gly Thr Gly Asn Asn

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130	135	140
Leu Pro Phe Ala Phe Gly	Trp Gly Lys Lys Asn	Pro Gly Thr Asp Arg
145	150	155
Thr Ala Val Glu Ser Phe	Leu Glu Gln Val Leu	Lys Ala Lys Val Met
165	170	175
Lys Ile Asp Asn Trp His	Ile Leu Met Arg Met	Lys Thr Pro Lys Glu
180	185	190
Gly Gly Ser Cys Asp Pro	Val Ala Pro Leu Glu	Leu Pro His Ser Leu
195	200	205
His Ala Phe His Arg Val	Ser Pro Thr Asp Glu	Leu Asn Lys Glu Gly
210	215	220
Cys His Thr Phe Arg Gly	Gly Phe Trp Asn Tyr	Phe Ser Leu Gly Met
225	230	235
Asp Ala Gln Ile Ser Tyr	Ala Phe His Ser Glu	Arg Lys Leu His Pro
245	250	255
Glu Lys Phe Lys Asn Gln	Leu Val Asn Gln Ser	Thr Tyr Val Lys Leu
260	265	270
Gly Cys Thr Gln Gly Trp	Phe Cys Ala Ser Leu	Phe His Pro Ala Ser
275	280	285
Arg Asn Ile Ala Gln Leu	Ala Lys Val Lys Ile	Ala Thr Arg Asn Gly
290	295	300
Gln Trp Gln Asp Leu His	Ile Pro His Ser Ile	Arg Ser Ile Val Cys
305	310	315
Leu Asn Leu Pro Ser Phe	Ser Gly Gly Leu Asn	Pro Trp Gly Thr Pro
325	330	335
Asn Pro Arg Lys Gln Arg	Asp Arg Gly Leu Thr	Pro Pro Phe Val Asp
340	345	350
Asp Gly Leu Ile Glu Val	Val Gly Phe Arg Asn	Ala Trp His Gly Leu
355	360	365
Val Leu Leu Ala Pro Asn	Gly His Gly Thr Arg	Leu Ala Gln Ala Asn
370	375	380
Arg Ile Arg Phe Glu Phe	His Lys Gly Ala Thr	Asp His Thr Phe Met
385	390	395
Arg Met Asp Gly Glu Pro	Trp Lys Gln Pro Leu	Pro Leu Asp Asp Glu
405	410	415
Thr Val Met Val Glu Ile	Ser His Leu Gly Gln	Val Asn Met Leu Ala
420	425	430
Thr His Asp Cys Arg Ser	Arg Ser Val Phe Asp	Pro Ser Thr Pro Arg
435	440	445
His Gln Asp Gly Ala Glu	Asp Tyr Asp Asp Asn	Glu Asp Asp Ser Xaa
450	455	460
Ala Glu Gly Glu Glu Phe	Arg Lys Phe Gly Ala	Ala Asp Thr Phe Lys
465	470	475
Ile Pro Asp Glu Val Asp	Ile Ser Gln Leu Ser	
485	490	

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Met Lys Ile Asp Asn Trp His Ile Leu Met Arg Met Lys Thr Pro Lys
1 5 10 15
Glu Gly Gly Ser Cys Asp Pro Val Ala Pro Leu Glu Leu Pro His Ser
20 25 30

Leu His Ala Phe His Arg Val Ser Pro Thr Asp Glu Leu Asn Lys Glu  
35 40 45  
Gly Cys His Thr Phe Arg Gly Gly Phe Trp Asn Tyr Phe Ser Leu Gly  
50 55 60  
Met Asp Ala Gln Ile Ser Tyr Ala Phe His Ser Glu Arg Lys Leu His  
65 70 75 80  
Pro Glu Lys Phe Lys Asn Gln Leu Val Asn Gln Ser Thr Tyr Val Lys  
85 90 95  
Leu Gly Cys Thr Gln Gly Trp Phe Cys Ala Ser Leu Phe His Pro Ala  
100 105 110  
Ser Arg Asn Ile Ala Gln Leu Ala Lys Val Lys Ile Ala Thr Arg Asn  
115 120 125  
Gly Gln Trp Gln Asp Leu His Ile Pro His Ser Ile Arg Ser Ile Val  
130 135 140  
Cys Leu Asn Leu Pro Ser Phe Ser Gly Gly Leu Asn Pro Trp Gly Thr  
145 150 155 160  
Pro Asn Pro Arg Lys Gln Arg Asp Arg Gly Leu Thr Pro Pro Phe Val  
165 170 175  
Asp Asp Gly Leu Ile Glu Val Val Gly Phe Arg Asn Ala Trp His Gly  
180 185 190  
Leu Val Leu Leu Ala Pro Asn Gly His Gly Thr Arg Leu Ala Gln Ala  
195 200 205  
Asn Arg Ile Arg Phe Glu Phe His Lys Gly Ala Thr Asp His Thr Phe  
210 215 220  
Met Arg Met Asp Gly Glu Pro Trp Lys Gln Pro Leu Pro Leu Asp Asp  
225 230 235 240  
Glu Thr Val Met Val Glu Ile Ser His Leu Gly Gln Val Asn Met Leu  
245 250 255  
Ala Thr His Asp Cys Arg Ser Arg Ser Val Phe Asp Pro Ser Thr Pro  
260 265 270  
Arg His Gln Asp Gly Ala Glu Asp Tyr Asp Asp Asn Glu Asp Asp Ser  
275 280 285  
Xaa Ala Glu Gly Glu Glu Phe Arg Lys Phe Gly Ala Ala Asp Thr Phe  
290 295 300  
Lys Ile Pro Asp Glu Val Asp Ile Ser Gln Leu Ser  
305 310 315

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

aaacaaaaaac agagcaaagt ttttcaaaaa aaaaaaaaac agagccacga agaaattttac	60
agaaaatttca aaaccatcga taaagatggg agatgtgatt ttgttcattg atgatacgaa	120
atcgaaagtg agaatcacgc gttgcagaat ttgccatgaa gaagaagaag aaagtttctt	180
cgaagtcca tgtgcttggt caggcaccgt taagttcgca cacagaaact gcatacaacg	240
ttggtgtaat gaaaaaggaa acacaacttg tgaaatctgt cttcaggtgt ataaagatgg	300
atatacagca gtttcaaaac aatcgaaatt gattgaacaa gaagtcacaa tcagagtaaa	360
tggaagaaga agaagaagaa gtagaagatt agtgtctata gctgaatccg atatttctca	420
gtgtaattct gttgctgata gaggagcttc gttttgcaga tcattaactt ttactctttc	480
agtatttttg ctgatgaaac atacattcga tgtgatttac ggaaccgaag aatatccatt	540
ctctgtattht acggtactaa cattaaaggc cattgggata ctattgcaa tgtccattat	600
aattcgaaca atctcaacta ttcagaaaac tcttcgtcgt cgatcatcaat atcctgaatc	660
tgaagaagaa gatagggtga gctctgacga cgacgatgac ttggaagatg aagatgaaga	720
gcaacaacaa catttggtt aaaccttcca attaacgaac ttaacgaaat tttttctttc	780

tttttttcta attcttttctt ttttaaaacg aaaagcatct atttgatgct catggtcatt 840  
tttactcgca aagtc

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Asn	Lys	Asn	Arg	Ala	Lys	Phe	Phe	Lys	Lys	Lys	Lys	Asn	Arg	Ala	Thr
1				5					10					15	
Lys	Lys	Phe	Thr	Glu	Asn	Ser	Lys	Pro	Ser	Ile	Lys	Met	Gly	Asp	Val
		20						25					30		
Ile	Leu	Phe	Ile	Asp	Asp	Thr	Lys	Ser	Lys	Val	Arg	Ile	Thr	Arg	Cys
		35					40					45			
Arg	Ile	Cys	His	Glu	Glu	Glu	Glu	Ser	Phe	Phe	Glu	Val	Pro	Cys	
		50				55				60					
Ala	Cys	Ser	Gly	Thr	Val	Lys	Phe	Ala	His	Arg	Asn	Cys	Ile	Gln	Arg
65					70				75					80	
Trp	Cys	Asn	Glu	Lys	Gly	Asn	Thr	Thr	Cys	Glu	Ile	Cys	Leu	Gln	Val
				85					90					95	
Tyr	Lys	Asp	Gly	Tyr	Thr	Ala	Val	Ser	Lys	Gln	Ser	Lys	Leu	Ile	Glu
			100					105					110		
Gln	Glu	Val	Thr	Ile	Arg	Val	Asn	Gly	Arg	Arg	Arg	Arg	Arg	Ser	Arg
		115					120					125			
Arg	Leu	Val	Ser	Ile	Ala	Glu	Ser	Asp	Ile	Ser	Gln	Cys	Asn	Ser	Val
		130				135					140				
Ala	Asp	Arg	Gly	Ala	Ser	Phe	Cys	Arg	Ser	Leu	Thr	Phe	Thr	Leu	Ser
145					150					155				160	
Val	Phe	Leu	Leu	Met	Lys	His	Thr	Phe	Asp	Val	Ile	Tyr	Gly	Thr	Glu
				165					170					175	
Glu	Tyr	Pro	Phe	Ser	Val	Phe	Thr	Val	Leu	Thr	Leu	Lys	Ala	Ile	Gly
		180						185					190		
Ile	Leu	Leu	Pro	Met	Ser	Ile	Ile	Ile	Arg	Thr	Ile	Ser	Thr	Ile	Gln
		195					200					205			
Lys	Thr	Leu	Arg	Arg	Arg	His	Gln	Tyr	Pro	Glu	Ser	Glu	Glu	Glu	Asp
		210				215				220					
Arg	Leu	Ser	Ser	Asp	Asp	Asp	Asp	Asp	Leu	Glu	Asp	Glu	Asp	Glu	Glu
225				230						235				240	
Gln	Gln	Gln	His	Leu	Ala										
				245											

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Met	Gly	Asp	Val	Ile	Leu	Phe	Ile	Asp	Asp	Thr	Lys	Ser	Lys	Val	Arg
1				5						10				15	
Ile	Thr	Arg	Cys	Arg	Ile	Cys	His	Glu	Glu	Glu	Glu	Glu	Ser	Phe	Phe

20	25	30
Glu Val Pro Cys Ala Cys Ser Gly Thr Val Lys Phe Ala His Arg Asn		
35	40	45
Cys Ile Gln Arg Trp Cys Asn Glu Lys Gly Asn Thr Thr Cys Glu Ile		
50	55	60
Cys Leu Gln Val Tyr Lys Asp Gly Tyr Thr Ala Val Ser Lys Gln Ser		
65	70	75
Lys Leu Ile Glu Gln Glu Val Thr Ile Arg Val Asn Gly Arg Arg Arg		
85	90	95
Arg Arg Ser Arg Arg Leu Val Ser Ile Ala Glu Ser Asp Ile Ser Gln		
100	105	110
Cys Asn Ser Val Ala Asp Arg Gly Ala Ser Phe Cys Arg Ser Leu Thr		
115	120	125
Phe Thr Leu Ser Val Phe Leu Leu Met Lys His Thr Phe Asp Val Ile		
130	135	140
Tyr Gly Thr Glu Glu Tyr Pro Phe Ser Val Phe Thr Val Leu Thr Leu		
145	150	155
Lys Ala Ile Gly Ile Leu Leu Pro Met Ser Ile Ile Ile Arg Thr Ile		
165	170	175
Ser Thr Ile Gln Lys Thr Leu Arg Arg Arg His Gln Tyr Pro Glu Ser		
180	185	190
Glu Glu Glu Asp Arg Leu Ser Ser Asp Asp Asp Asp Asp Leu Glu Asp		
195	200	205
Glu Asp Glu Glu Gln Gln Gln His Leu Ala		
210	215	

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1589
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

cattgaagtt	aacagtcagc	atcgttttgc	ttgcttggtgc	gtttctctcg	aactctctcc	60
atggctgttg	cgctccaatt	cagccgatta	tgcgttcgac	cggatacttt	cgtgcgggag	120
aatcatctct	ctggatccgg	atctctccgc	cgccggaaag	ctttatcagt	ccggtgctcg	180
tctggcgatg	agaacgctcc	ttcgccatcg	gtgggtgatg	actccgattt	cgacgccaag	240
gtgttccgta	agaacttgac	gagaagcgat	aattacaatc	gtaaaggggt	cggtcataag	300
gaggagacac	tcaagctcat	gaatcgagag	tacaccagtg	atatattgga	gacactgaaa	360
acaaatgggt	atacttattc	ttggggagat	gttactgtga	aactcgctaa	agcatatggt	420
ttttgctggg	gtgttgagcg	tgctgttcag	attgcataat	aagcacgaaa	gcagtttcca	480
gaggagaggc	tttggattac	taacgaaatc	attcataacc	cgaccgtcaa	taagaggttg	540
gaagatatgg	atgttaaaat	tattccgggt	gaggattcaa	agaaacagtt	tgatgtagta	600
gagaaagatg	atgtggttat	ccttcctgcg	tttggagctg	gtgttgacga	gatgtatggt	660
cttaatgata	aaaagggtgca	aattgttgac	acgacttgtc	cttgggtgac	aaaggtctgg	720
aacacggttg	agaagcacaa	gaagggggaa	tacacatcag	taatccatgg	taaatataat	780
catgaagaga	cgattgcaac	tgcgtctttt	gcaggaaagt	acatcattgt	aaagaacatg	840
aaagaggcaa	attacgtttg	tgattacatt	ctcgggtggc	aatacgatgg	atctagctcc	900
acaaaagagg	agttcatgga	gaaattcaaa	tacgcaattt	cgaaggggtt	cgatcccagc	960
aatgaccttg	tcaaagttgg	tattgcaaac	caaacaacga	tgctaaaggg	agaaacagag	1020
gagataggaa	gattactcga	gacaacaatg	atgcgcaagt	atggagtggg	aaatgtaagc	1080
ggacatttca	tcagcttcaa	cacaatatgc	gacgctactc	aagagcgaca	agacgcaatc	1140
tatgagctag	tggaagagaa	gattgacctc	atgctagtgg	ttggcgggatg	gaattcaagt	1200
aacacctctc	accttcagga	aatctcagag	gcacggggaa	tcccatctta	ctggatcgat	1260
agtgagaaac	ggataggacc	tgggaataaa	atagcctata	agctocacta	tggagaactg	1320
gtcgagkaag	gaaaactttc	tcccaaaggg	accaataaca	atcgggtgtga	catcaggtgc	1380
atcaaccccc	gataaggtcg	tggaagatgc	tttgggtgaag	gtgttcgaca	ttaaactgtga	1440

agagttattg cagctggcctt gattcggcat tgtgatcgta ttcaaatact atttgtcatg 1500  
tcaagagtgt actaaaatat atgtagttgt atgatttgtc tttataactt ttgtaagagg 1560  
ttttgtaatt caaagtcaac atcctcgtt

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

Met	Ala	Val	Ala	Leu	Gln	Phe	Ser	Arg	Leu	Cys	Val	Arg	Pro	Asp	Thr
1				5					10					15	
Phe	Val	Arg	Glu	Asn	His	Leu	Ser	Gly	Ser	Gly	Ser	Leu	Arg	Arg	Arg
			20					25					30		
Lys	Ala	Leu	Ser	Val	Arg	Cys	Ser	Gly	Asp	Glu	Asn	Ala	Pro	Ser	
		35					40				45				
Pro	Ser	Val	Val	Met	Asp	Ser	Asp	Phe	Asp	Ala	Lys	Val	Phe	Arg	Lys
		50				55					60				
Asn	Leu	Thr	Arg	Ser	Asp	Asn	Tyr	Asn	Arg	Lys	Gly	Phe	Gly	His	Lys
65					70					75				80	
Glu	Glu	Thr	Leu	Lys	Leu	Met	Asn	Arg	Glu	Tyr	Thr	Ser	Asp	Ile	Leu
				85					90					95	
Glu	Thr	Leu	Lys	Thr	Asn	Gly	Tyr	Thr	Tyr	Ser	Trp	Gly	Asp	Val	Thr
			100					105					110		
Val	Lys	Leu	Ala	Lys	Ala	Tyr	Gly	Phe	Cys	Trp	Gly	Val	Glu	Arg	Ala
		115					120					125			
Val	Gln	Ile	Ala	Tyr	Glu	Ala	Arg	Lys	Gln	Phe	Pro	Glu	Glu	Arg	Leu
		130					135				140				
Trp	Ile	Thr	Asn	Glu	Ile	Ile	His	Asn	Pro	Thr	Val	Asn	Lys	Arg	Leu
145					150					155				160	
Glu	Asp	Met	Asp	Val	Lys	Ile	Ile	Pro	Val	Glu	Asp	Ser	Lys	Lys	Gln
			165						170					175	
Phe	Asp	Val	Val	Glu	Lys	Asp	Asp	Val	Val	Ile	Leu	Pro	Ala	Phe	Gly
			180					185					190		
Ala	Gly	Val	Asp	Glu	Met	Tyr	Val	Leu	Asn	Asp	Lys	Lys	Val	Gln	Ile
		195					200					205			
Val	Asp	Thr	Thr	Cys	Pro	Trp	Val	Thr	Lys	Val	Trp	Asn	Thr	Val	Glu
		210				215					220				
Lys	His	Lys	Lys	Gly	Glu	Tyr	Thr	Ser	Val	Ile	His	Gly	Lys	Tyr	Asn
225					230					235				240	
His	Glu	Glu	Thr	Ile	Ala	Thr	Ala	Ser	Phe	Ala	Gly	Lys	Tyr	Ile	Ile
				245					250					255	
Val	Lys	Asn	Met	Lys	Glu	Ala	Asn	Tyr	Val	Cys	Asp	Tyr	Ile	Leu	Gly
			260					265					270		
Gly	Gln	Tyr	Asp	Gly	Ser	Ser	Ser	Thr	Lys	Glu	Glu	Phe	Met	Glu	Lys
			275				280						285		
Phe	Lys	Tyr	Ala	Ile	Ser	Lys	Gly	Phe	Asp	Pro	Asp	Asn	Asp	Leu	Val
		290				295					300				
Lys	Val	Gly	Ile	Ala	Asn	Gln	Thr	Thr	Met	Leu	Lys	Gly	Glu	Thr	Glu
305					310					315				320	
Glu	Ile	Gly	Arg	Leu	Leu	Glu	Thr	Thr	Met	Met	Arg	Lys	Tyr	Gly	Val
				325					330					335	
Glu	Asn	Val	Ser	Gly	His	Phe	Ile	Ser	Phe	Asn	Thr	Ile	Cys	Asp	Ala
				340				345					350		
Thr	Gln	Glu	Arg	Gln	Asp	Ala	Ile	Tyr	Glu	Leu	Val	Glu	Glu	Lys	Ile
		355					360						365		

Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His  
370 375 380  
Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp  
385 390 395 400  
Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His  
405 410 415  
Tyr Gly Glu Leu Val Glu Xaa Gly Lys Leu Ser Pro Lys Gly Thr Asn  
420 425 430  
Asn Asn Arg Cys Asp Ile Arg Cys Ile Asn Pro Gly  
435 440

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1498633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys Asn Leu Thr Arg  
1 5 10 15  
Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys Glu Glu Thr Leu  
20 25 30  
Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu Glu Thr Leu Lys  
35 40 45  
Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr Val Lys Leu Ala  
50 55 60  
Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala Val Gln Ile Ala  
65 70 75 80  
Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu Trp Ile Thr Asn  
85 90 95  
Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu Glu Asp Met Asp  
100 105 110  
Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln Phe Asp Val Val  
115 120 125  
Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly Ala Gly Val Asp  
130 135 140  
Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile Val Asp Thr Thr  
145 150 155 160  
Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu Lys His Lys Lys  
165 170 175  
Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn His Glu Glu Thr  
180 185 190  
Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile Val Lys Asn Met  
195 200 205  
Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly Gly Gln Tyr Asp  
210 215 220  
Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys Phe Lys Tyr Ala  
225 230 235 240  
Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val Lys Val Gly Ile  
245 250 255  
Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu Glu Ile Gly Arg  
260 265 270  
Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val Glu Asn Val Ser  
275 280 285  
Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala Thr Gln Glu Arg  
290 295 300  
Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile Asp Leu Met Leu

(2) INFORMATION FOR SEQ ID NO:549:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1498634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

Met 1	Asn	Arg	Glu	Tyr 5	Thr	Ser	Asp	Ile	Leu 10	Glu	Thr	Leu	Lys	Thr 15	Asn
Gly	Tyr	Thr	Tyr	Ser	Trp	Gly	Asp	Val	Thr	Val	Lys	Leu	Ala	Lys	Ala
			20				25						30		
Tyr	Gly	Phe	Cys	Trp	Gly	Val	Glu	Arg	Ala	Val	Gln	Ile	Ala	Tyr	Glu
		35					40					45			
Ala	Arg	Lys	Gln	Phe	Pro	Glu	Glu	Arg	Leu	Trp	Ile	Thr	Asn	Glu	Ile
	50					55					60				
Ile	His	Asn	Pro	Thr	Val	Asn	Lys	Arg	Leu	Glu	Asp	Met	Asp	Val	Lys
65				70						75				80	
Ile	Ile	Pro	Val	Glu	Asp	Ser	Lys	Lys	Gln	Phe	Asp	Val	Val	Glu	Lys
			85						90					95	
Asp	Asp	Val	Val	Ile	Leu	Pro	Ala	Phe	Gly	Ala	Gly	Val	Asp	Glu	Met
		100					105						110		
Tyr	Val	Leu	Asn	Asp	Lys	Lys	Val	Gln	Ile	Val	Asp	Thr	Thr	Cys	Pro
		115				120						125			
Trp	Val	Thr	Lys	Val	Trp	Asn	Thr	Val	Glu	Lys	His	Lys	Lys	Gly	Glu
	130					135					140				
Tyr	Thr	Ser	Val	Ile	His	Gly	Lys	Tyr	Asn	His	Glu	Glu	Thr	Ile	Ala
145				150						155				160	
Thr	Ala	Ser	Phe	Ala	Gly	Lys	Tyr	Ile	Ile	Val	Lys	Asn	Met	Lys	Glu
			165						170					175	
Ala	Asn	Tyr	Val	Cys	Asp	Tyr	Ile	Leu	Gly	Gly	Gln	Tyr	Asp	Gly	Ser
			180					185					190		
Ser	Ser	Thr	Lys	Glu	Glu	Phe	Met	Glu	Lys	Phe	Lys	Tyr	Ala	Ile	Ser
		195					200					205			
Lys	Gly	Phe	Asp	Pro	Asp	Asn	Asp	Leu	Val	Lys	Val	Gly	Ile	Ala	Asn
						215					220				
Gln	Thr	Thr	Met	Leu	Lys	Gly	Glu	Thr	Glu	Glu	Ile	Gly	Arg	Leu	Leu
225				230						235				240	
Glu	Thr	Thr	Met	Met	Arg	Lys	Tyr	Gly	Val	Glu	Asn	Val	Ser	Gly	His
			245						250					255	
Phe	Ile	Ser	Phe	Asn	Thr	Ile	Cys	Asp	Ala	Thr	Gln	Glu	Arg	Gln	Asp
			260					265					270		
Ala	Ile	Tyr	Glu	Leu	Val	Glu	Glu	Lys	Ile	Asp	Leu	Met	Leu	Val	Val
		275					280					285			
Gly	Gly	Trp	Asn	Ser	Ser	Asn	Thr	Ser	His	Leu	Gln	Glu	Ile	Ser	Glu
	290					295					300				



Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp Ser Glu Lys Arg Ile Gly  
305 310 315 320  
Pro Gly Asn Lys Ile Ala Tyr Lys Leu His Tyr Gly Glu Leu Val Glu  
325 330 335  
Xaa Gly Lys Leu Ser Pro Lys Gly Thr Asn Asn Asn Arg Cys Asp Ile  
340 345 350  
Arg Cys Ile Asn Pro Gly  
355

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

acatcaaagc	aattaacaaa	tacacaactt	gtaacttcaa	atagattact	ttcaaagaag	60
agagagagaa	agaaagatgg	agaagaacat	gaagtttcca	gtagtagact	tgtccaagct	120
caatggggaa	gagagagacc	aaaccatggc	tctaataaat	gaagcttggt	agaattgggg	180
cttctttgag	atagtgaacc	atggattacc	acatgactta	atggacaaga	tcgagaagat	240
gacaaaggac	cattacaaga	catgccaaga	acaaaagttc	aatgacatgc	tcaagtccaa	300
aggtttggat	aatcttgaga	cagaagtcga	agatgtcgat	tgggaaagca	ctttctacgt	360
tcgtcacctc	cctcaatcca	atctcaatga	catttcagat	gtgtctgatg	aatacgacgg	420
ccatgaaaga	ctttggttaag	agactggaga	atcttgctga	ggatttggtg	gatctactgt	480
gtgagaatct	aggggttagag	aaagggtatt	tgaagaaagt	gtttcatgga	acaaaaggcc	540
caaccttttg	gacaaagggtg	agcaattatc	caccatgtcc	taaaccagag	atgatcaaag	600
gtcttagggc	ccacactgat	gcaggaggca	tcattctgtt	gtttcaagac	gacaagggtca	660
gtgggtctcca	gcttcttaaa	gatggtgact	ggattgatgt	tcctcctctc	aaccactcta	720
ttgtcatcaa	tcttggtgac	caacttgagg	tgataaccaa	cgggaagtat	aagagtgtgc	780
tgcaccgtgt	ggtgactcaa	caagaaggaa	acaggatgtc	ggttgcatcg	ttttacaacc	840
cgggaagcga	tgcggagatc	tcaccagcta	cttcgcttgt	cgagaaagat	tccgagtacc	900
cgagtttctg	ctttgatgac	tacatgaagc	tttatgcagg	ggtcaagttt	cagcccaagg	960
agccacgggt	cgcagcaatg	aagaatgctt	ctgcagttac	agaactgaat	cctacagcag	1020
ccgtagagac	ttttctaaaa	tggatttgag	attcaagtga	agcagagaaa	gaamsmtgag	1080
tttgtgttgt	gtgttatggc	aataagttaa	aacttgattt	agtgttgatt	aattgttggt	1140
caattgggtg	gttttaaagt	gtggggtggt	tatgtttatg	gaagatgata	ataattataa	1200
aaatctaaat	tct					

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

Met Thr Cys Ser Ser Pro Lys Val Trp Ile Ile Leu Arg Gln Lys Ser	
1 5 10 15	
Lys Met Ser Ile Gly Lys Ala Leu Ser Thr Phe Val Thr Ser Leu Asn	
20 25 30	
Pro Ile Ser Met Thr Phe Gln Met Cys Leu Met Asn Thr Thr Ala Met	
35 40 45	
Lys Asp Phe Gly Lys Arg Leu Glu Asn Leu Ala Glu Asp Leu Leu Asp	
50 55 60	

```

Leu Leu Cys Glu Asn Leu Gly Leu Glu Lys Gly Tyr Leu Lys Lys Val
65          70          75          80
Phe His Gly Thr Lys Gly Pro Thr Phe Gly Thr Lys Val Ser Asn Tyr
          85          90          95
Pro Pro Cys Pro Lys Pro Glu Met Ile Lys Gly Leu Arg Ala His Thr
          100          105          110
Asp Ala Gly Gly Ile Ile Leu Leu Phe Gln Asp Asp Lys Val Ser Gly
          115          120          125
Leu Gln Leu Leu Lys Asp Gly Asp Trp Ile Asp Val Pro Pro Leu Asn
          130          135          140
His Ser Ile Val Ile Asn Leu Gly Asp Gln Leu Glu Val Ile Thr Asn
145          150          155          160
Gly Lys Tyr Lys Ser Val Leu His Arg Val Val Thr Gln Gln Glu Gly
          165          170          175
Asn Arg Met Ser Val Ala Ser Phe Tyr Asn Pro Gly Ser Asp Ala Glu
          180          185          190
Ile Ser Pro Ala Thr Ser Leu Val Glu Lys Asp Ser Glu Tyr Pro Ser
          195          200          205
Phe Val Phe Asp Asp Tyr Met Lys Leu Tyr Ala Gly Val Lys Phe Gln
210          215          220
Pro Lys Glu Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr
225          230          235          240
Glu Leu Asn Pro Thr Ala Ala Val Glu Thr Phe
          245          250

```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1498637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

```

Met Ser Ile Gly Lys Ala Leu Ser Thr Phe Val Thr Ser Leu Asn Pro
1          5          10          15
Ile Ser Met Thr Phe Gln Met Cys Leu Met Asn Thr Thr Ala Met Lys
          20          25          30
Asp Phe Gly Lys Arg Leu Glu Asn Leu Ala Glu Asp Leu Leu Asp Leu
          35          40          45
Leu Cys Glu Asn Leu Gly Leu Glu Lys Gly Tyr Leu Lys Lys Val Phe
          50          55          60
His Gly Thr Lys Gly Pro Thr Phe Gly Thr Lys Val Ser Asn Tyr Pro
65          70          75          80
Pro Cys Pro Lys Pro Glu Met Ile Lys Gly Leu Arg Ala His Thr Asp
          85          90          95
Ala Gly Gly Ile Ile Leu Leu Phe Gln Asp Asp Lys Val Ser Gly Leu
          100          105          110
Gln Leu Leu Lys Asp Gly Asp Trp Ile Asp Val Pro Pro Leu Asn His
          115          120          125
Ser Ile Val Ile Asn Leu Gly Asp Gln Leu Glu Val Ile Thr Asn Gly
          130          135          140
Lys Tyr Lys Ser Val Leu His Arg Val Val Thr Gln Gln Glu Gly Asn
145          150          155          160
Arg Met Ser Val Ala Ser Phe Tyr Asn Pro Gly Ser Asp Ala Glu Ile
          165          170          175
Ser Pro Ala Thr Ser Leu Val Glu Lys Asp Ser Glu Tyr Pro Ser Phe
          180          185          190
Val Phe Asp Asp Tyr Met Lys Leu Tyr Ala Gly Val Lys Phe Gln Pro

```

195 200 205  
Lys Glu Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr Glu  
210 215 220  
Leu Asn Pro Thr Ala Ala Val Glu Thr Phe  
225 230

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Met Thr Phe Gln Met Cys Leu Met Asn Thr Thr Ala Met Lys Asp Phe  
1 5 10 15  
Gly Lys Arg Leu Glu Asn Leu Ala Glu Asp Leu Leu Asp Leu Cys  
20 25 30  
Glu Asn Leu Gly Leu Glu Lys Gly Tyr Leu Lys Lys Val Phe His Gly  
35 40 45  
Thr Lys Gly Pro Thr Phe Gly Thr Lys Val Ser Asn Tyr Pro Pro Cys  
50 55 60  
Pro Lys Pro Glu Met Ile Lys Gly Leu Arg Ala His Thr Asp Ala Gly  
65 70 75 80  
Gly Ile Ile Leu Leu Phe Gln Asp Asp Lys Val Ser Gly Leu Gln Leu  
85 90 95  
Leu Lys Asp Gly Asp Trp Ile Asp Val Pro Pro Leu Asn His Ser Ile  
100 105 110  
Val Ile Asn Leu Gly Asp Gln Leu Glu Val Ile Thr Asn Gly Lys Tyr  
115 120 125  
Lys Ser Val Leu His Arg Val Val Thr Gln Gln Glu Gly Asn Arg Met  
130 135 140  
Ser Val Ala Ser Phe Tyr Asn Pro Gly Ser Asp Ala Glu Ile Ser Pro  
145 150 155 160  
Ala Thr Ser Leu Val Glu Lys Asp Ser Glu Tyr Pro Ser Phe Val Phe  
165 170 175  
Asp Asp Tyr Met Lys Leu Tyr Ala Gly Val Lys Phe Gln Pro Lys Glu  
180 185 190  
Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr Glu Leu Asn  
195 200 205  
Pro Thr Ala Ala Val Glu Thr Phe  
210 215

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1065
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

acttaaccga	raaagcaaaa	gagaagaaga	agaaggaatc	gaaaaatgaa	gactccgatc	60
cacgcggttt	cgacatgggt	gaggaggcag	cctccaaagg	tgaaagcttt	ccttgccgtc	120
gtatctggca	tggcggctct	tgttctcctc	aaactcatcg	ttcacgatca	cgacaatctc	180
ttcgttgccg	ccgaagctgt	tcattctatt	ggaatctctg	ttcttatsta	taaactcatg	240

```
aaggagaaga cttgtgctgg attgtcattg aaatctcagg agcttacggc gatatttcta 300
gctgtgaggg ttttattgcag ttttgaatg gaatatgata tacataccat tctggacttg 360
gctacttttg gaacaactct ctgggttata tatatgatcc gttttaacct caaagctact 420
tacatggagg aaaaagacaa cttcgctctc tattatgtgc tggcgccctg tgttgtgcta 480
gctgtatgga ttcattccatc aacgtcacac aatatattga atagaatatc ctggggattc 540
tgtgtttacc tcgaagctgt ttcagtactg ccacagttga gagtgatgca gaacacaaaag 600
attgtcgaac ccttcacggc tcattatgtt tttgcacttg gagtagcaag attttttagc 660
tgtgcacact gggttttaca gatgatggac acgcacggac gactgcttgt agtgctgggt 720
tatggactat ggccatcgat gggtataatc tcagaaatag tccaagcatt catattggca 780
gatttctgtt actactacgt taaaagtgtt ttccggtggcc agcttgttct aaggcttcca 840
tctgggggtg tgtaagtatt aaaggaaaaa agataagaca cattatgacg aaatttggtta 900
cacgaagata gatctcagct tgggtgaatc tgagtagcct ctgggttactc tcaagttact 960
ccctcaggcc aagtcctaatt tctattaact gtgttgata tttttgtgtg ggtcatcatc 1020
atagacagtc ccttgatat tattgacatg attttttyca ctgcc
```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

```
Met Lys Thr Pro Ile His Ala Val Ser Thr Trp Val Arg Arg Gln Pro
1          5          10          15
Pro Lys Val Lys Ala Phe Leu Ala Val Val Ser Gly Met Ala Ala Leu
20          25          30
Val Leu Leu Lys Leu Ile Val His Asp His Asp Asn Leu Phe Val Ala
35          40          45
Ala Glu Ala Val His Ser Ile Gly Ile Ser Val Leu Xaa Tyr Lys Leu
50          55          60
Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys Ser Gln Glu Leu
65          70          75          80
Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser Phe Val Met Glu
85          90          95
Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu Gly Thr Thr Leu
100          105          110
Trp Val Ile Tyr Met Ile Arg Phe Asn Leu Lys Ala Thr Tyr Met Glu
115          120          125
Glu Lys Asp Asn Phe Ala Leu Tyr Tyr Val Leu Ala Pro Cys Val Val
130          135          140
Leu Ala Val Trp Ile His Pro Ser Thr Ser His Asn Ile Leu Asn Arg
145          150          155          160
Ile Ser Trp Gly Phe Cys Val Tyr Leu Glu Ala Val Ser Val Leu Pro
165          170          175
Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu Pro Phe Thr Ala
180          185          190
His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Phe Ser Cys Ala His
195          200          205
Trp Val Leu Gln Met Met Asp Thr His Gly Arg Leu Leu Val Val Leu
210          215          220
Gly Tyr Gly Leu Trp Pro Ser Met Val Ile Ile Ser Glu Ile Val Gln
225          230          235          240
Ala Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val Lys Ser Val Phe
245          250          255
Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val Val
260          265
```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 241 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..241  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498641  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Met	Ala	Ala	Leu	Val	Leu	Leu	Lys	Leu	Ile	Val	His	Asp	His	Asp	Asn
1			5						10					15	
Leu	Phe	Val	Ala	Ala	Glu	Ala	Val	His	Ser	Ile	Gly	Ile	Ser	Val	Leu
			20					25					30		
Xaa	Tyr	Lys	Leu	Met	Lys	Glu	Lys	Thr	Cys	Ala	Gly	Leu	Ser	Leu	Lys
		35					40					45			
Ser	Gln	Glu	Leu	Thr	Ala	Ile	Phe	Leu	Ala	Val	Arg	Leu	Tyr	Cys	Ser
	50					55					60				
Phe	Val	Met	Glu	Tyr	Asp	Ile	His	Thr	Ile	Leu	Asp	Leu	Ala	Thr	Leu
65					70					75				80	
Gly	Thr	Thr	Leu	Trp	Val	Ile	Tyr	Met	Ile	Arg	Phe	Asn	Leu	Lys	Ala
			85						90					95	
Thr	Tyr	Met	Glu	Glu	Lys	Asp	Asn	Phe	Ala	Leu	Tyr	Tyr	Val	Leu	Ala
		100						105					110		
Pro	Cys	Val	Val	Leu	Ala	Val	Trp	Ile	His	Pro	Ser	Thr	Ser	His	Asn
		115					120						125		
Ile	Leu	Asn	Arg	Ile	Ser	Trp	Gly	Phe	Cys	Val	Tyr	Leu	Glu	Ala	Val
	130					135					140				
Ser	Val	Leu	Pro	Gln	Leu	Arg	Val	Met	Gln	Asn	Thr	Lys	Ile	Val	Glu
145				150					155					160	
Pro	Phe	Thr	Ala	His	Tyr	Val	Phe	Ala	Leu	Gly	Val	Ala	Arg	Phe	Phe
			165						170					175	
Ser	Cys	Ala	His	Trp	Val	Leu	Gln	Met	Met	Asp	Thr	His	Gly	Arg	Leu
		180						185					190		
Leu	Val	Val	Leu	Gly	Tyr	Gly	Leu	Trp	Pro	Ser	Met	Val	Ile	Ile	Ser
	195						200					205			
Glu	Ile	Val	Gln	Ala	Phe	Ile	Leu	Ala	Asp	Phe	Cys	Tyr	Tyr	Tyr	Val
	210					215					220				
Lys	Ser	Val	Phe	Gly	Gly	Gln	Leu	Val	Leu	Arg	Leu	Pro	Ser	Gly	Val
225					230					235					240
Val															

(2) INFORMATION FOR SEQ ID NO:557:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 205 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..205  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498642  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

Met	Lys	Glu	Lys	Thr	Cys	Ala	Gly	Leu	Ser	Leu	Lys	Ser	Gln	Glu	Leu
1				5					10					15	
Thr	Ala	Ile	Phe	Leu	Ala	Val	Arg	Leu	Tyr	Cys	Ser	Phe	Val	Met	Glu
			20					25					30		
Tyr	Asp	Ile	His	Thr	Ile	Leu	Asp	Leu	Ala	Thr	Leu	Gly	Thr	Thr	Leu
		35					40						45		

Trp Val Ile Tyr Met Ile Arg Phe Asn Leu Lys Ala Thr Tyr Met Glu  
50 55 60  
Glu Lys Asp Asn Phe Ala Leu Tyr Tyr Val Leu Ala Pro Cys Val Val  
65 70 75 80  
Leu Ala Val Trp Ile His Pro Ser Thr Ser His Asn Ile Leu Asn Arg  
85 90 95  
Ile Ser Trp Gly Phe Cys Val Tyr Leu Glu Ala Val Ser Val Leu Pro  
100 105 110  
Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu Pro Phe Thr Ala  
115 120 125  
His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Phe Ser Cys Ala His  
130 135 140  
Trp Val Leu Gln Met Met Asp Thr His Gly Arg Leu Leu Val Val Leu  
145 150 155 160  
Gly Tyr Gly Leu Trp Pro Ser Met Val Ile Ile Ser Glu Ile Val Gln  
165 170 175  
Ala Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val Lys Ser Val Phe  
180 185 190  
Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val Val  
195 200 205

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

agcgaaaatc ccaaacaataa aaataaaaga atggcggtctc tgtgcctttc tctccaccaa	60
accctaacta atcccctgtc ggctcccaga tgcagaccac tcagcctctc cttccccgga	120
tcctcaacct tctcgatccg cccctctagc agacgcgcaa ccgccttgac gaccgcgcc	180
tcctacaccc cgacgccggc gactgagcgc gtgatttoga tagcgtcgta cgcgctgccg	240
ttcttcaatt ctctgcagta cgggcgggttc ctgttcgcgc agtaccacaag gctgggattg	300
ctgttcgagc caatcttccc aatcctgaac ctgtacagat cggtgccgta cgcgagcttc	360
gtggcattct tcgggctgta cctgggagtg gtgaggaaca cgagtttcag taggtacgtg	420
aggttcaacg cgatgcaggc ggtgacgctg gatgtgctcc tggcggttcc ggtgctgctg	480
acccgaatac tggatccggg tcaaggaggc gggtttgaa tgaaggcgat gatgtggggg	540
cacacggggg ttttcgtctt cagctttatg tgttttgtgt atggagtcgt cagctcctta	600
ctcgcaaaa ctccatacat tccatttgtc gctgatgccg ccggtagaca actctaattc	660
cggccaatat ctacctact cagtgttcgg gttttcgatt ctagaatcgg ttattttctgg	720
tttataagag agaccaaatac aatcagtgtt gttaattaac cattaccgtt tc	

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

Ser Glu Asn Pro Lys Gln Lys Asn Lys Arg Met Ala Ser Leu Cys Leu	
1 5 10 15	
Ser Leu His Gln Thr Leu Thr Asn Pro Leu Ser Ala Pro Arg Cys Arg	
20 25 30	

Pro Leu Ser Leu Ser Phe Pro Gly Ser Ser Thr Phe Ser Ile Arg Pro  
35 40 45  
Ser Ser Arg Arg Ala Thr Ala Leu Thr Thr Arg Ala Ser Tyr Thr Pro  
50 55 60  
Thr Pro Ala Thr Glu Arg Val Ile Ser Ile Ala Ser Tyr Ala Leu Pro  
65 70 75 80  
Phe Phe Asn Ser Leu Gln Tyr Gly Arg Phe Leu Phe Ala Gln Tyr Pro  
85 90 95  
Arg Leu Gly Leu Leu Phe Glu Pro Ile Phe Pro Ile Leu Asn Leu Tyr  
100 105 110  
Arg Ser Val Pro Tyr Ala Ser Phe Val Ala Phe Phe Gly Leu Tyr Leu  
115 120 125  
Gly Val Val Arg Asn Thr Ser Phe Ser Arg Tyr Val Arg Phe Asn Ala  
130 135 140  
Met Gln Ala Val Thr Leu Asp Val Leu Leu Ala Val Pro Val Leu Leu  
145 150 155 160  
Thr Arg Ile Leu Asp Pro Gly Gln Gly Gly Gly Phe Gly Met Lys Ala  
165 170 175  
Met Met Trp Gly His Thr Gly Val Phe Val Phe Ser Phe Met Cys Phe  
180 185 190  
Val Tyr Gly Val Val Ser Ser Leu Gly Lys Thr Pro Tyr Ile Pro  
195 200 205  
Phe Val Ala Asp Ala Ala Gly Arg Gln Leu  
210 215

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1498645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met Ala Ser Leu Cys Leu Ser Leu His Gln Thr Leu Thr Asn Pro Leu  
1 5 10 15  
Ser Ala Pro Arg Cys Arg Pro Leu Ser Leu Ser Phe Pro Gly Ser Ser  
20 25 30  
Thr Phe Ser Ile Arg Pro Ser Ser Arg Arg Ala Thr Ala Leu Thr Thr  
35 40 45  
Arg Ala Ser Tyr Thr Pro Thr Pro Ala Thr Glu Arg Val Ile Ser Ile  
50 55 60  
Ala Ser Tyr Ala Leu Pro Phe Phe Asn Ser Leu Gln Tyr Gly Arg Phe  
65 70 75 80  
Leu Phe Ala Gln Tyr Pro Arg Leu Gly Leu Leu Phe Glu Pro Ile Phe  
85 90 95  
Pro Ile Leu Asn Leu Tyr Arg Ser Val Pro Tyr Ala Ser Phe Val Ala  
100 105 110  
Phe Phe Gly Leu Tyr Leu Gly Val Val Arg Asn Thr Ser Phe Ser Arg  
115 120 125  
Tyr Val Arg Phe Asn Ala Met Gln Ala Val Thr Leu Asp Val Leu Leu  
130 135 140  
Ala Val Pro Val Leu Leu Thr Arg Ile Leu Asp Pro Gly Gln Gly Gly  
145 150 155 160  
Gly Phe Gly Met Lys Ala Met Met Trp Gly His Thr Gly Val Phe Val  
165 170 175  
Phe Ser Phe Met Cys Phe Val Tyr Gly Val Val Ser Ser Leu Leu Gly  
180 185 190  
Lys Thr Pro Tyr Ile Pro Phe Val Ala Asp Ala Ala Gly Arg Gln Leu

195

200

205

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1645
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

```
amcaaaaaaaaaa aaaaagaaaaa aaggagataa taatcacaaa ctacaaaagt agaaagaaga      60
aaaaagaaca aagtatcagt tcttgaatat ttgcatcaat ggaggaatcc aaaacacctc      120
acgttgcgat cataccaagt ccgggaatgg gtcattctcat accactcgtc gagtttgcta      180
aacgactcgt ccattcttcac ggccctcaccg ttaccttcgt catcgccggc gaagggtccac      240
catcaaaagc tcagagaacc gtccctcgact ctctcccttc ttcaatctcc tccgtctttc      300
tccctcctgt tgatctcacc gatctctctt cgtccactcg catcgaatct cggatctccc      360
tcaccgtgac tcgttcaaac ccggagctcc ggaaagtctt cgactcgttc gtggaggggag      420
gtcgtttgcc aacggcgctc gtcgtcgatc tcttcggtac ggacgctttc gacgtggccg      480
tagaattttca cgtgccaccg tatattttct acccaacaac ggccaacgtc ttgtcgtttt      540
ttctccattt gcctaaacta kacgaaacgg tgtcgtgtga gttcaggga ttaaccgaac      600
cgcttatgct tcctggatgt gtaccggttg ccgggaaaga tttccttgac ccggcccaag      660
accggaagaa cgatgcatac aaatggcttc tccataacac caagaggtag aaagaagccg      720
aaggatttct tgtgaatacc ttctttgagc tagagccaaa tgctataaag gccttgcaag      780
aaccgggtct tgataaacca ccggtttatc cggttgagc gttggttaac attggtaacg      840
aagaggctaa gcaaaccgaa gagtctgaat gtttaaagtg gttggataac cagccgctcg      900
gttcggtttt atatgtgtcc tttggtagt gcggtaccct cacatgtgag cagctcaatg      960
agcttgctct tggctcttgc gatagtgagc aacggtttct ttgggtcata cgaagtccta      1020
gtgggatcgc taattcgctc tattttgatt cacatagcca aacagatcca ttgacatttt      1080
taccaccggg atttttagag cggactaaaa aaagagggtt tgtgatccct ttttgggctc      1140
cacaagccca agtcttggcg catccatcca cgggaggatt tttaaactcat tgtggatgga      1200
attcgactct agagagtgtg gtaagcggta ttccacttat agcatggcca ttatacgcac      1260
aacagaagat gaatgcggtt ttgttgagt aagatattcg tgcggcactt aggccgcgtg      1320
ccggggacga tgggttagtt agaagagaag aggtggctag agtggtaaaa ggattgatgg      1380
aaggtgaaga aggcaaagga gtgaggaaca agatgaagga gttgaaggaa gcagcttgta      1440
gggtgttgaa ggatgatggg acttcgacaa aagcacttag tcttgtggcc ttaaagtgga      1500
aagcccacaa aaaagagtta gagcaaaatg gcaaccacta aatatttgat gttctaatat      1560
gatttgata atcaacggtg ggatttgtgc aaatgtgttt ctgtatgtat atgtatgttc      1620
tacttttctt tgcttcgttt gtctc
```

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

```
Met Glu Glu Ser Lys Thr Pro His Val Ala Ile Ile Pro Ser Pro Gly
1           5           10           15
Met Gly His Leu Ile Pro Leu Val Glu Phe Ala Lys Arg Leu Val His
20           25           30
Leu His Gly Leu Thr Val Thr Phe Val Ile Ala Gly Glu Gly Pro Pro
35           40           45
```



Ser	Lys	Ala	Gln	Arg	Thr	Val	Leu	Asp	Ser	Leu	Pro	Ser	Ser	Ile	Ser
50						55					60				
Ser	Val	Phe	Leu	Pro	Pro	Val	Asp	Leu	Thr	Asp	Leu	Ser	Ser	Ser	Thr
65					70					75					80
Arg	Ile	Glu	Ser	Arg	Ile	Ser	Leu	Thr	Val	Thr	Arg	Ser	Asn	Pro	Glu
				85					90					95	
Leu	Arg	Lys	Val	Phe	Asp	Ser	Phe	Val	Glu	Gly	Gly	Arg	Leu	Pro	Thr
			100					105					110		
Ala	Leu	Val	Val	Asp	Leu	Phe	Gly	Thr	Asp	Ala	Phe	Asp	Val	Ala	Val
		115					120					125			
Glu	Phe	His	Val	Pro	Pro	Tyr	Ile	Phe	Tyr	Pro	Thr	Thr	Ala	Asn	Val
	130					135					140				
Leu	Ser	Phe	Phe	Leu	His	Leu	Pro	Lys	Leu	Xaa	Glu	Thr	Val	Ser	Cys
145					150					155					160
Glu	Phe	Arg	Glu	Leu	Thr	Glu	Pro	Leu	Met	Leu	Pro	Gly	Cys	Val	Pro
				165					170					175	
Val	Ala	Gly	Lys	Asp	Phe	Leu	Asp	Pro	Ala	Gln	Asp	Arg	Lys	Asp	Asp
			180					185					190		
Ala	Tyr	Lys	Trp	Leu	Leu	His	Asn	Thr	Lys	Arg	Tyr	Lys	Glu	Ala	Glu
	195						200					205			
Gly	Ile	Leu	Val	Asn	Thr	Phe	Glu	Leu	Glu	Pro	Asn	Ala	Ile	Lys	
	210					215				220					
Ala	Leu	Gln	Glu	Pro	Gly	Leu	Asp	Lys	Pro	Pro	Val	Tyr	Pro	Val	Gly
225					230					235					240
Pro	Leu	Val	Asn	Ile	Gly	Lys	Gln	Glu	Ala	Lys	Gln	Thr	Glu	Glu	Ser
				245					250					255	
Glu	Cys	Leu	Lys	Trp	Leu	Asp	Asn	Gln	Pro	Leu	Gly	Ser	Val	Leu	Tyr
			260					265					270		
Val	Ser	Phe	Gly	Ser	Gly	Gly	Thr	Leu	Thr	Cys	Glu	Gln	Leu	Asn	Glu
	275						280					285			
Leu	Ala	Leu	Gly	Leu	Ala	Asp	Ser	Glu	Gln	Arg	Phe	Leu	Trp	Val	Ile
	290					295					300				
Arg	Ser	Pro	Ser	Gly	Ile	Ala	Asn	Ser	Ser	Tyr	Phe	Asp	Ser	His	Ser
305					310					315					320
Gln	Thr	Asp	Pro	Leu	Thr	Phe	Leu	Pro	Pro	Gly	Phe	Leu	Glu	Arg	Thr
				325					330					335	
Lys	Lys	Arg	Gly	Phe	Val	Ile	Pro	Phe	Trp	Ala	Pro	Gln	Ala	Gln	Val
			340					345					350		
Leu	Ala	His	Pro	Ser	Thr	Gly	Gly	Phe	Leu	Thr	His	Cys	Gly	Trp	Asn
		355					360					365			
Ser	Thr	Leu	Glu	Ser	Val	Val	Ser	Gly	Ile	Pro	Leu	Ile	Ala	Trp	Pro
	370					375					380				
Leu	Tyr	Ala	Glu	Gln	Lys	Met	Asn	Ala	Val	Leu	Leu	Ser	Glu	Asp	Ile
385					390					395					400
Arg	Ala	Ala	Leu	Arg	Pro	Arg	Ala	Gly	Asp	Asp	Gly	Leu	Val	Arg	Arg
				405					410					415	
Glu	Glu	Val	Ala	Arg	Val	Val	Lys	Gly	Leu	Met	Glu	Gly	Glu	Glu	Gly
			420					425					430		
Lys	Gly	Val	Arg	Asn	Lys	Met	Lys	Glu	Leu	Lys	Glu	Ala	Ala	Cys	Arg
		435					440					445			
Val	Leu	Lys	Asp	Asp	Gly	Thr	Ser	Thr	Lys	Ala	Leu	Ser	Leu	Val	Ala
	450					455					460				
Leu	Lys	Trp	Lys	Ala	His	Lys	Lys	Glu	Leu	Glu	Gln	Asn	Gly	Asn	His
465					470					475					480

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:																
Met	Gly	His	Leu	Ile	Pro	Leu	Val	Glu	Phe	Ala	Lys	Arg	Leu	Val	His	
1				5					10					15		
Leu	His	Gly	Leu	Thr	Val	Thr	Phe	Val	Ile	Ala	Gly	Glu	Gly	Pro	Pro	
			20					25					30			
Ser	Lys	Ala	Gln	Arg	Thr	Val	Leu	Asp	Ser	Leu	Pro	Ser	Ser	Ile	Ser	
		35					40					45				
Ser	Val	Phe	Leu	Pro	Pro	Val	Asp	Leu	Thr	Asp	Leu	Ser	Ser	Ser	Thr	
	50					55					60					
Arg	Ile	Glu	Ser	Arg	Ile	Ser	Leu	Thr	Val	Thr	Arg	Ser	Asn	Pro	Glu	
65				70						75				80		
Leu	Arg	Lys	Val	Phe	Asp	Ser	Phe	Val	Glu	Gly	Gly	Arg	Leu	Pro	Thr	
			85					90						95		
Ala	Leu	Val	Val	Asp	Leu	Phe	Gly	Thr	Asp	Ala	Phe	Asp	Val	Ala	Val	
			100					105					110			
Glu	Phe	His	Val	Pro	Pro	Tyr	Ile	Phe	Tyr	Pro	Thr	Thr	Ala	Asn	Val	
		115					120					125				
Leu	Ser	Phe	Phe	Leu	His	Leu	Pro	Lys	Leu	Xaa	Glu	Thr	Val	Ser	Cys	
	130					135					140					
Glu	Phe	Arg	Glu	Leu	Thr	Glu	Pro	Leu	Met	Leu	Pro	Gly	Cys	Val	Pro	
145				150						155				160		
Val	Ala	Gly	Lys	Asp	Phe	Leu	Asp	Pro	Ala	Gln	Asp	Arg	Lys	Asp	Asp	
			165					170						175		
Ala	Tyr	Lys	Trp	Leu	Leu	His	Asn	Thr	Lys	Arg	Tyr	Lys	Glu	Ala	Glu	
		180						185					190			
Gly	Ile	Leu	Val	Asn	Thr	Phe	Phe	Glu	Leu	Glu	Pro	Asn	Ala	Ile	Lys	
	195						200					205				
Ala	Leu	Gln	Glu	Pro	Gly	Leu	Asp	Lys	Pro	Pro	Val	Tyr	Pro	Val	Gly	
	210					215					220					
Pro	Leu	Val	Asn	Ile	Gly	Lys	Gln	Glu	Ala	Lys	Gln	Thr	Glu	Glu	Ser	
225				230						235				240		
Glu	Cys	Leu	Lys	Trp	Leu	Asp	Asn	Gln	Pro	Leu	Gly	Ser	Val	Leu	Tyr	
			245					250						255		
Val	Ser	Phe	Gly	Ser	Gly	Gly	Thr	Leu	Thr	Cys	Glu	Gln	Leu	Asn	Glu	
		260						265					270			
Leu	Ala	Leu	Gly	Leu	Ala	Asp	Ser	Glu	Gln	Arg	Phe	Leu	Trp	Val	Ile	
		275					280					285				
Arg	Ser	Pro	Ser	Gly	Ile	Ala	Asn	Ser	Ser	Tyr	Phe	Asp	Ser	His	Ser	
	290					295					300					
Gln	Thr	Asp	Pro	Leu	Thr	Phe	Leu	Pro	Pro	Gly	Phe	Leu	Glu	Arg	Thr	
305				310						315				320		
Lys	Lys	Arg	Gly	Phe	Val	Ile	Pro	Phe								

Val Leu Lys Asp Asp Gly Thr Ser Thr Lys Ala Leu Ser Leu Val Ala  
435 440 445  
Leu Lys Trp Lys Ala His Lys Lys Glu Leu Glu Gln Asn Gly Asn His  
450 455 460

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1498649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

Met Leu Pro Gly Cys Val Pro Val Ala Gly Lys Asp Phe Leu Asp Pro  
1 5 10 15  
Ala Gln Asp Arg Lys Asp Asp Ala Tyr Lys Trp Leu Leu His Asn Thr  
20 25 30  
Lys Arg Tyr Lys Glu Ala Glu Gly Ile Leu Val Asn Thr Phe Phe Glu  
35 40 45  
Leu Glu Pro Asn Ala Ile Lys Ala Leu Gln Glu Pro Gly Leu Asp Lys  
50 55 60  
Pro Pro Val Tyr Pro Val Gly Pro Leu Val Asn Ile Gly Lys Gln Glu  
65 70 75 80  
Ala Lys Gln Thr Glu Ser Glu Cys Leu Lys Trp Leu Asp Asn Gln  
85 90 95  
Pro Leu Gly Ser Val Leu Tyr Val Ser Phe Gly Ser Gly Gly Thr Leu  
100 105 110  
Thr Cys Glu Gln Leu Asn Glu Leu Ala Leu Gly Leu Ala Asp Ser Glu  
115 120 125  
Gln Arg Phe Leu Trp Val Ile Arg Ser Pro Ser Gly Ile Ala Asn Ser  
130 135 140  
Ser Tyr Phe Asp Ser His Ser Gln Thr Asp Pro Leu Thr Phe Leu Pro  
145 150 155 160  
Pro Gly Phe Leu Glu Arg Thr Lys Lys Arg Gly Phe Val Ile Pro Phe  
165 170 175  
Trp Ala Pro Gln Ala Gln Val Leu Ala His Pro Ser Thr Gly Gly Phe  
180 185 190  
Leu Thr His Cys Gly Trp Asn Ser Thr Leu Glu Ser Val Val Ser Gly  
195 200 205  
Ile Pro Leu Ile Ala Trp Pro Leu Tyr Ala Glu Gln Lys Met Asn Ala  
210 215 220  
Val Leu Leu Ser Glu Asp Ile Arg Ala Ala Leu Arg Pro Arg Ala Gly  
225 230 235 240  
Asp Asp Gly Leu Val Arg Arg Glu Glu Val Ala Arg Val Val Lys Gly  
245 250 255  
Leu Met Glu Gly Glu Glu Gly Lys Gly Val Arg Asn Lys Met Lys Glu  
260 265 270  
Leu Lys Glu Ala Ala Cys Arg Val Leu Lys Asp Asp Gly Thr Ser Thr  
275 280 285  
Lys Ala Leu Ser Leu Val Ala Leu Lys Trp Lys Ala His Lys Lys Glu  
290 295 300  
Leu Glu Gln Asn Gly Asn His  
305 310

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1499 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

(2) INFORMATION FOR SEQ ID NO:566:

(A) LENGTH: 462 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1498651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Leu	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ala	Leu	Phe	Tyr	Phe	Pro	Arg	Lys
1				5					10					15	
Phe	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu	Gly	Phe	Pro	Leu
			20					25					30		
Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val
		35					40					45			
Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu
	50					55					60				
Ala	Pro	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg
65					70					75					80
Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val
				85					90					95	
Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu
			100					105					110		
Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly

115	120	125
Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr Arg Gly Lys Met		
130	135	140
Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala Val Ser Thr Gly		
145	150	155
Phe Ile Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg		
165	170	175
Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met		
180	185	190
Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly		
195	200	205
Ser Met His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala		
210	215	220
Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser		
225	230	235
Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val		
245	250	255
Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys		
260	265	270
Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu		
275	280	285
Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp		
290	295	300
Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His		
305	310	315
Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala		
325	330	335
Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu		
340	345	350
Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg		
355	360	365
Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala		
370	375	380
Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu		
385	390	395
Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu		
405	410	415
Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn		
420	425	430
Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr		
435	440	445
Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val		
450	455	460

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1498652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

Met Ala Thr Ala Phe Ala Pro Thr Lys Leu Thr Ala Thr Val Pro Leu		
1	5	10
His Gly Ser His Glu Asn Arg Leu Leu Leu Pro Ile Arg Leu Ala Pro		
20	25	30
Pro Ser Ser Phe Leu Gly Ser Thr Arg Ser Leu Ser Leu Arg Arg Leu		
35	40	45

Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val	Gln	Glu
50						55				60					
Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	Ile	Thr
65					70					75					80
Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	Arg	Ser
				85				90						95	
Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	Phe	Gly
			100				105						110		
Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	Phe	Ile
		115				120						125			
Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	Ser	Thr	Tyr	Arg	Asp	His
	130					135					140				
Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala	Arg	Ala	Val	Met	Ser	Glu
145					150					155					160
Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg	Gly	Gln	Gly	Gly	Ser	Met
				165					170					175	
His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu	Gly	Gly	Phe	Ala	Phe	Ile
			180				185						190		
Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala	Ala	Phe	Ser	Ser	Lys	Tyr
	195					200						205			
Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp	Asp	Val	Thr	Val	Ala	Phe
	210				215						220				
Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln	Phe	Phe	Glu	Cys	Leu	Asn
225					230					235					240
Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile	Phe	Val	Val	Glu	Asn	Asn
				245					250					255	
Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg	Ala	Thr	Ser	Asp	Pro	Glu
			260					265					270		
Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met	Pro	Gly	Val	His	Val	Asp
	275						280					285			
Gly	Met	Asp	Val	Leu	Lys	Val	Arg	Glu	Val	Ala	Lys	Glu	Ala	Val	Thr
	290					295					300				
Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu	Val	Glu	Cys	Glu	Thr	Tyr
	305				310					315					320
Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro	Asp	Glu	Leu	Arg	Asp	Ala
				325					330					335	
Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp	Pro	Ile	Ala	Ala	Leu	Lys
			340					345					350		
Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys	Glu	Ala	Glu	Leu	Lys	Ser
		355					360					365			
Ile	Glu	Lys	Lys	Ile	Asp	Glu	Leu	Val	Glu	Glu	Ala	Val	Glu	Phe	Ala
	370					375					380				
Asp	Ala	Ser	Pro	Gln	Pro	Gly	Arg	Ser	Gln	Leu	Leu	Glu	Asn	Val	Phe
	385				390					395					400
Ala	Asp	Pro	Lys	Gly	Phe	Gly	Ile	Gly	Pro	Asp	Gly	Arg	Tyr	Arg	Cys
				405					410					415	
Glu	Asp	Pro	Lys	Phe	Thr	Glu	Gly	Thr	Ala	Gln	Val				
			420					425							

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr

1	5	10	15
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala			
20	25	30	
Val Ser Thr Gly Phe Ile Lys Leu Thr Lys Ser Asp Ser Val Val			
35	40	45	
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala			
50	55	60	
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg			
65	70	75	80
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu			
85	90	95	
Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala			
100	105	110	
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp			
115	120	125	
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln			
130	135	140	
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile			
145	150	155	160
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg			
165	170	175	
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met			
180	185	190	
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val			
195	200	205	
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu			
210	215	220	
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro			
225	230	235	240
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp			
245	250	255	
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys			
260	265	270	
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu			
275	280	285	
Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln			
290	295	300	
Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro			
305	310	315	320
Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala			
325	330	335	
Gln Val			

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

atcctttctc tctgtatctc tgtgtattct tctctcatgg agcctgctca tatcgattgg	60
aagagaatcg attctcgttt tgttgaagac gttttttacg aacacatcag agctcctaaa	120
tggttcgatt tcttgcccc taccatttt gactccattg acgacgatgc ttggttctgc	180
aaacctgaat gtaatcatcc caagagacct gaggactttt tctcaacgcc gacttcttcc	240
aagcatccaa gtctgaggga tacgaatgag actctaacag agcagaatca gaggaggagg	300
ggatatgctt tatcaccttc tactccaaac aaccaagaaa gtgaaaatca gaacccgaac	360

ttagccacac	ctccaagcta	ccaagcaaaa	tcatggagag	cagcaattaa	atcaacttct	420
gtcaagaaga	tgaataaaga	agttccaaga	ctaaagagca	cacaatcagc	tagaaatctg	480
ttttcaggga	gagacatatt	tggtcatatc	tcagatttbt	gctatgaatt	gaagagatta	540
gccacaaggg	ttactgagag	agaagatact	gggaaatctg	aagtgaagga	gagtcatcaa	600
gtgggtggaa	tagtaaataca	gccttactct	gttcatgact	tggaattgaa	aaaggaaata	660
aagccactgc	ttgaagtaag	caaagataag	ctccctgagt	ccacggatgt	taaaggaagc	720
acattttaaag	agaaccgtag	aagaaagaag	agagtggatg	atgcagagaa	cattcctgtc	780
tcacttaatg	tggagactgt	aaaaaacaaa	ggagaggagg	gtagaagaaa	gaagagaatg	840
gatgatgcag	agaacatccc	agttcctcta	aaactggaga	ctataaagaa	caaaggacac	900
gaacgattcc	tgcagcaaat	caggacaaac	ccaccatctc	ctcaatgctt	ctctgagaac	960
cggacagcta	cattgaaacc	cttgaggacc	aaacctacgg	aagtgttgaa	gagaaaggaa	1020
gatgaagctg	aagaagaaaa	gaacagaaag	agtggagaaa	gcaaagaagc	aacaagggga	1080
ttggacgttc	tctggttctt	aaagccttgc	actttagcca	actagaaaac	cttcacaaaa	1140
ttctttctat	attgattcat	tcttttgtaa	atttcatttt	attcaactgt	aactaacgag	1200
atgattatct	tgctcagata	tataattctg	ggcaaatttg	attcaatctc	ttactttttac	1260
acatacaacg	atttgttt					

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1498655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Ile	Leu	Ser	Leu	Cys	Ile	Ser	Val	Tyr	Ser	Ser	Leu	Met	Glu	Pro	Ala
1			5					10					15		
His	Ile	Asp	Trp	Lys	Arg	Ile	Asp	Ser	Arg	Phe	Val	Glu	Asp	Val	Phe
			20					25				30			
Tyr	Glu	His	Ile	Arg	Ala	Pro	Lys	Trp	Phe	Asp	Phe	Leu	Ala	Pro	Thr
			35				40					45			
His	Phe	Asp	Ser	Ile	Asp	Asp	Asp	Ala	Trp	Phe	Cys	Lys	Pro	Glu	Cys
			50			55					60				
Asn	His	Pro	Lys	Arg	Pro	Glu	Asp	Phe	Phe	Ser	Thr	Pro	Thr	Ser	Ser
65					70					75				80	
Lys	His	Pro	Ser	Leu	Arg	Asp	Thr	Asn	Glu	Thr	Leu	Thr	Glu	Gln	Asn
			85					90						95	
Gln	Arg	Arg	Arg	Gly	Tyr	Ala	Leu	Ser	Pro	Ser	Thr	Pro	Asn	Asn	Gln
			100					105					110		
Glu	Ser	Glu	Asn	Gln	Asn	Pro	Asn	Leu	Ala	Thr	Pro	Pro	Ser	Tyr	Gln
			115				120					125			
Ala	Lys	Ser	Trp	Arg	Ala	Ala	Ile	Lys	Ser	Thr	Ser	Val	Lys	Lys	Met
			130			135					140				
Asn	Lys	Glu	Val	Pro	Arg	Leu	Lys	Ser	Thr	Gln	Ser	Ala	Arg	Asn	Leu
145				150					155					160	
Phe	Ser	Gly	Arg	Asp	Ile	Phe	Gly	His	Ile	Ser	Asp	Xaa	Cys	Tyr	Glu
			165					170						175	
Leu	Lys	Arg	Leu	Ala	Thr	Arg	Val	Thr	Glu	Arg	Glu	Asp	Thr	Gly	Lys
			180					185					190		
Ser	Glu	Val	Lys	Glu	Ser	His	Gln	Val	Gly	Gly	Ile	Val	Asn	Gln	Pro
			195				200				205				
Tyr	Ser	Val	His	Asp	Leu	Glu	Leu	Lys	Lys	Glu	Ile	Lys	Pro	Leu	Leu
			210				215				220				
Glu	Val	Ser	Lys	Asp	Lys	Leu	Pro	Glu	Ser	Thr	Asp	Val	Lys	Gly	Ser
225				230						235				240	
Thr	Phe	Lys	Glu	Asn	Arg	Arg	Arg	Lys	Lys	Arg	Val	Asp	Asp	Ala	Glu
			245							250				255	
Asn	Ile	Pro	Val	Ser	Leu	Asn	Val	Glu	Thr	Val	Lys	Asn	Lys	Gly	Glu



260	265	270
Glu Gly Arg Arg Lys Lys Arg Met Asp Asp Ala Glu Asn Ile Pro Val		
275	280	285
Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His Glu Arg Phe Leu		
290	295	300
Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys Phe Ser Glu Asn		
305	310	315
Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro Thr Glu Val Leu		
325	330	335
Lys Arg Lys Glu Asp Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser Gly		
340	345	350
Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu Trp Phe Leu Lys		
355	360	365
Pro Cys Thr Leu Ala Asn		
370		

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..362
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

Met Glu Pro Ala His Ile Asp Trp Lys Arg Ile Asp Ser Arg Phe Val		
1	5	10
Glu Asp Val Phe Tyr Glu His Ile Arg Ala Pro Lys Trp Phe Asp Phe		
20	25	30
Leu Ala Pro Thr His Phe Asp Ser Ile Asp Asp Asp Ala Trp Phe Cys		
35	40	45
Lys Pro Glu Cys Asn His Pro Lys Arg Pro Glu Asp Phe Phe Ser Thr		
50	55	60
Pro Thr Ser Ser Lys His Pro Ser Leu Arg Asp Thr Asn Glu Thr Leu		
65	70	75
Thr Glu Gln Asn Gln Arg Arg Arg Gly Tyr Ala Leu Ser Pro Ser Thr		
85	90	95
Pro Asn Asn Gln Glu Ser Glu Asn Gln Asn Pro Asn Leu Ala Thr Pro		
100	105	110
Pro Ser Tyr Gln Ala Lys Ser Trp Arg Ala Ala Ile Lys Ser Thr Ser		
115	120	125
Val Lys Lys Met Asn Lys Glu Val Pro Arg Leu Lys Ser Thr Gln Ser		
130	135	140
Ala Arg Asn Leu Phe Ser Gly Arg Asp Ile Phe Gly His Ile Ser Asp		
145	150	155
Xaa Cys Tyr Glu Leu Lys Arg Leu Ala Thr Arg Val Thr Glu Arg Glu		
165	170	175
Asp Thr Gly Lys Ser Glu Val Lys Glu Ser His Gln Val Gly Gly Ile		
180	185	190
Val Asn Gln Pro Tyr Ser Val His Asp Leu Glu Leu Lys Lys Glu Ile		
195	200	205
Lys Pro Leu Leu Glu Val Ser Lys Asp Lys Leu Pro Glu Ser Thr Asp		
210	215	220
Val Lys Gly Ser Thr Phe Lys Glu Asn Arg Arg Arg Lys Lys Arg Val		
225	230	235
Asp Asp Ala Glu Asn Ile Pro Val Ser Leu Asn Val Glu Thr Val Lys		
245	250	255
Asn Lys Gly Glu Glu Gly Arg Arg Lys Lys Arg Met Asp Asp Ala Glu		
260	265	270

Asn Ile Pro Val Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His  
275 280 285  
Glu Arg Phe Leu Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys  
290 295 300  
Phe Ser Glu Asn Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro  
305 310 315 320  
Thr Glu Val Leu Lys Arg Lys Glu Asp Glu Ala Glu Glu Glu Lys Asn  
325 330 335  
Arg Lys Ser Gly Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu  
340 345 350  
Trp Phe Leu Lys Pro Cys Thr Leu Ala Asn  
355 360

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

Met Asn Lys Glu Val Pro Arg Leu Lys Ser Thr Gln Ser Ala Arg Asn  
1 5 10 15  
Leu Phe Ser Gly Arg Asp Ile Phe Gly His Ile Ser Asp Xaa Cys Tyr  
20 25 30  
Glu Leu Lys Arg Leu Ala Thr Arg Val Thr Glu Arg Glu Asp Thr Gly  
35 40 45  
Lys Ser Glu Val Lys Glu Ser His Gln Val Gly Gly Ile Val Asn Gln  
50 55 60  
Pro Tyr Ser Val His Asp Leu Glu Leu Lys Lys Glu Ile Lys Pro Leu  
65 70 75 80  
Leu Glu Val Ser Lys Asp Lys Leu Pro Glu Ser Thr Asp Val Lys Gly  
85 90 95  
Ser Thr Phe Lys Glu Asn Arg Arg Arg Lys Lys Arg Val Asp Asp Ala  
100 105 110  
Glu Asn Ile Pro Val Ser Leu Asn Val Glu Thr Val Lys Asn Lys Gly  
115 120 125  
Glu Glu Gly Arg Arg Lys Lys Arg Met Asp Asp Ala Glu Asn Ile Pro  
130 135 140  
Val Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His Glu Arg Phe  
145 150 155 160  
Leu Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys Phe Ser Glu  
165 170 175  
Asn Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro Thr Glu Val  
180 185 190  
Leu Lys Arg Lys Glu Asp Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser  
195 200 205  
Gly Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu Trp Phe Leu  
210 215 220  
Lys Pro Cys Thr Leu Ala Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1135

(D) OTHER INFORMATION: / Ceres Seq. ID 1498658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

acaaactcat	catcataagc	aacaatggtg	gtgtcactct	tctcttccag	aaatgttttc	60
tatacgtaa	gcttatgctt	atttgcagca	ttataccagc	cggttatgag	tagaccggct	120
aagtttgaag	atgacttttag	gatcgcatgg	tccgatactc	atatcactca	aattgacgga	180
ggcatagcca	ttcagctcaa	attggaccct	agctcaggat	gtggatttgc	ttcgaagaag	240
caatacttgt	tcggccgtgt	gagcatgaaa	atcaaaactga	tccccgggtga	ttctgccggg	300
actgtcactg	ccttctacat	gaattcagat	accgattcgg	tacgagacga	gcttgatttt	360
gagttcttag	gaaatcgaag	tggacaacct	tacacagtgc	aaaccaatgt	gtttgctcat	420
ggtaaaggcg	atagagagca	aagagttaac	ctttggttcg	acccttctcg	tgatttccac	480
gaatatgcca	tctcatggaa	ccatctccgt	attgtcttct	acgtagacaa	tgtgcccac	540
agggtttaca	agaacaatga	ggcaaggaaa	gtaccatacc	caagattcca	accaatgggt	600
gtatattcca	cgttatggga	agccgatgat	tgggcgacac	gtggaggaat	agagaaaatc	660
aattggtcga	gagcgccatt	ttatgcttat	tacaaagatt	ttgatataga	aggatgtccg	720
gttccaggac	cgcgagattg	tcccgtctaat	tcgaagaatt	ggtgggaagg	cagtgcgtac	780
caccagttga	gtccggtgga	agctcgaagt	tatagatggg	tccgagtga	ccatatggtc	840
tacgattatt	gcactgacaa	atctcgtttt	cctgttccac	ctccagaatg	ctcggctgga	900
atctgatcca	aacattattg	tcttaaaagc	aaaacaagtg	cgaagtgggt	ccataagcaa	960
cgttgcaatg	tatgtgaagt	gattaatgag	tcttgtggta	tgtggtgaat	tgctcataat	1020
cgatctgatt	gtggtcaa	gttcatatat	atatgtatat	ctttgaattt	tactttgttt	1080
tcgatgatgc	ttatgttttg	ttgatctatt	gaagagaacc	atgtttgttt	gttgc	

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1498659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Met	Val	Val	Ser	Phe	Ser	Ser	Arg	Val	Phe	Tyr	Thr	Leu	Ser	
1			5				10					15		
Leu	Cys	Leu	Phe	Ala	Ala	Leu	Tyr	Gln	Pro	Val	Met	Ser	Arg	Pro
			20				25					30		
Lys	Phe	Glu	Asp	Asp	Phe	Arg	Ile	Ala	Trp	Ser	Asp	Thr	His	Ile
			35				40					45		
Gln	Ile	Asp	Gly	Gly	Ile	Ala	Ile	Gln	Leu	Lys	Leu	Asp	Pro	Ser
			50				55				60			
Gly	Cys	Gly	Phe	Ala	Ser	Lys	Lys	Gln	Tyr	Leu	Phe	Gly	Arg	Val
65					70				75					80
Met	Lys	Ile	Lys	Leu	Ile	Pro	Gly	Asp	Ser	Ala	Gly	Thr	Val	Thr
			85				90						95	
Phe	Tyr	Met	Asn	Ser	Asp	Thr	Asp	Ser	Val	Arg	Asp	Glu	Leu	Asp
			100				105					110		
Glu	Phe	Leu	Gly	Asn	Arg	Ser	Gly	Gln	Pro	Tyr	Thr	Val	Gln	Thr
			115				120					125		
Val	Phe	Ala	His	Gly	Lys	Gly	Asp	Arg	Glu	Gln	Arg	Val	Asn	Leu
			130				135				140			
Phe	Asp	Pro	Ser	Arg	Asp	Phe	His	Glu	Tyr	Ala	Ile	Ser	Trp	Asn
145					150				155					160
Leu	Arg	Ile	Val	Phe	Tyr	Val	Asp	Asn	Val	Pro	Ile	Arg	Val	Tyr
			165				170					175		
Asn	Asn	Glu	Ala	Arg	Lys	Val	Pro	Tyr	Pro	Arg	Phe	Gln	Pro	Met
			180				185					190		
Val	Tyr	Ser	Thr	Leu	Trp	Glu	Ala	Asp	Asp	Trp	Ala	Thr	Arg	Gly

195 200 205  
Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe Tyr Ala Tyr Tyr Lys  
210 215 220  
Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Ala Asp Cys Pro  
225 230 235 240  
Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala Tyr His Gln Leu Ser  
245 250 255  
Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg Val Asn His Met Val  
260 265 270  
Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro Val Pro Pro Pro Glu  
275 280 285  
Cys Ser Ala Gly Ile  
290

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Met Ser Arg Pro Ala Lys Phe Glu Asp Asp Phe Arg Ile Ala Trp Ser  
1 5 10 15  
Asp Thr His Ile Thr Gln Ile Asp Gly Gly Ile Ala Ile Gln Leu Lys  
20 25 30  
Leu Asp Pro Ser Ser Gly Cys Gly Phe Ala Ser Lys Lys Gln Tyr Leu  
35 40 45  
Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala  
50 55 60  
Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp Thr Asp Ser Val Arg  
65 70 75 80  
Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr  
85 90 95  
Thr Val Gln Thr Asn Val Phe Ala His Gly Lys Gly Asp Arg Glu Gln  
100 105 110  
Arg Val Asn Leu Trp Phe Asp Pro Ser Arg Asp Phe His Glu Tyr Ala  
115 120 125  
Ile Ser Trp Asn His Leu Arg Ile Val Phe Tyr Val Asp Asn Val Pro  
130 135 140  
Ile Arg Val Tyr Lys Asn Asn Glu Ala Arg Lys Val Pro Tyr Pro Arg  
145 150 155 160  
Phe Gln Pro Met Gly Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp  
165 170 175  
Ala Thr Arg Gly Gly Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe  
180 185 190  
Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly  
195 200 205  
Pro Ala Asp Cys Pro Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala  
210 215 220  
Tyr His Gln Leu Ser Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg  
225 230 235 240  
Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro  
245 250 255  
Val Pro Pro Pro Glu Cys Ser Ala Gly Ile  
260 265

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..213  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498661  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met	Lys	Ile	Lys	Leu	Ile	Pro	Gly	Asp	Ser	Ala	Gly	Thr	Val	Thr	Ala
1			5				10				15				
Phe	Tyr	Met	Asn	Ser	Asp	Thr	Asp	Ser	Val	Arg	Asp	Glu	Leu	Asp	Phe
			20				25				30				
Glu	Phe	Leu	Gly	Asn	Arg	Ser	Gly	Gln	Pro	Tyr	Thr	Val	Gln	Thr	Asn
			35				40				45				
Val	Phe	Ala	His	Gly	Lys	Gly	Asp	Arg	Glu	Gln	Arg	Val	Asn	Leu	Trp
			50				55				60				
Phe	Asp	Pro	Ser	Arg	Asp	Phe	His	Glu	Tyr	Ala	Ile	Ser	Trp	Asn	His
65						70				75				80	
Leu	Arg	Ile	Val	Phe	Tyr	Val	Asp	Asn	Val	Pro	Ile	Arg	Val	Tyr	Lys
				85					90					95	
Asn	Asn	Glu	Ala	Arg	Lys	Val	Pro	Tyr	Pro	Arg	Phe	Gln	Pro	Met	Gly
			100						105				110		
Val	Tyr	Ser	Thr	Leu	Trp	Glu	Ala	Asp	Asp	Trp	Ala	Thr	Arg	Gly	Gly
			115				120				125				
Ile	Glu	Lys	Ile	Asn	Trp	Ser	Arg	Ala	Pro	Phe	Tyr	Ala	Tyr	Tyr	Lys
			130				135				140				
Asp	Phe	Asp	Ile	Glu	Gly	Cys	Pro	Val	Pro	Gly	Pro	Ala	Asp	Cys	Pro
145					150					155				160	
Ala	Asn	Ser	Lys	Asn	Trp	Trp	Glu	Gly	Ser	Ala	Tyr	His	Gln	Leu	Ser
				165					170					175	
Pro	Val	Glu	Ala	Arg	Ser	Tyr	Arg	Trp	Val	Arg	Val	Asn	His	Met	Val
			180					185					190		
Tyr	Asp	Tyr	Cys	Thr	Asp	Lys	Ser	Arg	Phe	Pro	Val	Pro	Pro	Pro	Glu
		195				200					205				
Cys	Ser	Ala	Gly	Ile											
			210												

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1519 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1519  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

aaaaataact	taatcacaca	caaggagaga	agagagaaaag	agagaaagag	agacagagat	60
aatggcgtag	agtgcgtggt	tcctacacca	gagcgcattg	gcttcatcag	ccgcacgatc	120
atcatcttcc	tcctcatccc	agcgtcacgt	gtcgtctctc	aaacctgttc	agatcatctg	180
taaagctcaa	cagtcctcatg	aagacgataa	ctccgccgtc	tcccgccgtc	ttgctctcac	240
tctcctcgtc	ggcgccgctg	ctgttggttc	caaagtatct	cctgctgatg	ccgcctacgg	300
tgaagctgca	aacgtgtttg	ggaagccaaa	gacgaacaca	gacttcttgc	catacaatgg	360
agatgggttc	aaagtgcagg	ttccagcaaa	atggaaccca	agcaaagaga	ttgagtatcc	420
aggacaagtc	cttaggttcg	aagacaactt	cgatgctact	agcaatctca	atgtcatggg	480
cactcctacc	gacaagaagt	ccatcactga	ttacggttct	cccgaagagt	tcctctctca	540
ggttaattac	ctcctaggga	aacaagctta	cttcgggtgag	actgcctctg	agggaggctt	600
tgacaacaat	gcagtggcaa	cagcaaacat	tctggagtca	tcattctcagg	aagttggtgg	660

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gaaaccctac tattacttgt ctgtgttgac aagaacggct gatggagacg aaggtgggaa 720
gcatcagctg atcacagcaa ccgtgaagga gggaagcktt acatctgcaa agcacaagct 780
ggagacaaga ggtggttcaa gggagccagg aaatttgtcg agagcgcagc cacttctttc 840
agtgttgctt gmgrtgaaag caacacaacg taacaatgct ctgcttgctt tcttcatttg 900
tctcttgtaa aaaatggaaa atgaaactga gcttttgaga actatcaaga tgatgttacc 960
ttttcggcat cacttgtgta cctatgatac cagactcgtt tccaagtttt cttaaaaaaac 1020
aactatattc aatagatatt ttctcaaatt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080
aaaaaamcaa aaaaaaaaaa aaaaaagctt ctcgkgccgt tttttttttt ttttttttga 1140
gttttttggtt ggacgggtgga gattggagaa gctagaagga ttgacgggtg agggccaacg 1200
tgcacaggag tttgtgtgtg ggtagctca gaggattaga cgccttcaag agcgtgcaga 1260
cgagagagct aagaagctta agaagacca tgaggtttgc tttagtgtga tcttcgataa 1320
gcagattagt gtgtaaacctc ttgaaaatat caaacctttc ctttctccgt ttcttgtttt 1380
tttactctaa tgaggcctac tcatggttgt gtgagtgggt cctcaagtat cattgtccaa 1440
taaggagcca atttatttat ggctggctgt tttattacaa attatgtgta tgtgttaata 1500
attaaagatt gaattatct
```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1498663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

```
Met Ala Tyr Ser Ala Cys Phe Leu His Gln Ser Ala Leu Ala Ser Ser
1      5      10      15
Ala Ala Arg Ser Ser Ser Ser Ser Ser Ser Gln Arg His Val Ser Leu
20      25      30
Ser Lys Pro Val Gln Ile Ile Cys Lys Ala Gln Gln Ser His Glu Asp
35      40      45
Asp Asn Ser Ala Val Ser Arg Arg Leu Ala Leu Thr Leu Leu Val Gly
50      55      60
Ala Ala Ala Val Gly Ser Lys Val Ser Pro Ala Asp Ala Ala Tyr Gly
65      70      75      80
Glu Ala Ala Asn Val Phe Gly Lys Pro Lys Thr Asn Thr Asp Phe Leu
85      90      95
Pro Tyr Asn Gly Asp Gly Phe Lys Val Gln Val Pro Ala Lys Trp Asn
100     105     110
Pro Ser Lys Glu Ile Glu Tyr Pro Gly Gln Val Leu Arg Phe Glu Asp
115     120     125
Asn Phe Asp Ala Thr Ser Asn Leu Asn Val Met Val Thr Pro Thr Asp
130     135     140
Lys Lys Ser Ile Thr Asp Tyr Gly Ser Pro Glu Glu Phe Leu Ser Gln
145     150     155     160
Val Asn Tyr Leu Leu Gly Lys Gln Ala Tyr Phe Gly Glu Thr Ala Ser
165     170     175
Glu Gly Gly Phe Asp Asn Asn Ala Val Ala Thr Ala Asn Ile Leu Glu
180     185     190
Ser Ser Ser Gln Glu Val Gly Gly Lys Pro Tyr Tyr Tyr Leu Ser Val
195     200     205
Leu Thr Arg Thr Ala Asp Gly Asp Glu Gly Gly Lys His Gln Leu Ile
210     215     220
Thr Ala Thr Val Lys Glu Gly Ser Xaa Thr Ser Ala Lys His Lys Leu
225     230     235     240
Glu Thr Arg Gly Gly Ser Arg Glu Pro Gly Asn Leu Ser Arg Ala Gln
245     250     255
Pro Leu Leu Ser Val Leu Leu Xaa Xaa Lys Ala Thr Gln Arg Asn Asn
260     265     270
```

Ala Leu Leu Ala Phe Phe Ile Cys Leu Leu  
275 280

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met	Val	Thr	Pro	Thr	Asp	Lys	Lys	Ser	Ile	Thr	Asp	Tyr	Gly	Ser	Pro
1				5				10						15	
Glu	Glu	Phe	Leu	Ser	Gln	Val	Asn	Tyr	Leu	Leu	Gly	Lys	Gln	Ala	Tyr
			20					25					30		
Phe	Gly	Glu	Thr	Ala	Ser	Glu	Gly	Gly	Phe	Asp	Asn	Asn	Ala	Val	Ala
			35				40					45			
Thr	Ala	Asn	Ile	Leu	Glu	Ser	Ser	Ser	Gln	Glu	Val	Gly	Gly	Lys	Pro
			50			55					60				
Tyr	Tyr	Tyr	Leu	Ser	Val	Leu	Thr	Arg	Thr	Ala	Asp	Gly	Asp	Glu	Gly
65					70					75				80	
Gly	Lys	His	Gln	Leu	Ile	Thr	Ala	Thr	Val	Lys	Glu	Gly	Ser	Xaa	Thr
			85						90					95	
Ser	Ala	Lys	His	Lys	Leu	Glu	Thr	Arg	Gly	Gly	Ser	Arg	Glu	Pro	Gly
			100					105					110		
Asn	Leu	Ser	Arg	Ala	Gln	Pro	Leu	Leu	Ser	Val	Leu	Leu	Xaa	Xaa	Lys
			115				120					125			
Ala	Thr	Gln	Arg	Asn	Asn	Ala	Leu	Leu	Ala	Phe	Phe	Ile	Cys	Leu	Leu
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

tctctctctc	tctctctctc	tgttctttta	tttagagaga	aaaaataagc	attcttcctt	60
ctctgttttc	gagcgggaaa	ttctggagat	ggctatacaa	gcgcagttga	attacaacgc	120
tccgaatgcg	aatcaaatac	gttttggttg	gtccgagttt	tctttgatca	acaacaatgg	180
cgttattgga	atcgcatcat	caacaacaac	agtctccttc	tcaaagcttt	ttagctgctc	240
agatggagaa	acagaagcaa	gagatcgatc	agttcatcaa	aatacagaac	gagaggttga	300
gatatgtggt	gcaagaacag	aggaagcgag	aaatggagat	gattttaagg	aaaatggaga	360
gtaaagcttt	gcttttgatg	agtcagaagg	aagaagaaat	gtcgaaagca	ttgaacaaga	420
acattggaact	cgaagatctg	ttgagaaaaa	tggaatgga	gaatcagacg	tggcag	

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Leu	Ser	Leu	Ser	Leu	Ser	Leu	Phe	Phe	Asn	Leu	Glu	Arg	Lys	Asn	Lys
1				5					10					15	
His	Ser	Ser	Phe	Ser	Val	Phe	Glu	Arg	Glu	Ile	Leu	Glu	Met	Ala	Ile
			20					25					30		
Gln	Ala	Gln	Leu	Asn	Tyr	Asn	Ala	Pro	Asn	Ala	Asn	Gln	Ile	Gly	Phe
		35				40						45			
Gly	Gly	Ser	Glu	Phe	Ser	Leu	Ile	Asn	Asn	Asn	Gly	Val	Ile	Gly	Ile
	50					55					60				
Ala	Ser	Ser	Thr	Thr	Thr	Val	Ser	Phe	Ser	Lys	Leu	Phe	Ser	Cys	Ser
65					70					75				80	
Asp	Gly	Glu	Thr	Glu	Ala	Arg	Asp	Arg	Ser	Val	His	Gln	Asn	Thr	Glu
			85					90					95		
Arg	Glu	Val	Glu	Ile	Cys	Val	Ala	Arg	Thr	Glu	Glu	Ala	Arg	Asn	Gly
		100						105					110		
Asp	Asp	Phe	Lys	Glu	Asn	Gly	Glu								
	115					120									

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1498667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met	Ala	Ile	Gln	Ala	Gln	Leu	Asn	Tyr	Asn	Ala	Pro	Asn	Ala	Asn	Gln
1				5					10					15	
Ile	Gly	Phe	Gly	Gly	Ser	Glu	Phe	Ser	Leu	Ile	Asn	Asn	Asn	Gly	Val
			20					25					30		
Ile	Gly	Ile	Ala	Ser	Ser	Thr	Thr	Thr	Val	Ser	Phe	Ser	Lys	Leu	Phe
		35				40						45			
Ser	Cys	Ser	Asp	Gly	Glu	Thr	Glu	Ala	Arg	Asp	Arg	Ser	Val	His	Gln
	50				55					60					
Asn	Thr	Glu	Arg	Glu	Val	Glu	Ile	Cys	Val	Ala	Arg	Thr	Glu	Glu	Ala
65				70					75					80	
Arg	Asn	Gly	Asp	Asp	Phe	Lys	Glu	Asn	Gly	Glu					
			85					90							

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1498668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met	Ala	Leu	Leu	Glu	Ser	His	His	Gln	Gln	Gln	Gln	Ser	Pro	Ser	Gln
1				5					10					15	
Ser	Phe	Leu	Ala	Ala	Gln	Met	Glu	Lys	Gln	Lys	Gln	Glu	Ile	Asp	Gln
		20						25					30		



Phe Ile Lys Ile Gln Asn Glu Arg Leu Arg Tyr Val Leu Gln Glu Gln  
35 40 45  
Arg Lys Arg Glu Met Glu Met Ile Leu Arg Lys Met Glu Ser Lys Ala  
50 55 60  
Leu Leu Leu Met Ser Gln Lys Glu Glu Glu Met Ser Lys Ala Leu Asn  
65 70 75 80  
Lys Asn Met Glu Leu Glu Asp Leu Leu Arg Lys Met Glu Met Glu Asn  
85 90 95  
Gln Thr Trp Gln  
100

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..777
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

attggaacaa aatattttct tagaaaaaaa attatgggat tttgcttctc caaatttggc	60
aaatcacaaa cacatgagat cccaatctct tcctcttccg attcaagccc tcctcatcac	120
taccaacctc tccctaaacc aactgtttct caaggtcaaa ccagtaatcc cacctccaat	180
cctcagccca aacccaaacc cgctcctcct cctcctccgt caacatcctc cggttcacaa	240
atcgggtccaa tcctaaaccg accaatgatc gatctctcag ctctctacga cctccacaaa	300
gaactcggcc gtggccaatt cggaatcact tacaaatgca cggacaaatc caacggtcga	360
gaatacgccct gcaaatccat ctcaaaacgt aaactcatc gtcgcaaaga catcgaagac	420
gtgagacgtg aggtcatgat cttgcaacac cttactggtc aaccaaacad agtcgagttt	480
cgaggcgcggt atgaagacaa agacaatctt catttggtta tggagctctg ttctggagga	540
gattatgttg gtggtggcca tcaatgatga gtggtgaggc tcatgtctcat gcattcgtaa	600
cgttgttata ttatttaatt aaatggaaaa tgataaatta attattgcaa taaaatgata	660
cattagcaat tgtgtatgtc gttattttta ttttgagtcg cattgtatgc tgattccata	720
tgttcggcctt tggtcgggtt caagtgtggt taataaaatg gttattttac ttttgcc	

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

Ile Gly Thr Lys Tyr Phe Leu Arg Lys Lys Ile Met Gly Phe Cys Phe	
1 5 10 15	
Ser Lys Phe Gly Lys Ser Gln Thr His Glu Ile Pro Ile Ser Ser Ser	
20 25 30	
Ser Asp Ser Ser Pro Pro His His Tyr Gln Pro Leu Pro Lys Pro Thr	
35 40 45	
Val Ser Gln Gly Gln Thr Ser Asn Pro Thr Ser Asn Pro Gln Pro Lys	
50 55 60	
Pro Lys Pro Ala Pro Pro Pro Pro Pro Ser Thr Ser Ser Gly Ser Gln	
65 70 75 80	
Ile Gly Pro Ile Leu Asn Arg Pro Met Ile Asp Leu Ser Ala Leu Tyr	
85 90 95	
Asp Leu His Lys Glu Leu Gly Arg Gly Gln Phe Gly Ile Thr Tyr Lys	
100 105 110	

Cys	Thr	Asp	Lys	Ser	Asn	Gly	Arg	Glu	Tyr	Ala	Cys	Lys	Ser	Ile	Ser
	115						120					125			
Lys	Arg	Lys	Leu	Ile	Arg	Arg	Lys	Asp	Ile	Glu	Asp	Val	Arg	Arg	Glu
	130					135					140				
Val	Met	Ile	Leu	Gln	His	Leu	Thr	Gly	Gln	Pro	Asn	Ile	Val	Glu	Phe
	145				150					155					160
Arg	Gly	Ala	Tyr	Glu	Asp	Lys	Asp	Asn	Leu	His	Leu	Val	Met	Glu	Leu
				165					170					175	
Cys	Ser	Gly	Gly	Asp	Tyr	Val	Gly	Gly	Gly	His	His				
		180					185								

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1498673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met	Gly	Phe	Cys	Phe	Ser	Lys	Phe	Gly	Lys	Ser	Gln	Thr	His	Glu	Ile
1			5						10					15	
Pro	Ile	Ser	Ser	Ser	Ser	Asp	Ser	Ser	Pro	Pro	His	His	Tyr	Gln	Pro
			20					25					30		
Leu	Pro	Lys	Pro	Thr	Val	Ser	Gln	Gly	Gln	Thr	Ser	Asn	Pro	Thr	Ser
		35					40					45			
Asn	Pro	Gln	Pro	Lys	Pro	Lys	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Ser	Thr
		50				55					60				
Ser	Ser	Gly	Ser	Gln	Ile	Gly	Pro	Ile	Leu	Asn	Arg	Pro	Met	Ile	Asp
		65			70				75					80	
Leu	Ser	Ala	Leu	Tyr	Asp	Leu	His	Lys	Glu	Leu	Gly	Arg	Gly	Gln	Phe
			85						90					95	
Gly	Ile	Thr	Tyr	Lys	Cys	Thr	Asp	Lys	Ser	Asn	Gly	Arg	Glu	Tyr	Ala
		100						105					110		
Cys	Lys	Ser	Ile	Ser	Lys	Arg	Lys	Leu	Ile	Arg	Arg	Lys	Asp	Ile	Glu
		115					120					125			
Asp	Val	Arg	Arg	Glu	Val	Met	Ile	Leu	Gln	His	Leu	Thr	Gly	Gln	Pro
		130				135						140			
Asn	Ile	Val	Glu	Phe	Arg	Gly	Ala	Tyr	Glu	Asp	Lys	Asp	Asn	Leu	His
		145			150				155					160	
Leu	Val	Met	Glu	Leu	Cys	Ser	Gly	Gly	Asp	Tyr	Val	Gly	Gly	Gly	His
			165						170					175	

His

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1498674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met	Ile	Asp	Leu	Ser	Ala	Leu	Tyr	Asp	Leu	His	Lys	Glu	Leu	Gly	Arg
1			5						10					15	
Gly	Gln	Phe	Gly	Ile	Thr	Tyr	Lys	Cys	Thr	Asp	Lys	Ser	Asn	Gly	Arg

20 25 30  
Glu Tyr Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Ile Arg Arg Lys  
35 40 45  
Asp Ile Glu Asp Val Arg Arg Glu Val Met Ile Leu Gln His Leu Thr  
50 55 60  
Gly Gln Pro Asn Ile Val Glu Phe Arg Gly Ala Tyr Glu Asp Lys Asp  
65 70 75 80  
Asn Leu His Leu Val Met Glu Leu Cys Ser Gly Gly Asp Tyr Val Gly  
85 90 95  
Gly Gly His His  
100

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..489
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

aatacaagt	g	atttccatta	tttctcgtct	acgtatacaa	ttgatcttcc	cccatctcca	60
attcagattt	g	ggacagaggt	atTTTTtgat	ccgattctta	cgaatcctga	atcttcctcg	120
tagattaatc	g	gatcgatcgg	ttcttaattc	gcggaatt	gtttcagtaa	cctgtgatcg	180
tgtcggttg	g	ggtagaagag	atcgaagtgg	gagcaaatc	atgatgaatc	ggctattcgg	240
gaaacccaag	g	caggaggcta	atgctctcca	aactttagac	aagcttaacg	agacgcttgg	300
agatgctaga	g	gaaaaaggag	aaagtactct	tgaagaaagc	tggtgcagag	gttgagaagg	360
caaaagaata	c	ctccgggct	aagaacaaac	gagcggctat	acagtstttg	aaaaggaaga	420
ggtyatatga	g	gggacaagtc	gaacagcttg	ggaatttctt	ttgccttctc	acctctatca	480
tcacatcatc							

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Ile Gln Val Ile Ser Ile Ile Ser Arg Leu Arg Ile Gln Leu Ile Phe  
1 5 10 15  
Pro His Leu Gln Phe Arg Phe Gly Gln Arg Tyr Phe Leu Ile Arg Phe  
20 25 30  
Leu Arg Ile Leu Asn Leu Pro Arg Arg Leu Ile Asp Arg Ser Val Leu  
35 40 45  
Asn Ser Arg Lys Ile Val Ser Val Thr Cys Asp Arg Val Gly Trp Gly  
50 55 60  
Arg Arg Asp Arg Ser Gly Ser Lys Ile Met Met Asn Arg Leu Phe Gly  
65 70 75 80  
Lys Pro Lys Gln Glu Ala Asn Ala Leu Gln Thr Leu Asp Lys Leu Asn  
85 90 95  
Glu Thr Leu Gly Asp Ala Arg Glu Lys Gly Glu Ser Thr Leu Glu Glu  
100 105 110  
Ser Trp Cys Arg Gly  
115

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 62 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..62  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498681  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:  
Met Leu Glu Lys Lys Glu Lys Val Leu Leu Lys Lys Ala Gly Ala Glu  
1                    5                    10                    15  
Val Glu Lys Ala Lys Glu Tyr Ser Arg Ala Lys Asn Lys Arg Ala Ala  
                    20                    25                    30  
Ile Gln Xaa Leu Lys Arg Lys Arg Xaa Tyr Glu Gly Gln Val Glu Gln  
                    35                    40                    45  
Leu Gly Asn Phe Phe Cys Leu Leu Thr Ser Ile Ile Ile Tyr  
50                    55                    60

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..2409  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

aaaaaaaaaga	tttctagtag	aaagagagaa	gggcgtgaat	tcctgagcga	gagattcttc	60
gccggagtaa	tctctttgcg	tgatcttacc	ggctgcttaa	ttcgtcttcg	cctgattcgt	120
tggtttcaaa	attcgtctct	ctctttcaat	cggagggttaa	ttgtttttct	gtttgggggt	180
caaagcgaag	atggtgaacg	ctatggtgga	gagagcgacg	agcgangatg	ctgatcgggc	240
ctgattgggc	tatgaacctc	gagatctgtg	atatgctcaa	tagcgatcca	gcgcaasaaa	300
agatgttgtg	aaaggcatta	aaaaacggat	tggtagcagg	aatccaaaag	ctcagcttct	360
tgccttaact	ctgcttgaga	caatagtga	gaactgtggt	gacatgggtc	atatgcatgt	420
ggctgagaaa	ggtgttatct	atgagatggt	ccggatagtt	aagaagaagc	cggacttcca	480
tgtcaaagag	aagattctgg	tccttatcga	tacatggcaa	gaggcctttg	gtggccctag	540
ggcaagatat	ccacaatact	atgcaggata	ccaggaattg	ttgcgtgctg	gtgctgtttt	600
ccctcagaga	tcagagagat	cagctcctgt	gttcacacct	cctcaaacac	agcctttgac	660
atcttaccct	ccaaatcttc	gtaacgctgg	acctggtaat	gatgtgcctg	aaccttcagc	720
agagccagaa	tttccgactc	taagtttgtc	ggagattcaa	aatgcaaaa	gtatcatgga	780
tgtgcttgcg	gagatgctga	gtgcattaga	gcccggaaac	aaggaggatc	tcaaacaaga	840
ggttatggtc	gatctggtgg	agcagtgctg	tacatacaaa	caaagagtgg	tgacctcgt	900
caactcgact	tcggacgagt	ctttgttatg	tcaaggtctg	gctttgaatg	atgacttgca	960
gcgtgtctta	accaattatg	aagcaattgc	ttctggatta	cctggaactt	cttctcagat	1020
cgagaagccc	aagtccgaga	caggaaaatc	ccttgttgat	gttgatggtc	cacttattga	1080
tacaggggac	agcagtaatc	aggcgaacgg	agctacatcg	agctctggta	acgggggttct	1140
aaatcagttg	gccctccctg	caccacctgt	aactaatggt	tcagccaatt	ccaaaataga	1200
cctcctcagt	ggcgatgac	ttgcccttgt	tcctgttggg	accttcctca	gccagcaagt	1260
ccggttgcat	cagatcaaaa	tgcactcgcc	cttatcgaca	tgttctcaga	taataactaat	1320
aatccaagtc	ctgcaactgc	accaagtggc	aatccagctc	agaatattcc	tttgaatcct	1380
caagggcacc	aacaacccaa	tagtcaagct	ggagaagctg	gattacaaca	atccaatgga	1440
tttgccctc	aagtgggtta	ttcgcagttt	gagcagccat	catacgggca	aggagtctct	1500
tctccctgga	gcagtcagcc	tgcacagcaa	ccagtccagc	catcttatga	agggtgcccc	1560
gacagtacgg	catttccacc	tccccatgg	gaagctcagc	tccaagacta	tagtccctct	1620
gcgagtcag	gaagtccggt	ttctcctgga	atgcatccaa	ctcagactgc	cttcacacat	1680
gctcaaccag	ttaacaacaa	caatccatat	cctcaaattc	cccaaaccgg	gccaccagtc	1740
aacaataaca	gtccatatgc	tcaaatgccc	caaacaggtc	aagcagttgc	caacatcagt	1800

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ccatatacctc aaattccaca aaacggcgtg tacatgccar actttcaacc aaatcaggct 1860
cttgggtcag gctatcaacc acagcaacaa cagcagcagc agatgatgat ggctcagtac 1920
tatgccaac agcaacagct acagcaacaa caacagcaac aggcgtatgg aaaccagatg 1980
ggaggatacg gatatggcta ntamtcaaca gcaacaagga agcagcccat atctggacca 2040
gcaaatgtac ggtttatcca tgagagacca gacatcgcat caggtagcat catcatcatc 2100
taccacatct tatctgcctc caatgaaacc taagaataaa ccagaggaca agctatttgg 2160
ggatcttgtg gacatctcca aattcaagcc tacaaaaccg acttccggaa gagctggtac 2220
catgtgaaaa ttctccatc cattcatcat ttaccagtat tcatctcctc tatcctcctc 2280
agctaaactct ctttcttctc tttgttaagc ttttttcatc attgatttta ttaccctctt 2340
gggagataca tagatataca tatgtgttat gttcttcctt ataatttacc gttggttatg 2400
ggtttgttc
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(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```
Met Val His Met His Val Ala Glu Lys Gly Val Ile His Glu Met Val
1          5          10          15
Arg Ile Val Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys Ile Leu
20          25          30
Val Leu Ile Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg Ala Arg
35          40          45
Tyr Pro Gln Tyr Tyr Ala Gly Tyr Gln Glu Leu Leu Arg Ala Gly Ala
50          55          60
Val Phe Pro Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr Pro Pro
65          70          75          80
Gln Thr Gln Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn Ala Gly
85          90          95
Pro Gly Asn Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe Pro Thr
100          105          110
Leu Ser Leu Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp Val Leu
115          120          125
Ala Glu Met Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp Leu Lys
130          135          140
Gln Glu Val Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr Lys Gln
145          150          155          160
Arg Val Val His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu Leu Cys
165          170          175
Gln Gly Leu Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr Asn Tyr
180          185          190
Glu Ala Ile Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile Glu Lys
195          200          205
Pro Lys Ser Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly Pro Leu
210          215          220
Ile Asp Thr Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr Ser Ser
225          230          235          240
Ser Gly Asn Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro Pro Val
245          250          255
Thr Asn Gly Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly Asp Asp
260          265          270
Leu Ala Leu Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val Arg Leu
275          280          285
His Gln Ile Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln Ile Ile
290          295          300
```

Leu Ile Ile Gln Val Leu Gln Leu His Gln Val Ala Ile Gln Leu Arg  
305 310 315 320  
Ile Phe Leu

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..320
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met His Val Ala Glu Lys Gly Val Ile His Glu Met Val Arg Ile Val  
1 5 10 15  
Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys Ile Leu Val Leu Ile  
20 25 30  
Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg Ala Arg Tyr Pro Gln  
35 40 45  
Tyr Tyr Ala Gly Tyr Gln Glu Leu Leu Arg Ala Gly Ala Val Phe Pro  
50 55 60  
Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr Pro Pro Gln Thr Gln  
65 70 75 80  
Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn Ala Gly Pro Gly Asn  
85 90 95  
Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe Pro Thr Leu Ser Leu  
100 105 110  
Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp Val Leu Ala Glu Met  
115 120 125  
Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp Leu Lys Gln Glu Val  
130 135 140  
Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr Lys Gln Arg Val Val  
145 150 155 160  
His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu Leu Cys Gln Gly Leu  
165 170 175  
Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr Asn Tyr Glu Ala Ile  
180 185 190  
Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile Glu Lys Pro Lys Ser  
195 200 205  
Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly Pro Leu Ile Asp Thr  
210 215 220  
Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr Ser Ser Ser Gly Asn  
225 230 235 240  
Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro Pro Val Thr Asn Gly  
245 250 255  
Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly Asp Asp Leu Ala Leu  
260 265 270  
Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val Arg Leu His Gln Ile  
275 280 285  
Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln Ile Ile Leu Ile Ile  
290 295 300  
Gln Val Leu Gln Leu His Gln Val Ala Ile Gln Leu Arg Ile Phe Leu  
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..309  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498685  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:  
Met Val Arg Ile Val Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys  
1                  5                  10                  15  
Ile Leu Val Leu Ile Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg  
                  20                  25                  30  
Ala Arg Tyr Pro Gln Tyr Tyr Ala Gly Tyr Gln Glu Leu Leu Arg Ala  
                  35                  40                  45  
Gly Ala Val Phe Pro Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr  
                  50                  55                  60  
Pro Pro Gln Thr Gln Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn  
65                  70                  75                  80  
Ala Gly Pro Gly Asn Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe  
                  85                  90                  95  
Pro Thr Leu Ser Leu Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp  
                  100                 105                 110  
Val Leu Ala Glu Met Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp  
                 115                 120                 125  
Leu Lys Gln Glu Val Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr  
                 130                 135                 140  
Lys Gln Arg Val Val His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu  
145                 150                 155                 160  
Leu Cys Gln Gly Leu Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr  
                 165                 170                 175  
Asn Tyr Glu Ala Ile Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile  
                 180                 185                 190  
Glu Lys Pro Lys Ser Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly  
                 195                 200                 205  
Pro Leu Ile Asp Thr Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr  
210                 215                 220  
Ser Ser Ser Gly Asn Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro  
225                 230                 235                 240  
Pro Val Thr Asn Gly Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly  
                 245                 250                 255  
Asp Asp Leu Ala Leu Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val  
                 260                 265                 270  
Arg Leu His Gln Ile Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln  
275                 280                 285  
Ile Ile Leu Ile Ile Gln Val Leu Gln Leu His Gln Val Ala Ile Gln  
290                 295                 300  
Leu Arg Ile Phe Leu  
305

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..860
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

aaacacaaaa	aaaaaaactt	aagaaaattt	gaaatcctca	gaattgcaga	gcaaagaaca	60
accatggcga	atcctattca	agagattctg	gagaaccaag	ttctaacggt	ggctaaagct	120
atggaagata	agatagacaa	cgagatcgcc	tctttagaaa	agcttgacga	ggacgatcta	180
gaggttttga	gagagagaag	gttaaagcaa	atgaagaaaa	tggcagagaa	gaagaaacgt	240
tggattagtc	ttggacatgg	tgaatactct	gagatccatt	ctgagaaaga	cttcttctcc	300
gtcgttaaag	ccagcgaacg	cgtcgtctgc	catttctacc	gcgagaattg	gccatgtaaa	360
gtgatggata	mscacatgag	tatattggca	aagcaacaca	ttgagacacg	ttttgtgaag	420
atccaagctg	agaaaagtcc	gttcttggct	gagaggctca	agattgttgt	tctacctact	480
cttgcactta	ttaagaacac	taaagtcgat	gattatgttg	ttgggttcaa	tgagcttgga	540
gggaaagatg	atttcagcac	tgaggatttg	gaagagagaa	tagctagagc	gcaagtgatt	600
cattacgatg	gagagtcatc	gtcgcttaaa	ccaaagtcga	caacacaagt	tagaaggaat	660
gtgaggcaga	gtgctcggtc	agattcagac	tccgaataga	ctctcgggtt	tttcagcaaa	720
cgtttgttgg	tatgttcatt	atcttcactc	tatcttcagc	ccttttttgg	tgtgagtttg	780
tattgtgcga	attcagttgt	gatgtgtaat	acaaagtagg	agatgatctt	atatgcatat	840
ttgatgagtt	tttaaccttg					

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1498687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

Lys	Pro	Lys	Lys	Lys	Asn	Leu	Arg	Lys	Phe	Glu	Ile	Leu	Arg	Ile	Ala
1				5					10					15	
Glu	Gln	Arg	Thr	Thr	Met	Ala	Asn	Pro	Ile	Gln	Glu	Ile	Leu	Glu	Asn
			20					25					30		
Gln	Val	Leu	Thr	Val	Ala	Lys	Ala	Met	Glu	Asp	Lys	Ile	Asp	Asn	Glu
		35					40					45			
Ile	Ala	Ser	Leu	Glu	Lys	Leu	Asp	Glu	Asp	Asp	Leu	Glu	Val	Leu	Arg
	50					55					60				
Glu	Arg	Arg	Leu	Lys	Gln	Met	Lys	Lys	Met	Ala	Glu	Lys	Lys	Lys	Arg
65					70					75				80	
Trp	Ile	Ser	Leu	Gly	His	Gly	Glu	Tyr	Ser	Glu	Ile	His	Ser	Glu	Lys
			85					90					95		
Asp	Phe	Phe	Ser	Val	Val	Lys	Ala	Ser	Glu	Arg	Val	Val	Cys	His	Phe
			100					105					110		
Tyr	Arg	Glu	Asn	Trp	Pro	Cys	Lys	Val	Met	Asp	Xaa	His	Met	Ser	Ile
		115					120					125			
Leu	Ala	Lys	Gln	His	Ile	Glu	Thr	Arg	Phe	Val	Lys	Ile	Gln	Ala	Glu
	130					135					140				
Lys	Ser	Pro	Phe	Leu	Ala	Glu	Arg	Leu	Lys	Ile	Val	Val	Leu	Pro	Thr
145				150					155					160	
Leu	Ala	Leu	Ile	Lys	Asn	Thr	Lys	Val	Asp	Asp	Tyr	Val	Val	Gly	Phe
			165						170					175	
Asn	Glu	Leu	Gly	Gly	Lys	Asp	Asp	Phe	Ser	Thr	Glu	Asp	Leu	Glu	Glu
		180						185					190		
Arg	Ile	Ala	Arg	Ala	Gln	Val	Ile	His	Tyr	Asp	Gly	Glu	Ser	Ser	Ser
	195					200					205				
Leu	Lys	Pro	Lys	Ser	Thr	Thr	Gln	Val	Arg	Arg	Asn	Val	Arg	Gln	Ser
	210					215					220				
Ala	Arg	Ser	Asp	Ser	Asp	Ser	Glu								
225					230										

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid



- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..211  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498688  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

Met	Ala	Asn	Pro	Ile	Gln	Glu	Ile	Leu	Glu	Asn	Gln	Val	Leu	Thr	Val
1				5				10						15	
Ala	Lys	Ala	Met	Glu	Asp	Lys	Ile	Asp	Asn	Glu	Ile	Ala	Ser	Leu	Glu
			20					25					30		
Lys	Leu	Asp	Glu	Asp	Asp	Leu	Glu	Val	Leu	Arg	Glu	Arg	Arg	Leu	Lys
		35					40					45			
Gln	Met	Lys	Lys	Met	Ala	Glu	Lys	Lys	Lys	Arg	Trp	Ile	Ser	Leu	Gly
	50					55					60				
His	Gly	Glu	Tyr	Ser	Glu	Ile	His	Ser	Glu	Lys	Asp	Phe	Phe	Ser	Val
65					70					75				80	
Val	Lys	Ala	Ser	Glu	Arg	Val	Val	Cys	His	Phe	Tyr	Arg	Glu	Asn	Trp
			85						90					95	
Pro	Cys	Lys	Val	Met	Asp	Xaa	His	Met	Ser	Ile	Leu	Ala	Lys	Gln	His
			100					105					110		
Ile	Glu	Thr	Arg	Phe	Val	Lys	Ile	Gln	Ala	Glu	Lys	Ser	Pro	Phe	Leu
		115					120					125			
Ala	Glu	Arg	Leu	Lys	Ile	Val	Val	Leu	Pro	Thr	Leu	Ala	Leu	Ile	Lys
	130					135					140				
Asn	Thr	Lys	Val	Asp	Asp	Tyr	Val	Val	Gly	Phe	Asn	Glu	Leu	Gly	Gly
145					150					155				160	
Lys	Asp	Asp	Phe	Ser	Thr	Glu	Asp	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ala
			165						170					175	
Gln	Val	Ile	His	Tyr	Asp	Gly	Glu	Ser	Ser	Ser	Leu	Lys	Pro	Lys	Ser
			180					185					190		
Thr	Thr	Gln	Val	Arg	Arg	Asn	Val	Arg	Gln	Ser	Ala	Arg	Ser	Asp	Ser
		195				200						205			
Asp	Ser	Glu													
		210													

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..192  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met	Glu	Asp	Lys	Ile	Asp	Asn	Glu	Ile	Ala	Ser	Leu	Glu	Lys	Leu	Asp
1				5					10					15	
Glu	Asp	Asp	Leu	Glu	Val	Leu	Arg	Glu	Arg	Arg	Leu	Lys	Gln	Met	Lys
			20					25					30		
Lys	Met	Ala	Glu	Lys	Lys	Lys	Arg	Trp	Ile	Ser	Leu	Gly	His	Gly	Glu
		35					40					45			
Tyr	Ser	Glu	Ile	His	Ser	Glu	Lys	Asp	Phe	Phe	Ser	Val	Val	Lys	Ala
	50					55					60				
Ser	Glu	Arg	Val	Val	Cys	His	Phe	Tyr	Arg	Glu	Asn	Trp	Pro	Cys	Lys
65					70					75				80	
Val	Met	Asp	Xaa	His	Met	Ser	Ile	Leu	Ala	Lys	Gln	His	Ile	Glu	Thr
			85						90					95	
Arg	Phe	Val	Lys	Ile	Gln	Ala	Glu	Lys	Ser	Pro	Phe	Leu	Ala	Glu	Arg

	100					105						110			
Leu	Lys	Ile	Val	Val	Leu	Pro	Thr	Leu	Ala	Leu	Ile	Lys	Asn	Thr	Lys
	115						120					125			
Val	Asp	Asp	Tyr	Val	Val	Gly	Phe	Asn	Glu	Leu	Gly	Gly	Lys	Asp	Asp
	130					135					140				
Phe	Ser	Thr	Glu	Asp	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ala	Gln	Val	Ile
145					150					155					160
His	Tyr	Asp	Gly	Glu	Ser	Ser	Ser	Leu	Lys	Pro	Lys	Ser	Thr	Thr	Gln
			165					170						175	
Val	Arg	Arg	Asn	Val	Arg	Gln	Ser	Ala	Arg	Ser	Asp	Ser	Asp	Ser	Glu
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

aacttagcct	tggtcttctt	cttcacgcg	atatctccg	tgctcttctt	gtctccatca	60
gaagaagaag	ctctctgtat	ccatccatat	cgaaaaacca	gagatcggag	gaaggagaga	120
gagataccaa	tctctgttgc	tttggtttta	agggtttaga	ggagatgtca	aaccacccga	180
agatcacatc	ggcgcatcag	aatgtggagg	agaagctaag	ggaacttcag	gagaggttct	240
gtcatcttca	agctgctagg	aaagaagggc	ggcatggtga	ccttgcgctt	ttagaagccc	300
aaatctctca	gaatattcgg	gagtggcaag	ctgaactcac	tgctccttct	cctgaatctt	360
ctctgttggg	tgaaggtatt	agccaattcc	ttgaggagtt	tgctcctctg	ttgaaattag	420
acgaggagga	tgatgcaact	agtacgctaa	aagaacatgc	tggagcaaag	cctgatcctg	480
agggtttttc	tcaaagcttg	tgccctcctg	aatggacatc	tgagaatttt	agtcaaagtc	540
ctttcaacgg	aaattttctc	tgcggttttg	aggatgctct	taatagcaca	gaaacacatg	600
gccagcaact	ccattatgga	tatgaagggt	ttgatccaag	cataaactcc	gctcctgatt	660
tccatgacca	aaaactcagc	agcaacttgg	atataacttc	tcagtatgat	tatatcttct	720
ccgaagtgcg	tcaggaacta	gataacagcc	cttccactaa	gcttgattct	tctgaagaga	780
ttgacaactt	tgctgaattt	tctactccat	caagtgtccg	tgtgcctcca	tctgcttttc	840
tgggacctaa	gtgtgcacta	tgggattgca	caaggcctgc	tcagggctcc	gagtgggtacc	900
tggattactg	cagtaactac	catgggactc	tagctctgaa	tgaagattcg	cctggcacag	960
cacctgtatt	gaggccaggg	ggcatcagtt	tgaagataaa	tctattgatt	gatgctcttc	1020
gtgcaaagac	tcagggttaag	aatgttggga	tcccagtggt	tgaaggagct	gttaacacaa	1080
aatgcccatt	gaacgcagca	gagctatttc	atcttgaact	ggttgaaggc	gaaacaatta	1140
gagagtggct	cttctttgac	aaacctagaa	gagcatatga	tagcggaaac	cgaaagcaaa	1200
gatcacttcc	agattacagt	ggaagagggt	ggcatgaatc	aagaaaacaa	ctgatgaagg	1260
aacaagaagg	ccagaagaga	tcttactata	tggatccaca	acctccaggt	ccctttgagt	1320
ggcatctctt	tgaataccaa	atcaatgaat	ctgacgcgat	tgcggttatat	cgccatgaac	1380
ttaaagtagg	aaatggaaa	aagagtccta	agggaaaag			

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Leu	Ser	Leu	Val	Leu	Leu	His	Arg	Asp	Ile	Ser	Gly	Val	Phe	Phe
1			5					10					15	
Val	Ser	Ile	Arg	Arg	Ser	Ser	Leu	Tyr	Pro	Ser	Ile	Ser	Lys	Asn
		20					25					30		
Gln	Arg	Ser	Glu	Glu	Gly	Glu	Arg	Asp	Thr	Asn	Leu	Cys	Cys	Phe
		35					40					45		Gly
Phe	Lys	Gly	Leu	Glu	Glu	Met	Ser	Asn	His	Pro	Lys	Ile	Thr	Ser
	50					55					60			Ala
His	Gln	Asn	Val	Glu	Glu	Lys	Leu	Arg	Glu	Leu	Gln	Glu	Arg	Phe
65					70					75				Cys
His	Leu	Gln	Ala	Ala	Arg	Lys	Glu	Gly	Arg	His	Gly	Asp	Leu	Ala
			85						90					Leu
Leu	Glu	Ala	Gln	Ile	Ser	Gln	Asn	Ile	Arg	Glu	Trp	Gln	Ala	Glu
			100					105					110	Leu
Thr	Ala	Pro	Ser	Pro	Glu	Ser	Ser	Leu	Leu	Gly	Glu	Gly	Ile	Ser
		115					120					125		Gln
Phe	Leu	Glu	Glu	Phe	Ala	Pro	Leu	Leu	Lys	Leu	Asp	Glu	Glu	Asp
	130					135					140			Asp
Ala	Thr	Ser	Thr	Leu	Lys	Glu	His	Ala	Gly	Ala	Lys	Pro	Asp	Pro
145					150					155				Glu
Gly	Phe	Ser	Gln	Ser	Leu	Cys	Pro	Pro	Glu	Trp	Thr	Ser	Glu	Asn
			165						170					Phe
Ser	Gln	Ser	Pro	Phe	Asn	Gly	Asn	Phe	Ser	Cys	Gly	Phe	Glu	Asp
			180					185					190	Ala
Leu	Asn	Ser	Thr	Glu	Thr	His	Gly	Gln	Gln	Leu	His	Tyr	Gly	Tyr
	195						200					205		Glu
Gly	Phe	Asp	Pro	Ser	Ile	Asn	Ser	Ala	Pro	Asp	Phe	His	Asp	Gln
	210					215					220			Lys
Leu	Ser	Ser	Asn	Leu	Asp	Ile	Thr	Ser	Gln	Tyr	Asp	Tyr	Ile	Phe
225				230						235				Ser
Glu	Val	Arg	Gln	Glu	Leu	Asp	Asn	Ser	Pro	Ser	Thr	Lys	Leu	Asp
			245						250				255	Ser
Ser	Glu	Glu	Ile	Asp	Asn	Phe	Ala	Glu	Phe	Ser	Thr	Pro	Ser	Ser
			260					265					270	Val
Arg	Val	Pro	Pro	Ser	Ala	Phe	Leu	Gly	Pro	Lys	Cys	Ala	Leu	Trp
		275					280					285		Asp
Cys	Thr	Arg	Pro	Ala	Gln	Gly	Ser	Glu	Trp	Tyr	Leu	Asp	Tyr	Cys
	290					295					300			Ser
Asn	Tyr	His	Gly	Thr	Leu	Ala	Leu	Asn	Glu	Asp	Ser	Pro	Gly	Thr
305					310					315				Ala
Pro	Val	Leu	Arg	Pro	Gly	Gly	Ile	Ser	Leu	Lys	Asp	Asn	Leu	Leu
			325						330					Ile
Asp	Ala	Leu	Arg	Ala	Lys	Thr	Gln	Gly	Lys	Asn	Val	Gly	Ile	Pro
			340					345					350	Val
Cys	Glu	Gly	Ala	Val	Asn	Thr	Lys	Cys	Pro	Trp	Asn	Ala	Ala	Glu
	355						360					365		Leu
Phe	His	Leu	Glu	Leu	Val	Glu	Gly	Glu	Thr	Ile	Arg	Glu	Trp	Leu
	370					375					380			Phe
Phe	Asp	Lys	Pro	Arg	Arg	Ala	Tyr	Asp	Ser	Gly	Asn	Arg	Lys	Gln
385					390					395				Arg
Ser	Leu	Pro	Asp	Tyr	Ser	Gly	Arg	Gly	Trp	His	Glu	Ser	Arg	Lys
			405						410					Gln
Leu	Met	Lys	Glu	Gln	Glu	Gly	Gln	Lys	Arg	Ser	Tyr	Tyr	Met	Asp
			420					425					430	Pro
Gln	Pro	Pro	Gly	Pro	Phe	Glu	Trp	His	Leu	Phe	Glu	Tyr	Gln	Ile
		435					440					445		Asn
Glu	Ser	Asp	Ala	Cys	Ala	Leu	Tyr	Arg	Leu	Glu	Leu	Lys	Val	Gly
	450					455					460			Asn
Gly	Lys	Lys	Ser	Pro	Lys	Gly	Lys							
465					470									

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 418 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..418  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498692  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Met	Ser	Asn	His	Pro	Lys	Ile	Thr	Ser	Ala	His	Gln	Asn	Val	Glu	Glu
1				5				10						15	
Lys	Leu	Arg	Glu	Leu	Gln	Glu	Arg	Phe	Cys	His	Leu	Gln	Ala	Ala	Arg
			20					25					30		
Lys	Glu	Gly	Arg	His	Gly	Asp	Leu	Ala	Leu	Leu	Glu	Ala	Gln	Ile	Ser
			35				40					45			
Gln	Asn	Ile	Arg	Glu	Trp	Gln	Ala	Glu	Leu	Thr	Ala	Pro	Ser	Pro	Glu
			50			55					60				
Ser	Ser	Leu	Leu	Gly	Glu	Gly	Ile	Ser	Gln	Phe	Leu	Glu	Glu	Phe	Ala
65				70						75				80	
Pro	Leu	Leu	Lys	Leu	Asp	Glu	Glu	Asp	Asp	Ala	Thr	Ser	Thr	Leu	Lys
			85					90						95	
Glu	His	Ala	Gly	Ala	Lys	Pro	Asp	Pro	Glu	Gly	Phe	Ser	Gln	Ser	Leu
			100					105					110		
Cys	Pro	Pro	Glu	Trp	Thr	Ser	Glu	Asn	Phe	Ser	Gln	Ser	Pro	Phe	Asn
			115				120					125			
Gly	Asn	Phe	Ser	Cys	Gly	Phe	Glu	Asp	Ala	Leu	Asn	Ser	Thr	Glu	Thr
			130			135					140				
His	Gly	Gln	Gln	Leu	His	Tyr	Gly	Tyr	Glu	Gly	Phe	Asp	Pro	Ser	Ile
145				150						155				160	
Asn	Ser	Ala	Pro	Asp	Phe	His	Asp	Gln	Lys	Leu	Ser	Ser	Asn	Leu	Asp
			165					170						175	
Ile	Thr	Ser	Gln	Tyr	Asp	Tyr	Ile	Phe	Ser	Glu	Val	Arg	Gln	Glu	Leu
			180				185						190		
Asp	Asn	Ser	Pro	Ser	Thr	Lys	Leu	Asp	Ser	Ser	Glu	Glu	Ile	Asp	Asn
			195			200					205				
Phe	Ala	Glu	Phe	Ser	Thr	Pro	Ser	Ser	Val	Arg	Val	Pro	Pro	Ser	Ala
			210			215					220				
Phe	Leu	Gly	Pro	Lys	Cys	Ala	Leu	Trp	Asp	Cys	Thr	Arg	Pro	Ala	Gln
225				230						235				240	
Gly	Ser	Glu	Trp	Tyr	Leu	Asp	Tyr	Cys	Ser	Asn	Tyr	His	Gly	Thr	Leu
			245				250						255		
Ala	Leu	Asn	Glu	Asp	Ser	Pro	Gly	Thr	Ala	Pro	Val	Leu	Arg	Pro	Gly
			260				265					270			
Gly	Ile	Ser	Leu	Lys	Asp	Asn	Leu	Ile	Asp	Ala	Leu	Arg	Ala	Lys	
			275			280					285				
Thr	Gln	Gly	Lys	Asn	Val	Gly	Ile	Pro	Val	Cys	Glu	Gly	Ala	Val	Asn
			290			295					300				
Thr	Lys	Cys	Pro	Trp	Asn	Ala	Ala	Glu	Leu	Phe	His	Leu	Glu	Leu	Val
305				310						315				320	
Glu	Gly	Glu	Thr	Ile	Arg	Glu	Trp	Leu	Phe	Phe	Asp	Lys	Pro	Arg	Arg
			325				330						335		
Ala	Tyr	Asp	Ser	Gly	Asn	Arg	Lys	Gln	Arg	Ser	Leu	Pro	Asp	Tyr	Ser
			340				345					350			
Gly	Arg	Gly	Trp	His	Glu	Ser	Arg	Lys	Gln	Leu	Met	Lys	Glu	Gln	Glu
			355			360					365				
Gly	Gln	Lys	Arg	Ser	Tyr	Tyr	Met	Asp	Pro	Gln	Pro	Pro	Gly	Pro	Phe
			370			375				380					
Glu	Trp	His	Leu	Phe	Glu	Tyr	Gln	Ile	Asn	Glu	Ser	Asp	Ala	Cys	Ala
385				390						395				400	

Leu Tyr Arg Leu Glu Leu Lys Val Gly Asn Gly Lys Lys Ser Pro Lys  
405 410 415  
Gly Lys

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1896
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

aaaaactcgc	cgccgtggag	agagaagaga	gaatggagga	tatcgaggat	ttgttggccg	60
gaggagtcgg	tgggtcacca	ccgggattcc	gattaccctt	gaatgcagtc	gggattaatc	120
cgaagacgaa	taagagcaaa	cgtattagct	cgaaacccga	tcaaattact	gcttcgaatc	180
gtgactcgct	tgctccacca	tcgatgaaga	ttccaggaac	tcagacgata	tacatcaaga	240
cgtttgatg	ttctcataat	cagagtata	gtgagtatat	ggctggtcag	ctttctgcat	300
ttggctatgc	gttgacagaa	gtcccggagg	aagctgattt	atggctcatt	aacacctgta	360
ctgtgaagtc	ccctagccag	tctgcgatgt	ctactttgat	aacgaggggt	agaagtggga	420
aaaagcctct	tgtgattgca	ggatgtgttc	ctcagggcag	tcgtgatctt	aaagaactgg	480
aaggcgtag	tgtagttgga	gtccaacaga	ttgatcgtgt	tgttgagatt	gttgaagaaa	540
ctcttaagg	tcataagta	cgggtgctga	ctcgggaagac	tttgccctgc	cttgatctcc	600
caaaggtgcg	gaggaacaat	tttatcgaaa	ttctcccat	taatgttggc	tgtttgggtg	660
cctgtactta	ctgcaagacc	aagcatgccc	gtggtcattt	aggaagttac	acagttgata	720
gtcttgtgga	gcgggtgaga	actgtaatct	ctgaaggagt	caaggagatt	tggttaagca	780
gcgaggacac	tgagcatat	ggctgtgaca	taggagttaa	tcttccaata	ctgcttaatg	840
ctatcggtta	ggaacttcct	tctgatcaaa	gcacaatgct	aaggattggg	atgactaatc	900
ctccctttat	tttagagcat	ttgaaagaaa	tagcggcagt	gttacgtcac	ccatgtgtct	960
acacctttct	tcattgtccct	gtgcaatctg	gtagcgattc	tgtgttgacg	gccatgaaca	1020
gggaatatac	agcaagttag	ttcaggactg	tggtagacac	cttaacagag	cttggtgccag	1080
gaatgcaa	tgctactgat	ataatatgcg	gttttcctgg	tgaaaccgat	gaagattttt	1140
ctcagacagt	tgaactcatc	aaggattaca	agtttcctca	agttcatatt	tctcagtttt	1200
accccagacc	agggacccca	gcagcaaaga	tgaagaagg	acaaagtaaa	atagtgaagc	1260
aacgaagccg	tgaattgact	tctgtctttg	aggcttttgc	accttacacc	ggaatggagt	1320
gcagagaaga	gaggatatgg	ataactgaag	tagctactga	tggaattcat	ttgggtggac	1380
atacgaagg	atatgtacag	gtcttagtta	ctggaccaga	aagtatgctt	gggacttcag	1440
ctatggcgag	gataacatct	gtggggagat	ggtcagtatt	tggggaagt	attgagacat	1500
ttagctctgc	aaatagagaa	acaaaatccc	gagaggaaac	aaagctgcct	tggtcgtcga	1560
atgttagcac	ttgtgagact	tgcaattgct	ctgctgagag	ctgtggagaa	gagagatcag	1620
gagaggcgtg	taacatttct	ggaaatatct	caggacaaga	tgataacaag	ggaaagtcaa	1680
agaaagaaga	gaaggaggta	caagaggctg	tcgtaccggg	aagcagcgta	gcaaattggg	1740
gtttcattga	taaggcactt	gtctgtggag	tggtcgtaa	ctctgtcacc	attcttgttt	1800
tggtgattag	cattgcatgt	agagttttgc	tgcggtaatg	aatcagtgtg	tccgactaat	1860
gtagtctttc	gaataatttt	cgtctttttac	ttgtct			

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..611
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Lys Leu Ala Ala Val Glu Arg Glu Glu Arg Met Glu Asp Ile Glu Asp

1	5	10	15
Leu Leu Ala Gly Val Gly Gly Ala Pro Pro Gly Phe Arg Leu Pro			
20	25	30	
Leu Asn Ala Val Gly Ile Asn Pro Lys Thr Asn Lys Ser Lys Arg Ile			
35	40	45	
Ser Ser Lys Pro Asp Gln Ile Thr Ala Ser Asn Arg Asp Ser Leu Ala			
50	55	60	
Pro Pro Ser Met Lys Ile Pro Gly Thr Gln Thr Ile Tyr Ile Lys Thr			
65	70	75	80
Phe Gly Cys Ser His Asn Gln Ser Asp Ser Glu Tyr Met Ala Gly Gln			
85	90	95	
Leu Ser Ala Phe Gly Tyr Ala Leu Thr Glu Val Pro Glu Glu Ala Asp			
100	105	110	
Leu Trp Leu Ile Asn Thr Cys Thr Val Lys Ser Pro Ser Gln Ser Ala			
115	120	125	
Met Ser Thr Leu Ile Thr Arg Gly Arg Ser Gly Lys Lys Pro Leu Val			
130	135	140	
Ile Ala Gly Cys Val Pro Gln Gly Ser Arg Asp Leu Lys Glu Leu Glu			
145	150	155	160
Gly Val Ser Val Val Gly Val Gln Gln Ile Asp Arg Val Val Glu Ile			
165	170	175	
Val Glu Glu Thr Leu Lys Gly His Glu Val Arg Leu Leu Thr Arg Lys			
180	185	190	
Thr Leu Pro Ala Leu Asp Leu Pro Lys Val Arg Arg Asn Asn Phe Ile			
195	200	205	
Glu Ile Leu Pro Ile Asn Val Gly Cys Leu Gly Ala Cys Thr Tyr Cys			
210	215	220	
Lys Thr Lys His Ala Arg Gly His Leu Gly Ser Tyr Thr Val Asp Ser			
225	230	235	240
Leu Val Glu Arg Val Arg Thr Val Ile Ser Glu Gly Val Lys Glu Ile			
245	250	255	
Trp Leu Ser Ser Glu Asp Thr Gly Ala Tyr Gly Arg Asp Ile Gly Val			
260	265	270	
Asn Leu Pro Ile Leu Leu Asn Ala Ile Val Lys Glu Leu Pro Ser Asp			
275	280	285	
Gln Ser Thr Met Leu Arg Ile Gly Met Thr Asn Pro Pro Phe Ile Leu			
290	295	300	
Glu His Leu Lys Glu Ile Ala Ala Val Leu Arg His Pro Cys Val Tyr			
305	310	315	320
Thr Phe Leu His Val Pro Val Gln Ser Gly Ser Asp Ser Val Leu Thr			
325	330	335	
Ala Met Asn Arg Glu Tyr Thr Ala Ser Glu Phe Arg Thr Val Val Asp			
340	345	350	
Thr Leu Thr Glu Leu Val Pro Gly Met Gln Ile Ala Thr Asp Ile Ile			
355	360	365	
Cys Gly Phe Pro Gly Glu Thr Asp Glu Asp Phe Ser Gln Thr Val Glu			
370	375	380	
Leu Ile Lys Asp Tyr Lys Phe Pro Gln Val His Ile Ser Gln Phe Tyr			
385	390	395	400
Pro Arg Pro Gly Thr Pro Ala Ala Lys Met Lys Lys Val Gln Ser Lys			
405	410	415	
Ile Val Lys Gln Arg Ser Arg Glu Leu Thr Ser Val Phe Glu Ala Phe			
420	425	430	
Ala Pro Tyr Thr Gly Met Glu Cys Arg Glu Glu Arg Ile Trp Ile Thr			
435	440	445	
Glu Val Ala Thr Asp Gly Ile His Leu Val Gly His Thr Lys Gly Tyr			
450	455	460	
Val Gln Val Leu Val Thr Gly Pro Glu Ser Met Leu Gly Thr Ser Ala			
465	470	475	480
Met Ala Arg Ile Thr Ser Val Gly Arg Trp Ser Val Phe Gly Glu Val			
485	490	495	

Ile Glu Thr Phe Ser Ser Ala Asn Arg Glu Thr Lys Ser Arg Glu Glu  
500 505 510  
Thr Lys Leu Pro Cys Ser Ser Asn Val Ser Thr Cys Glu Thr Cys Thr  
515 520 525  
Cys Ser Ala Glu Ser Cys Gly Glu Glu Arg Ser Gly Glu Ala Cys Asn  
530 535 540  
Ile Ser Gly Asn Ile Ser Gly Gln Asp Asp Asn Lys Gly Lys Ser Lys  
545 550 555 560  
Lys Glu Glu Lys Glu Val Gln Glu Val Val Pro Gly Ser Ser Val  
565 570 575  
Ala Asn Trp Gly Phe Ile Asp Lys Ala Leu Val Cys Gly Val Phe Val  
580 585 590  
Ser Ser Val Thr Ile Leu Val Leu Leu Ile Ser Ile Ala Cys Arg Val  
595 600 605  
Leu Leu Arg  
610

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..601

(D) OTHER INFORMATION: / Ceres Seq. ID 1498705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Glu Asp Ile Glu Asp Leu Leu Ala Gly Gly Val Gly Gly Ala Pro  
1 5 10 15  
Pro Gly Phe Arg Leu Pro Leu Asn Ala Val Gly Ile Asn Pro Lys Thr  
20 25 30  
Asn Lys Ser Lys Arg Ile Ser Ser Lys Pro Asp Gln Ile Thr Ala Ser  
35 40 45  
Asn Arg Asp Ser Leu Ala Pro Pro Ser Met Lys Ile Pro Gly Thr Gln  
50 55 60  
Thr Ile Tyr Ile Lys Thr Phe Gly Cys Ser His Asn Gln Ser Asp Ser  
65 70 75 80  
Glu Tyr Met Ala Gly Gln Leu Ser Ala Phe Gly Tyr Ala Leu Thr Glu  
85 90 95  
Val Pro Glu Glu Ala Asp Leu Trp Leu Ile Asn Thr Cys Thr Val Lys  
100 105 110  
Ser Pro Ser Gln Ser Ala Met Ser Thr Leu Ile Thr Arg Gly Arg Ser  
115 120 125  
Gly Lys Lys Pro Leu Val Ile Ala Gly Cys Val Pro Gln Gly Ser Arg  
130 135 140  
Asp Leu Lys Glu Leu Glu Gly Val Ser Val Val Gly Val Gln Gln Ile  
145 150 155 160  
Asp Arg Val Val Glu Ile Val Glu Glu Thr Leu Lys Gly His Glu Val  
165 170 175  
Arg Leu Leu Thr Arg Lys Thr Leu Pro Ala Leu Asp Leu Pro Lys Val  
180 185 190  
Arg Arg Asn Asn Phe Ile Glu Ile Leu Pro Ile Asn Val Gly Cys Leu  
195 200 205  
Gly Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg Gly His Leu Gly  
210 215 220  
Ser Tyr Thr Val Asp Ser Leu Val Glu Arg Val Arg Thr Val Ile Ser  
225 230 235 240  
Glu Gly Val Lys Glu Ile Trp Leu Ser Ser Glu Asp Thr Gly Ala Tyr  
245 250 255  
Gly Arg Asp Ile Gly Val Asn Leu Pro Ile Leu Leu Asn Ala Ile Val

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1															
Met	Lys	Ile	Pro	Gly	Thr	Gln	Thr	Ile	Tyr	Ile	Lys	Thr	Phe	Gly	Cys
1				5				10						15	
Ser	His	Asn	Gln	Ser	Asp	Ser	Glu	Tyr	Met	Ala	Gly	Gln	Leu	Ser	Ala
		20						25					30		
Phe	Gly	Tyr	Ala	Leu	Thr	Glu	Val	Pro	Glu	Glu	Ala	Asp	Leu	Trp	Leu
		35					40					45			



Ile	Asn	Thr	Cys	Thr	Val	Lys	Ser	Pro	Ser	Gln	Ser	Ala	Met	Ser	Thr
50						55				60					
Leu	Ile	Thr	Arg	Gly	Arg	Ser	Gly	Lys	Lys	Pro	Leu	Val	Ile	Ala	Gly
65					70					75					80
Cys	Val	Pro	Gln	Gly	Ser	Arg	Asp	Leu	Lys	Glu	Leu	Glu	Gly	Val	Ser
				85					90					95	
Val	Val	Gly	Val	Gln	Gln	Ile	Asp	Arg	Val	Val	Glu	Ile	Val	Glu	Glu
			100					105					110		
Thr	Leu	Lys	Gly	His	Glu	Val	Arg	Leu	Leu	Thr	Arg	Lys	Thr	Leu	Pro
		115					120					125			
Ala	Leu	Asp	Leu	Pro	Lys	Val	Arg	Arg	Asn	Asn	Phe	Ile	Glu	Ile	Leu
	130					135					140				
Pro	Ile	Asn	Val	Gly	Cys	Leu	Gly	Ala	Cys	Thr	Tyr	Cys	Lys	Thr	Lys
145					150					155					160
His	Ala	Arg	Gly	His	Leu	Gly	Ser	Tyr	Thr	Val	Asp	Ser	Leu	Val	Glu
			165						170					175	
Arg	Val	Arg	Thr	Val	Ile	Ser	Glu	Gly	Val	Lys	Glu	Ile	Trp	Leu	Ser
			180					185					190		
Ser	Glu	Asp	Thr	Gly	Ala	Tyr	Gly	Arg	Asp	Ile	Gly	Val	Asn	Leu	Pro
	195						200					205			
Ile	Leu	Leu	Asn	Ala	Ile	Val	Lys	Glu	Leu	Pro	Ser	Asp	Gln	Ser	Thr
	210					215					220				
Met	Leu	Arg	Ile	Gly	Met	Thr	Asn	Pro	Pro	Phe	Ile	Leu	Glu	His	Leu
225					230					235					240
Lys	Glu	Ile	Ala	Ala	Val	Leu	Arg	His	Pro	Cys	Val	Tyr	Thr	Phe	Leu
			245						250					255	
His	Val	Pro	Val	Gln	Ser	Gly	Ser	Asp	Ser	Val	Leu	Thr	Ala	Met	Asn
			260					265					270		
Arg	Glu	Tyr	Thr	Ala	Ser	Glu	Phe	Arg	Thr	Val	Val	Asp	Thr	Leu	Thr
	275						280					285			
Glu	Leu	Val	Pro	Gly	Met	Gln	Ile	Ala	Thr	Asp	Ile	Ile	Cys	Gly	Phe
	290					295					300				
Pro	Gly	Glu	Thr	Asp	Glu	Asp	Phe	Ser	Gln	Thr	Val	Glu	Leu	Ile	Lys
305					310					315					320
Asp	Tyr	Lys	Phe	Pro	Gln	Val	His	Ile	Ser	Gln	Phe	Tyr	Pro	Arg	Pro
			325						330					335	
Gly	Thr	Pro	Ala	Ala	Lys	Met	Lys	Lys	Val	Gln	Ser	Lys	Ile	Val	Lys
		340						345					350		
Gln	Arg	Ser	Arg	Glu	Leu	Thr	Ser	Val	Phe	Glu	Ala	Phe	Ala	Pro	Tyr
		355					360					365			
Thr	Gly	Met	Glu	Cys	Arg	Glu	Glu	Arg	Ile	Trp	Ile	Thr	Glu	Val	Ala
	370					375					380				
Thr	Asp	Gly	Ile	His	Leu	Val	Gly	His	Thr	Lys	Gly	Tyr	Val	Gln	Val
385					390					395					400
Leu	Val	Thr	Gly	Pro	Glu	Ser	Met	Leu	Gly	Thr	Ser	Ala	Met	Ala	Arg
			405						410					415	
Ile	Thr	Ser	Val	Gly	Arg	Trp	Ser	Val	Phe	Gly	Glu	Val	Ile	Glu	Thr
			420					425					430		
Phe	Ser	Ser	Ala	Asn	Arg	Glu	Thr	Lys	Ser	Arg	Glu	Glu	Thr	Lys	Leu
		435					440					445			
Pro	Cys	Ser	Ser	Asn	Val	Ser	Thr	Cys	Glu	Thr	Cys	Thr	Cys	Ser	Ala
		450				455					460				
Glu	Ser	Cys	Gly	Glu	Glu	Arg	Ser	Gly	Glu	Ala	Cys	Asn	Ile	Ser	Gly
465					470					475					480
Asn	Ile	Ser	Gly	Gln	Asp	Asp	Asn	Lys	Gly	Lys	Ser	Lys	Lys	Glu	Glu
			485						490					495	
Lys	Glu	Val	Gln	Glu	Val	Val	Val	Pro	Gly	Ser	Ser	Val	Ala	Asn	Trp
			500					505					510		
Gly	Phe	Ile	Asp	Lys	Ala	Leu	Val	Cys	Gly	Val	Phe	Val	Ser	Ser	Val
		515						520				525			
Thr	Ile	Leu	Val	Leu	Leu	Ile	Ser	Ile	Ala	Cys	Arg	Val	Leu	Leu	Arg

530

535

540

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

```
ctcttttcctt aagtgtcaaa ctcttgaaaa aactactttg aaggaaaaaa tgtctaagaa      60
gaagaaaggc agcaacaact ttaagcttct ctgtttcttc ctgttttttg gtgggttggt      120
tcagacagat gcttcttttg gagtaggagg cggcggttga gtaggaatcg gcggcgggcg      180
cgggtggcggt ggcgggtggtg tttgggttgg cgggtggatac aacaacggtt gaaatcgtaa      240
tgctgttcca ggatcatcag ctccaaacag ggtagcttac aatgctcttc aagtttggaa      300
atcagccatg agagaggatc catcaaagt tctctgggtca atctataacc tctatagatc ttaacctatgc      360
ttcttacaaa ggtgtgttct gttctgggtca atctataacc tctatagatc ttaacctatgc      420
aaatctcaaa ggcacacttg tcaaagacct agctttactc tcagacctca atattctcca      480
tctcaacagt aacagattct caggggcaaat cccagattct ttcaaactct tagcttctct      540
tcaagaactt gatctaagca acaataaact ctccaggtcct ttcccttttag tcacactcta      600
cataccaaat ctgggtttacc tcgatctccg gtttaatatg ttaaccggtt tcatccctga      660
agagcttttc aacaaacggt tagacgcgat tctcctcaat aacaatcaat tcgtcggaga      720
aatcccaaga aacctcggaa attctccggc ttccggttatt aatctcgcga ataacagatt      780
ttccggcgaa attccgacga gttttggtct gacgggatcg aggggttaagg aagttttgct      840
tttgaataac cagttaaccg gttgtatacc ggaatctggt ggtatgttct ctgaaattga      900
agtctttgac gttagctaca atgcattgat gggctcatgt ccagatacga tctcttgctt      960
gtcggcgatt gaaattttga atcttgctca caataaattc tctggggagg ttcttgattt      1020
ggtttggtcg ttgaggaatc ttattaatct cactgttgcg ttcaatttct tctctgggtt      1080
tagctctgaa tggtcttcca gggtagtatt cgggtttgat ttcgttggga attgtattcc      1140
cgggaggaat tcgcagcggc cgcagccgga ttgttccggt tattccggcg gagctatgag      1200
ctgttttagg attccgacgc agcctttggc ttgtgtgcgc ataagtgttg gattgagaga      1260
gagtaataat caatactaca ctcatctcc tccatgaaag tttctaaagt tagaagcttt      1320
tttttattaa tggttgatgc tgaatgatct atcttttttg taacttatta attagttgat      1380
tagtgaccaa attaaacggt aattcctctt ctgtgtaatc caatcgttgc taatgttggt      1440
ttgt
```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..329
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```
Met Arg Glu Asp Pro Ser Asn Val Leu Lys Thr Trp Val Gly Ser Asp
1          5          10          15
Val Cys Ser Tyr Lys Gly Val Phe Cys Ser Gly Gln Ser Ile Thr Ser
20          25          30
Ile Asp Leu Asn His Ala Asn Leu Lys Gly Thr Leu Val Lys Asp Leu
35          40          45
Ala Leu Leu Ser Asp Leu Asn Ile Leu His Leu Asn Ser Asn Arg Phe
50          55          60
Ser Gly Gln Ile Pro Asp Ser Phe Lys Ser Leu Ala Ser Leu Gln Glu
```

65		70		75		80
Leu	Asp	Leu	Ser	Asn	Lys	Leu
		85		90		95
Leu	Tyr	Ile	Pro	Asn	Leu	Val
		100		105		110
Thr	Gly	Phe	Ile	Pro	Glu	Glu
		115		120		125
Leu	Leu	Asn	Asn	Asn	Gln	Phe
		130		135		140
Asn	Ser	Pro	Ala	Ser	Val	Ile
		145		150		155
Glu	Ile	Pro	Thr	Ser	Phe	Gly
		165		170		175
Leu	Leu	Leu	Asn	Asn	Gln	Leu
		180		185		190
Met	Phe	Ser	Glu	Ile	Glu	Val
		195		200		205
Gly	His	Val	Pro	Asp	Thr	Ile
		210		215		220
Asn	Leu	Ala	His	Asn	Lys	Phe
		225		230		235
Ser	Leu	Arg	Asn	Leu	Ile	Asn
		245		250		255
Gly	Phe	Ser	Ser	Glu	Cys	Ser
		260		265		270
Val	Gly	Asn	Cys	Ile	Pro	Gly
		275		280		285
Cys	Ser	Gly	Tyr	Ser	Gly	Gly
		290		295		300
Gln	Pro	Leu	Ala	Cys	Ala	Ile
		305		310		315
Asn	Gln	Tyr	Tyr	Thr	Ser	Ser
		325				

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1981
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

atcggttcacg	caaaacttca	cgattcagat	ctgtgtgtg	cagaatttga	atcgaagcat	60
aggatcaatc	cggtaagcag	ccgtaacttg	caatcgatcg	ccgatctgga	tccgttaaag	120
gatccctcgc	agtccttgaa	gatatacgcg	tcctccgccca	ccgggaacag	gatccgttac	180
cgttcacctt	ccgcttctga	gctattggag	tctggactag	ccaccggatt	atccggtaac	240
cattctccta	cttccgactc	tcatacaggga	cttgtgtcta	tcgacggagg	aaaaatgacg	300
gcgaagcgag	cgatcggacg	gcacgaatcc	cttgctgaca	aggtccatcg	acatcggtgt	360
cttctacttg	tgatttcgat	ccccattgtg	ttgatagctc	ttgtgcttct	gttaatgccg	420
gggacgtcga	cgtccgtctc	tgatcatcgag	tacacgatga	aaaaccacga	gggaggttcc	480
aattcgaggg	gtccgaagaa	ttacgctgtg	atttttgatg	ctggaagtgc	tgggaagccgt	540
gtgcatgttt	actgttttca	tcagaatttg	gatcttggtc	ctttggagaa	tgagctcgag	600
ctcttcttac	agctaaaacc	gggtttaagt	gcataccta	atgatcctcg	gcaatcagca	660
aactctttag	taactcttct	ggacaaagca	gaagcttccg	ttccccgtga	gttgcgacca	720
aagactcctg	tcagagttgg	ggcaactgca	ggtttgagag	ctttgggtca	ccaagcctct	780
gaaaacattt	tgcaagcggg	agctcctcaa	aggtagaagt	aggctgaaga	ctgaggcaaaa	840
tgcagtgact	gttctggatg	gtactcagga	aggatcttat	cagtgggtga	caattaatta	900
cttgctaagg	actttgggaa	agccgtactc	ggacacagtt	ggagtgggtg	atcttgaggg	960

```

ggggtcgggtt caaatggcat atgctatacc agaggaagat gctgcaactg caccaaaacc 1020
agtagaaggc gaggattctt atgtcagaga aatgtatttg aaggacgaa agtatttcct 1080
ctatgttcat agctacctac attacgggtt actggctgct cgggctgaga ttttgaaagt 1140
ttctgaggac tctaacaacc cctgtatcgc gactggatat gctgggtacct acaaatatgg 1200
aggaaaagcg tttaaagctg cagcttctcc atccgggtgca agtctagatg agtgccggcg 1260
agtagctatt aacgcactca aagtcaataa ttcatgtgac acacacatga aatgcacttt 1320
tggtggagta tggaatggtg gaggcggtgg tggccagaag aaaatgtttg ttgcatcatt 1380
tttcttcgat cgagccgcag aggctgggtt tgttgaccca aaccaacctg tggctgaggt 1440
tcgaccactt gactttgaga aagcggccaa caaagcttgt aacatgagaa tggaagaagg 1500
gaaatcgaag ttcccacgtg tggaggaaga taatcttcct tacttgtgct tggatcttgt 1560
ttaccaatat actcttctcg tcgatggatt cggattgaag ccatcacaga caataacgtt 1620
agtgaagaag gtgaaatacg gagattacgc cgtggaagct gcgtggccac taggaagcgc 1680
catagaagca gtatcctcac catgaggaag gcaatttttg gtatttgcac taaacctctt 1740
attcttttag tttctcccaa aatcacccca agcttttttt gccttacctc aaattttttt 1800
tatcgtcaac atcttcttta catcaatttt tgttacaata atcatctaga gaaaagagtt 1860
tcaattctta atatacctat aattttattt ttcttgaat cttaaactgct taccgcatac 1920
gtaacctctg tttctttctt ataaaatatt ttccttgctt ttttttttct tttgacgact 1980

```

g

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1498736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

Ile Val His Ala Lys Leu His Asp Ser Asp Leu Cys Val Ala Glu Phe
1           5           10           15
Glu Ser Lys His Arg Ile Asn Pro Val Ser Ser Arg Asn Leu Gln Ser
20           25           30
Ile Ala Asp Leu Asp Pro Leu Lys Asp Pro Ser Gln Ser Leu Lys Ile
35           40           45
Ser Ala Ser Ser Ala Thr Gly Asn Arg Ile Arg Tyr Arg Ser Pro Ser
50           55           60
Ala Ser Glu Leu Leu Glu Ser Gly Leu Ala Thr Gly Leu Ser Gly Asn
65           70           75           80
His Ser Pro Thr Ser Asp Ser His Gln Gly Leu Val Ser Ile Asp Gly
85           90           95
Gly Lys Met Thr Ala Lys Arg Ala Ile Gly Arg His Glu Ser Leu Ala
100          105          110
Asp Lys Val His Arg His Arg Gly Leu Leu Leu Val Ile Ser Ile Pro
115          120          125
Ile Val Leu Ile Ala Leu Val Leu Leu Met Pro Gly Thr Ser Thr
130          135          140
Ser Val Ser Val Ile Glu Tyr Thr Met Lys Asn His Glu Gly Gly Ser
145          150          155          160
Asn Ser Arg Gly Pro Lys Asn Tyr Ala Val Ile Phe Asp Ala Gly Ser
165          170          175
Ser Gly Ser Arg Val His Val Tyr Cys Phe Asp Gln Asn Leu Asp Leu
180          185          190
Val Pro Leu Glu Asn Glu Leu Glu Phe Leu Gln Leu Lys Pro Gly
195          200          205
Leu Ser Ala Tyr Pro Asn Asp Pro Arg Gln Ser Ala Asn Ser Leu Val
210          215          220
Thr Leu Leu Asp Lys Ala Glu Ala Ser Val Pro Arg Glu Leu Arg Pro
225          230          235          240
Lys Thr Pro Val Arg Val Gly Ala Thr Ala Gly Leu Arg Ala Leu Gly

```

245 250 255  
His Gln Ala Ser Glu Asn Ile Leu Gln Ala Gly Ala Pro Gln Arg  
260 265 270

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Met Ala Tyr Ala Ile Pro Glu Glu Asp Ala Ala Thr Ala Pro Lys Pro  
1 5 10 15  
Val Glu Gly Glu Asp Ser Tyr Val Arg Glu Met Tyr Leu Lys Gly Arg  
20 25 30  
Lys Tyr Phe Leu Tyr Val His Ser Tyr Leu His Tyr Gly Leu Leu Ala  
35 40 45  
Ala Arg Ala Glu Ile Leu Lys Val Ser Glu Asp Ser Asn Asn Pro Cys  
50 55 60  
Ile Ala Thr Gly Tyr Ala Gly Thr Tyr Lys Tyr Gly Gly Lys Ala Phe  
65 70 75 80  
Lys Ala Ala Ala Ser Pro Ser Gly Ala Ser Leu Asp Glu Cys Arg Arg  
85 90 95  
Val Ala Ile Asn Ala Leu Lys Val Asn Asn Ser Leu Cys Thr His Met  
100 105 110  
Lys Cys Thr Phe Gly Gly Val Trp Asn Gly Gly Gly Gly Gly Gly Gln  
115 120 125  
Lys Lys Met Phe Val Ala Ser Phe Phe Phe Asp Arg Ala Ala Glu Ala  
130 135 140  
Gly Phe Val Asp Pro Asn Gln Pro Val Ala Glu Val Arg Pro Leu Asp  
145 150 155 160  
Phe Glu Lys Ala Ala Asn Lys Ala Cys Asn Met Arg Met Glu Glu Gly  
165 170 175  
Lys Ser Lys Phe Pro Arg Val Glu Glu Asp Asn Leu Pro Tyr Leu Cys  
180 185 190  
Leu Asp Leu Val Tyr Gln Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu  
195 200 205  
Lys Pro Ser Gln Thr Ile Thr Leu Val Lys Lys Val Lys Tyr Gly Asp  
210 215 220  
Tyr Ala Val Glu Ala Ala Trp Pro Leu Gly Ser Ala Ile Glu Ala Val  
225 230 235 240  
Ser Ser Pro

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met Tyr Leu Lys Gly Arg Lys Tyr Phe Leu Tyr Val His Ser Tyr Leu  
1 5 10 15

His Tyr Gly Leu Leu Ala Ala Arg Ala Glu Ile Leu Lys Val Ser Glu  
20 25 30  
Asp Ser Asn Asn Pro Cys Ile Ala Thr Gly Tyr Ala Gly Thr Tyr Lys  
35 40 45  
Tyr Gly Gly Lys Ala Phe Lys Ala Ala Ala Ser Pro Ser Gly Ala Ser  
50 55 60  
Leu Asp Glu Cys Arg Arg Val Ala Ile Asn Ala Leu Lys Val Asn Asn  
65 70 75 80  
Ser Leu Cys Thr His Met Lys Cys Thr Phe Gly Gly Val Trp Asn Gly  
85 90 95  
Gly Gly Gly Gly Gly Gln Lys Lys Met Phe Val Ala Ser Phe Phe  
100 105 110  
Asp Arg Ala Ala Glu Ala Gly Phe Val Asp Pro Asn Gln Pro Val Ala  
115 120 125  
Glu Val Arg Pro Leu Asp Phe Glu Lys Ala Ala Asn Lys Ala Cys Asn  
130 135 140  
Met Arg Met Glu Glu Gly Lys Ser Lys Phe Pro Arg Val Glu Glu Asp  
145 150 155 160  
Asn Leu Pro Tyr Leu Cys Leu Asp Leu Val Tyr Gln Tyr Thr Leu Leu  
165 170 175  
Val Asp Gly Phe Gly Leu Lys Pro Ser Gln Thr Ile Thr Leu Val Lys  
180 185 190  
Lys Val Lys Tyr Gly Asp Tyr Ala Val Glu Ala Ala Trp Pro Leu Gly  
195 200 205  
Ser Ala Ile Glu Ala Val Ser Ser Pro  
210 215

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

ttctctccgg	atctttctag	gttttcaatt	tttgttttac	cttcaaaggt	tggttcctttg	60
tgatataaaa	atatagtttt	caccttcttt	caatctctgc	ggtttctaaa	tagaacattg	120
gagagatttg	tttctgcatt	tgtaaatttt	gatttctttg	accatctctc	tggttttgrt	180
ggcaacacac	gtattccaat	ccaaatcgac	aataatcgcg	tctctgatgg	atatgttttg	240
gattcagtga	gaaacagaga	ttgatttttg	ttttctttta	tcatgggtga	gccttatgag	300
acacgtaaca	acggtgaagc	atcccagatg	atcagatatc	agagttataa	ccatcacaat	360
tccagactac	catcttcatt	atcatcgcca	ttgcttgatt	tgagagtgtt	ctatgtcaga	420
atcagtaatt	tcaaggtgga	tcattcgaca	cctgagggtc	tcaccattac	tcattatcct	480
ttggatccag	attcacttct	ggagattaat	ggtgttagaa	tgagcatgta	ctctgaagga	540
gtttctttct	agcttaggcg	tgatcgtggt	gataagaaat	ctgaagttgc	tactttttatc	600
agcacggata	atatcaggtt	atctggtagt	gtgaagtttg	aggttttatga	taaagatgag	660
ctgggttttg	ctggaacgct	tgagatgtct	ggtagtaatg	gtttcactgg	tgaatctaag	720
catagcgtga	agcgttgga	catgaattgt	gaagctgaga	tcactgcagg	gtctgggttc	780
ttgaaggaga	aacatattgg	tggttcggag	ttatcttctc	cattgccaac	tattgaagtc	840
tatgtcactg	gctgcttttc	tggaactcct	atcatcctaa	cgaagactct	acagcttggt	900
ttcagaaaga	agcacggtag	agtgactgca	ttagattcga	ttcccgaata	tgaaactgat	960
gagcctcata	aaggaaactc	atctgagctt	gattatcagg	ttactgaata	tggaagttat	1020
aaacaagaat	atgaaggaga	acacagcgac	atgtactgga	atagagagta	cgcagatggt	1080
gaagatgggt	agatgtcgtg	gttcaacgct	ggtgtgaggg	ttggtgtggg	aattggtctt	1140
ggtgtctgtg	taggtctttg	cattgggggt	ggccttctgg	tgcgtacctc	tcaatcgacc	1200
accagaaact	tcagaaggag	gattatctag	tttcattcaa	attgcctcaa	gcttcatcta	1260
ctctctccct	ctaactccaa	tccgttgac	atcacttttg	actgcagAAC	tctaagctat	1320
atagtctaag	ctaatactgc	tgtgtagtat	aatttttgtt	ttatgtactt	tttaactctt	1380

ttgtgccttc aaattttgaa agaaatcatt ttcccttg

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met	Val	Glu	Pro	Tyr	Glu	Thr	Arg	Asn	Asn	Gly	Glu	Ala	Ser	Gln	Met
1			5						10					15	
Ile	Arg	Tyr	Gln	Ser	Tyr	Asn	His	His	Asn	Ser	Arg	Leu	Pro	Ser	Ser
			20				25						30		
Leu	Ser	Ser	Pro	Leu	Leu	Asp	Leu	Arg	Val	Phe	Tyr	Val	Arg	Ile	Ser
		35				40					45				
Asn	Phe	Lys	Val	Asp	His	Ser	Thr	Pro	Glu	Val	Leu	Thr	Ile	Thr	His
	50				55					60					
Ile	Pro	Leu	Asp	Pro	Asp	Ser	Leu	Leu	Glu	Ile	Asn	Gly	Val	Arg	Met
65					70				75						80
Ser	Met	Tyr	Ser	Glu	Gly	Val	Ser	Ser	Gln	Leu	Arg	Arg	Asp	Arg	Val
			85						90				95		
Asp	Lys	Lys	Ser	Glu	Val	Ala	Thr	Phe	Ile	Ser	Thr	Asp	Asn	Ile	Arg
			100					105					110		
Leu	Ser	Gly	Ser	Val	Lys	Phe	Glu	Val	Tyr	Asp	Lys	Asp	Glu	Leu	Val
		115					120					125			
Leu	Ser	Gly	Thr	Leu	Glu	Met	Ser	Gly	Ser	Asn	Gly	Phe	Thr	Gly	Glu
		130				135					140				
Ser	Lys	His	Ser	Val	Lys	Arg	Trp	Asn	Met	Asn	Cys	Glu	Ala	Glu	Ile
145					150					155					160
Thr	Ala	Gly	Ser	Gly	Phe	Leu	Lys	Glu	Lys	His	Ile	Gly	Gly	Ser	Glu
			165						170					175	
Leu	Ser	Ser	Pro	Leu	Pro	Thr	Ile	Glu	Val	Tyr	Val	Thr	Gly	Cys	Phe
			180					185					190		
Ser	Gly	Thr	Pro	Ile	Ile	Leu	Thr	Lys	Thr	Leu	Gln	Leu	Gly	Phe	Arg
		195				200						205			
Lys	Lys	His	Gly	Arg	Val	Thr	Ala	Leu	Asp	Ser	Ile	Pro	Glu	Tyr	Glu
		210				215					220				
Thr	Asp	Glu	Pro	His	Lys	Gly	Asn	Ser	Ser	Glu	Leu	Asp	Tyr	Gln	Val
225					230					235					240
Thr	Glu	Tyr	Gly	Ser	Tyr	Lys	Gln	Glu	Tyr	Glu	Gly	Glu	His	Ser	Asp
			245						250					255	
Met	Tyr	Trp	Asn	Arg	Glu	Tyr	Ala	Asp	Gly	Glu	Asp	Gly	Glu	Met	Ser
			260					265					270		
Trp	Phe	Asn	Ala	Gly	Val	Arg	Val	Gly	Val	Gly	Ile	Gly	Leu	Gly	Val
		275					280					285			
Cys	Val	Gly	Leu	Gly	Ile	Gly	Val	Gly	Leu	Leu	Val	Arg	Thr	Tyr	Gln
		290				295					300				
Ser	Thr	Thr	Arg	Asn	Phe	Arg	Arg	Arg	Ile	Ile					
305					310					315					

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1498741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```
Met Ile Arg Tyr Gln Ser Tyr Asn His His Asn Ser Arg Leu Pro Ser
1           5           10           15
Ser Leu Ser Ser Pro Leu Leu Asp Leu Arg Val Phe Tyr Val Arg Ile
          20           25           30
Ser Asn Phe Lys Val Asp His Ser Thr Pro Glu Val Leu Thr Ile Thr
          35           40           45
His Ile Pro Leu Asp Pro Asp Ser Leu Leu Glu Ile Asn Gly Val Arg
          50           55           60
Met Ser Met Tyr Ser Glu Gly Val Ser Ser Gln Leu Arg Arg Asp Arg
65           70           75           80
Val Asp Lys Lys Ser Glu Val Ala Thr Phe Ile Ser Thr Asp Asn Ile
          85           90           95
Arg Leu Ser Gly Ser Val Lys Phe Glu Val Tyr Asp Lys Asp Glu Leu
          100          105          110
Val Leu Ser Gly Thr Leu Glu Met Ser Gly Ser Asn Gly Phe Thr Gly
          115          120          125
Glu Ser Lys His Ser Val Lys Arg Trp Asn Met Asn Cys Glu Ala Glu
130          135          140
Ile Thr Ala Gly Ser Gly Phe Leu Lys Glu Lys His Ile Gly Gly Ser
145          150          155          160
Glu Leu Ser Ser Pro Leu Pro Thr Ile Glu Val Tyr Val Thr Gly Cys
          165          170          175
Phe Ser Gly Thr Pro Ile Ile Leu Thr Lys Thr Leu Gln Leu Gly Phe
          180          185          190
Arg Lys Lys His Gly Arg Val Thr Ala Leu Asp Ser Ile Pro Glu Tyr
          195          200          205
Glu Thr Asp Glu Pro His Lys Gly Asn Ser Ser Glu Leu Asp Tyr Gln
210          215          220
Val Thr Glu Tyr Gly Ser Tyr Lys Gln Glu Tyr Glu Gly Glu His Ser
225          230          235          240
Asp Met Tyr Trp Asn Arg Glu Tyr Ala Asp Gly Glu Asp Gly Glu Met
          245          250          255
Ser Trp Phe Asn Ala Gly Val Arg Val Gly Val Gly Ile Gly Leu Gly
          260          265          270
Val Cys Val Gly Leu Gly Ile Gly Val Gly Leu Leu Val Arg Thr Tyr
          275          280          285
Gln Ser Thr Thr Arg Asn Phe Arg Arg Arg Ile Ile
290          295          300
```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1498742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```
Met Ser Met Tyr Ser Glu Gly Val Ser Gln Leu Arg Arg Asp Arg
1           5           10           15
Val Asp Lys Lys Ser Glu Val Ala Thr Phe Ile Ser Thr Asp Asn Ile
          20           25           30
Arg Leu Ser Gly Ser Val Lys Phe Glu Val Tyr Asp Lys Asp Glu Leu
          35           40           45
Val Leu Ser Gly Thr Leu Glu Met Ser Gly Ser Asn Gly Phe Thr Gly
```



50	55	60
Glu Ser Lys His Ser Val Lys Arg Trp Asn Met Asn Cys Glu Ala Glu		
65	70	75
Ile Thr Ala Gly Ser Gly Phe Leu Lys Glu Lys His Ile Gly Gly Ser		80
	85	90
Glu Leu Ser Ser Pro Leu Pro Thr Ile Glu Val Tyr Val Thr Gly Cys		95
	100	105
Phe Ser Gly Thr Pro Ile Ile Leu Thr Lys Thr Leu Gln Leu Gly Phe		110
	115	120
Arg Lys Lys His Gly Arg Val Thr Ala Leu Asp Ser Ile Pro Glu Tyr		125
	130	135
Glu Thr Asp Glu Pro His Lys Gly Asn Ser Ser Glu Leu Asp Tyr Gln		140
	145	150
Val Thr Glu Tyr Gly Ser Tyr Lys Gln Glu Tyr Glu Gly Glu His Ser		155
	165	170
Asp Met Tyr Trp Asn Arg Glu Tyr Ala Asp Gly Glu Asp Gly Glu Met		175
	180	185
Ser Trp Phe Asn Ala Gly Val Arg Val Gly Val Gly Ile Gly Leu Gly		190
	195	200
Val Cys Val Gly Leu Gly Ile Gly Val Gly Leu Leu Val Arg Thr Tyr		205
	210	215
Gln Ser Thr Thr Arg Asn Phe Arg Arg Arg Ile Ile		220
	225	230
		235

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1608
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

aatcgagat	tttctctcct	tctcttttca	gccgccaatc	gccgccgcaa	tcttcttcat	60
cggcctccgt	tctacatcga	cgggtgtttgc	cgtaacttct	gtcaaactct	cagaatttgc	120
ttaagtatac	cacctaaactc	gagacgctat	gaccgttttc	tcagttcagt	ccactatctt	180
cagtcgagcc	tccgtagctc	ttctctcgag	caatggcttc	aaacgatttt	cattcgtttc	240
ttcgttttct	tcctccgcgc	cttactctcc	acctaaaatg	aggaagcgtc	gctacccaat	300
cgtctctgct	gttgatattg	gtggcgctgc	aatcgctaga	aatgatgtgg	tgagagagga	360
tgatccaaca	aataatgtac	cagattcgat	tttctctaaa	ctaggaatsc	agctacacag	420
aagagataag	catccgattg	gtatcttaaa	aaacgcatac	tacgattact	ttgattccaa	480
ttactcaaac	aagtttgaga	agttcgaaga	cctttcccca	attgttacca	caaagcaaaa	540
ctttgatgat	gtgctagtcc	ctgctgatca	tgtaagcaga	agtcttaatg	acacgtacta	600
gttagactca	caaactgttt	tgagatgtca	tacgagtgtc	caccaagctg	agctgttgag	660
gaaaggatcat	agtcgtttcc	ttgtaaccgg	ggatgtttac	cgaagagatt	ctattgactc	720
tactcattat	cgggttttcc	atcagatgga	aggtttttgt	gttttctctc	ctgaggactg	780
gaacgggtct	ggcaaggatt	ccactttgta	tgctgctgag	gatttgaaga	aatgtcttga	840
gggattggca	cgccacttat	ttggttcggt	ggagatgaga	tgggttgata	catatttccc	900
atttaccat	ccatcttttg	agcttgagat	atattttaag	gaagactggt	tggagggttt	960
gggctgtggg	gtgaccgagc	aagtaattct	gaaacaaagt	ggataagaaa	ataatgttgc	1020
ttgggccttc	ggacttgga	ttgagagact	tgctatgggt	ttgtttgaca	tacctgat	1080
acgatttttc	tggtcatccg	atgaacgatt	cacgtcccag	tttggaaaag	gagaacttgg	1140
agtgaatttc	aagccatatt	caaagtatcc	tccttggtac	aaggacatca	gtttctggat	1200
aagtgtattg	ttcacagaga	ataatttttg	tgaagtgtt	agaggaattg	ctggggatct	1260
tggtgaagag	gtgaagttaa	ttgaccaatt	caccaataag	aagaaagggc	tgacgagtca	1320
ttgttacaga	atcgtgttcc	gttccatgga	gcggtctctt	acggacgagg	aggtoaatga	1380
tctgcagagt	aaagtgcgtg	atgaggtgca	gaagaagcta	aatgtcgaat	taaggtgaga	1440
attttgaaaa	gagtagcggt	gttgacagaca	gtgatgaata	ttgaaggttt	ggcattgtta	1500
ttcctacata	aactttattt	acttctggca	gaattgcatt	accctcaaaa	aaatatatgt	1560

acattggttt cgttattcta aaggaatgaa aaataagggtg tccgtttt

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1498744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Met	Thr	Val	Phe	Ser	Val	Gln	Ser	Thr	Ile	Phe	Ser	Arg	Ala	Ser	Val
1				5					10					15	
Ala	Leu	Leu	Ser	Ser	Asn	Gly	Phe	Lys	Arg	Phe	Ser	Phe	Val	Ser	Ser
			20					25					30		
Phe	Ser	Ser	Ser	Ala	Ala	Tyr	Ser	Pro	Pro	Lys	Met	Arg	Lys	Arg	Arg
			35				40					45			
Tyr	Pro	Ile	Val	Ser	Ala	Val	Asp	Ile	Gly	Gly	Val	Ala	Ile	Ala	Arg
	50					55					60				
Asn	Asp	Val	Val	Arg	Glu	Asp	Asp	Pro	Thr	Asn	Asn	Val	Pro	Asp	Ser
65					70					75				80	
Ile	Phe	Ser	Lys	Leu	Gly	Xaa	Gln	Leu	His	Arg	Arg	Asp	Lys	His	Pro
			85						90					95	
Ile	Gly	Ile	Leu	Lys	Asn	Ala	Ile	Tyr	Asp	Tyr	Phe	Asp	Ser	Asn	Tyr
			100				105						110		
Ser	Asn	Lys	Phe	Glu	Lys	Phe	Glu	Asp	Leu	Ser	Pro	Ile	Val	Thr	Thr
		115					120					125			
Lys	Gln	Asn	Phe	Asp	Asp	Val	Leu	Val	Pro	Ala	Asp	His	Val	Ser	Arg
		130				135					140				
Ser	Leu	Asn	Asp	Thr	Tyr	Tyr	Val	Asp	Ser	Gln	Thr	Val	Leu	Arg	Cys
145					150					155				160	
His	Thr	Ser	Ala	His	Gln	Ala	Glu	Leu	Leu	Arg	Lys	Gly	His	Ser	Arg
			165					170						175	
Phe	Leu	Val	Thr	Gly	Asp	Val	Tyr	Arg	Arg	Asp	Ser	Ile	Asp	Ser	Thr
			180					185					190		
His	Tyr	Pro	Val	Phe	His	Gln	Met	Glu	Gly	Phe	Cys	Val	Phe	Ser	Pro
		195					200					205			
Glu	Asp	Trp	Asn	Gly	Ser	Gly	Lys	Asp	Ser	Thr	Leu	Tyr	Ala	Ala	Glu
		210				215					220				
Asp	Leu	Lys	Lys	Cys	Leu	Glu	Gly	Leu	Ala	Arg	His	Leu	Phe	Gly	Ser
225					230					235				240	
Val	Glu	Met	Arg	Trp	Val	Asp	Thr	Tyr	Phe	Pro	Phe	Thr	Asn	Pro	Ser
			245						250					255	
Phe	Glu	Leu	Glu	Ile	Tyr	Phe	Lys	Glu	Asp	Trp	Leu	Glu	Val	Leu	Gly
		260					265						270		
Cys	Gly	Val	Thr	Glu	Gln	Val	Ile	Leu	Lys	Gln	Ser	Gly			
		275				280						285			

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1498745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

```

Met Arg Lys Arg Arg Tyr Pro Ile Val Ser Ala Val Asp Ile Gly Gly
1      5      10      15
Val Ala Ile Ala Arg Asn Asp Val Val Arg Glu Asp Asp Pro Thr Asn
20      25      30
Asn Val Pro Asp Ser Ile Phe Ser Lys Leu Gly Xaa Gln Leu His Arg
35      40      45
Arg Asp Lys His Pro Ile Gly Ile Leu Lys Asn Ala Ile Tyr Asp Tyr
50      55      60
Phe Asp Ser Asn Tyr Ser Asn Lys Phe Glu Lys Phe Glu Asp Leu Ser
65      70      75      80
Pro Ile Val Thr Thr Lys Gln Asn Phe Asp Asp Val Leu Val Pro Ala
85      90      95
Asp His Val Ser Arg Ser Leu Asn Asp Thr Tyr Tyr Val Asp Ser Gln
100     105     110
Thr Val Leu Arg Cys His Thr Ser Ala His Gln Ala Glu Leu Leu Arg
115     120     125
Lys Gly His Ser Arg Phe Leu Val Thr Gly Asp Val Tyr Arg Arg Asp
130     135     140
Ser Ile Asp Ser Thr His Tyr Pro Val Phe His Gln Met Glu Gly Phe
145     150     155     160
Cys Val Phe Ser Pro Glu Asp Trp Asn Gly Ser Gly Lys Asp Ser Thr
165     170     175
Leu Tyr Ala Ala Glu Asp Leu Lys Lys Cys Leu Glu Gly Leu Ala Arg
180     185     190
His Leu Phe Gly Ser Val Glu Met Arg Trp Val Asp Thr Tyr Phe Pro
195     200     205
Phe Thr Asn Pro Ser Phe Glu Leu Glu Ile Tyr Phe Lys Glu Asp Trp
210     215     220
Leu Glu Val Leu Gly Cys Gly Val Thr Glu Gln Val Ile Leu Lys Gln
225     230     235     240
Ser Gly

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

accagaagaa gagccacaca ctcaaaatt aaaaagagag agagagagag agagacagag      60
agagagagag attctgcgga ggagcttctt ctctgtaggg tgttcacgtg tattaacggt      120
atcgccccta cgtcagctcc atctccagaa acatgggtgc aggtggaaga atgccgggtc      180
ctacttcttc caagaaatcg gaaaccgaca ccacaaagcg tgtgccgtgc gagaaaccgc      240
ctttctcggt gggagatctg aagaaagcaa tcccgccgca ttgtttcaaa cgctcaatcc      300
ctcgtctctt ctctacctt atcagtgaca tcattatagc ctcattgctt tactacgtcg      360
ccaccaatta ctctctctc ctccctcagc ctctctctta cttggcttgg ccactctatt      420
gggcctgtca aggtgtgtc ctaactggta tctgggtcat agcccacgaa tgcggtcacc      480
acgcattcag cgactaccaa tggctggatg acacagttgg tcttatcttc cattccttc      540
tcctcgtccc ttacttctcc tggaagtata gtcatcgccg tcaccattcc aacactggat      600
ccctcgaaag agatgaagta tttgtcccaa agcagaaaac agcaatcaag tggtagcgga      660
aataacctca caacctctt ggacgcatca tgatgttaac cgtccagttt gtcctcgggt      720
ggcccttgta cttagccttt aacgtctctg gcagaccgta tgacgggttc gcttgccatt      780
tcttcccaa cgctcccac tacaatgacc gagaacgcct ccagatatat ctctctgatg      840
cgggtattct agccgtctgt tttggctctt accgttacgc tgctgcacaa gggatggcct      900
cgatgatctg cctctacgga gtaccgcttc tgatagttaa tgcgttcctc gtcttgatca      960
cttacttgca gcacactcat ccctcgttgc ctactacga ttcacagag tgggactggc      1020

```

tcaggggagc tttggctacc gtagacagag actacggaat cttgaacaag gtgttccaca 1080  
acattacaga cacacacgtg gctcatcacc tgttctcgac aatgccgcat tataacgcaa 1140  
tggaagctac aaaggcgata aagccaattc tgggagacta ttaccagttc gatggaacac 1200  
cgtggtatgt ggcgatgtat agggaggcaa aggagtgtat ctatgtagaa ccggacaggg 1260  
aagggtgacaa gaaaggtgtg tactggtaca acaataagtt atgaggatga tgggtgaagaa 1320  
attgtcgact tttctcttgt ctgtttgtct tttgttaaag aagctatgct tcgttttaat 1380  
aatcttattg tccattttgt tgtgttatga cattttggct gctcattatg ttatgtggga 1440  
agttagtgtt c

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1498747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met	Gly	Ala	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser	
1			5					10					15		
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser
			20					25					30		
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
			35				40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser
	50					55				60					
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65				70					75						80
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
			85						90					95	
Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
	115					120						125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
	130					135					140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
			165						170					175	
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu
		180						185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys
	195						200					205			
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln
	210					215					220				
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr
225					230					235					240
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly
			245						250					255	
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu
		260						265					270		
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp
	275						280					285			
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu
	290					295					300				
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu
305					310					315					320
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile

Met 1	Pro	Val	Pro	Thr 5	Ser	Ser	Lys	Lys	Ser 10	Glu	Thr	Asp	Thr	Thr 15	Lys
Arg	Val	Pro	Cys 20	Glu	Lys	Pro	Pro	Phe 25	Ser	Val	Gly	Asp	Leu 30	Lys	Lys
Ala	Ile	Pro	Pro	His	Cys	Phe	Lys 40	Arg	Ser	Ile	Pro	Arg 45	Ser	Phe	Ser
Tyr	Leu 50	Ile	Ser	Asp	Ile	Ile 55	Ile	Ala	Ser	Cys	Phe 60	Tyr	Tyr	Val	Ala
Thr 65	Asn	Tyr	Phe	Ser 70	Leu	Pro	Gln	Pro	Leu 75	Ser	Tyr	Leu	Ala	Trp 80	
Pro	Leu	Tyr	Trp	Ala 85	Cys	Gln	Gly	Cys 90	Val	Leu	Thr	Gly	Ile	Trp 95	Val
Ile	Ala	His	Glu 100	Cys	Gly	His	His 105	Ala	Phe	Ser	Asp	Tyr	Gln 110	Trp	Leu
Asp	Asp	Thr 115	Val	Gly	Leu	Ile 120	Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr
Phe	Ser 130	Trp	Lys	Tyr	Ser	His 135	Arg	Arg	His	His 140	Ser	Asn	Thr	Gly	Ser
Leu 145	Glu	Arg	Asp	Glu 150	Val	Phe	Val	Pro	Lys	Gln 155	Lys	Ser	Ala	Ile	Lys 160
Trp	Tyr	Gly	Lys	Tyr 165	Leu	Asn	Asn	Pro	Leu 170	Gly	Arg	Ile	Met	Met	Leu
Thr	Val	Gln	Phe 180	Val	Leu	Gly	Trp 185	Pro	Leu	Tyr	Leu	Ala	Phe 190	Asn	Val
Ser	Gly	Arg 195	Pro	Tyr	Asp	Gly 200	Phe	Ala	Cys	His	Phe	Phe 205	Pro	Asn	Ala
Pro	Ile 210	Tyr	Asn	Asp	Arg	Glu 215	Arg	Leu	Gln	Ile	Tyr 220	Leu	Ser	Asp	Ala
Gly 225	Ile	Leu	Ala	Val 230	Cys	Phe	Gly	Leu	Tyr	Arg 235	Tyr	Ala	Ala	Ala	Gln 240
Gly	Met	Ala	Ser	Met 245	Ile	Cys	Leu	Tyr	Gly 250	Val	Pro	Leu	Leu	Ile 255	Val
Asn	Ala	Phe 260	Leu	Val	Leu	Ile	Thr 265	Tyr	Leu	Gln	His	Thr 270	His	Pro	Ser
Leu	Pro	His 275	Tyr	Asp	Ser	Ser	Glu 280	Trp	Asp	Trp	Leu	Arg 285	Gly	Ala	Leu
Ala	Thr 290	Val	Asp	Arg	Asp	Tyr 295	Gly	Ile	Leu	Asn	Lys 300	Val	Phe	His	Asn
Ile 305	Thr	Asp	Thr	His 310	Val	Ala	His	His	Leu	Phe 315	Ser	Thr	Met	Pro	His 320
Tyr	Asn	Ala	Met	Glu 325	Ala	Thr	Lys	Ala 330	Ile	Lys	Pro	Ile	Leu	Gly 335	Asp

Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu  
340 345 350  
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys  
355 360 365  
Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1498749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala  
1 5 10 15  
Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe  
20 25 30  
Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu  
35 40 45  
Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala  
50 55 60  
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu  
65 70 75 80  
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr  
85 90 95  
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg  
100 105 110  
Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val  
115 120 125  
Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr  
130 135 140  
Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  
145 150 155 160  
Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met  
165 170 175  
Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly  
180 185 190  
Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1813

(D) OTHER INFORMATION: / Ceres Seq. ID 1498750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

ctccttttaga gagagcgtgc catttttatt ttctcttttc ttctctcatt tttattttct	60
tttctttttt ttcacctttt tttttccttt ttttttcttt cttcttcttc ttacttgatt	120
ttgaacccta gcttaagggg aattttctcg ggaaacaaaa gagatatttt tatcgagtg	180
agaaagaaac acaaaaaatg cagaatcaaa ggcttattaa gcagcaacaa caacaacaac	240
aacagcaaca tcaacaagct atgattcaac aagctatgat gcaacaacat ccttctcttt	300

```
atcatcctgg tgttatggct cctcctcaga tggagccttt accaagtgga aaccttcctc 360
ctggttttga tccaactact tgccgtagtg tgtatgctgg aaacattcat acgcagggtca 420
cagagattct tcttcaagag atttttgcaa gtactgggtcc tattgaaagc tgtaaactca 480
tcagaaagga taagtcatca tatggatttg ttcactactt tgatcgaaga tgtgctagta 540
tggtctataat gactcttaac ggaaggcata tatttggaac gcctatgaaa gtttaattggg 600
cgtatgcaac tgggtcaaagg gaagatacat caagtcattt caacattttt gttggagatc 660
ttagtccaga gggtactgat gcagcattgt ttgatagctt ttctgctttt aacagctgct 720
cggacgcaag agtaatgtgg gaccagaaaa ctggacgctc aagaggcttt ggttttgttt 780
ccttccgtaa tcagcaggat gctcaaactg ccattaatga gatgaatggt aaatgggtaa 840
gtagcagaca gatcagatgc aactgggcga caaaagggtc tacttttggc gaggacaaac 900
atagctctga tgaaaaaagt gttgtagaac ttactaacgg atcttcagag gatggtagag 960
agctgtcaaa tgaagatgcc cctgaaaaca atcctcaatt tacaactgtc tatgtaggaa 1020
atctctctcc agaaataact cagcttgatc tacaccgtct attctatacc cttggtgctg 1080
gagtgatcga agagggtcgt gtccagcgag acaaaggggt tggttttgtg agatataaca 1140
ctcatgacga ggctgctctt gctattcaga tgggcaacgc tcagcctttc ctcttttagca 1200
gacagataag gtgttccttg ggaaacaaac caactccatc aggcacagcc tcaaacccac 1260
ttccccacc agccccggca tcagtcctct ctctgtctgc aatggacctc ttagcctacg 1320
agaggcaact ggctctagcc aagatgcac ctcaggctca acattctctg aggcaagcag 1380
gtcttgaggt caatgttgct ggaggaactg cagctatgta tgatgggtggc tatcagaatg 1440
tagctgcggc ccatcagcag ctcatgtact atcagtaata aaccctcttc actggctctg 1500
agataccttt ttctgtttct ttctttttct tcttcttaat tttataactt tcttgctttt 1560
tctagacctt ccttggttcaa gagtctttat gtatgtgtct ctttcattta aagccgttg 1620
ttttatttat gtatgcagag ctttatgtct agtttgtaac ctataggtct tacttggtt 1680
gtaagccaag caataagaca acatcaaata aaaggggatt tggttttctg gggttaatgt 1740
tgtttggtgt tctgtaatga taggtttgaa acaaagtaat ttgtctttta taaaagtttt 1800
atagtttcat ttc
```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1498751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

```
Met Gln Asn Gln Arg Leu Ile Lys Gln Gln Gln Gln Gln Gln Gln
1          5          10          15
Gln His Gln Gln Ala Met Ile Gln Gln Ala Met Met Gln Gln His Pro
20          25          30
Ser Leu Tyr His Pro Gly Val Met Ala Pro Pro Gln Met Glu Pro Leu
35          40          45
Pro Ser Gly Asn Leu Pro Pro Gly Phe Asp Pro Thr Thr Cys Arg Ser
50          55          60
Val Tyr Ala Gly Asn Ile His Thr Gln Val Thr Glu Ile Leu Leu Gln
65          70          75          80
Glu Ile Phe Ala Ser Thr Gly Pro Ile Glu Ser Cys Lys Leu Ile Arg
85          90          95
Lys Asp Lys Ser Ser Tyr Gly Phe Val His Tyr Phe Asp Arg Arg Cys
100          105          110
Ala Ser Met Ala Ile Met Thr Leu Asn Gly Arg His Ile Phe Gly Gln
115          120          125
Pro Met Lys Val Asn Trp Ala Tyr Ala Thr Gly Gln Arg Glu Asp Thr
130          135          140
Ser Ser His Phe Asn Ile Phe Val Gly Asp Leu Ser Pro Glu Val Thr
145          150          155          160
Asp Ala Ala Leu Phe Asp Ser Phe Ser Ala Phe Asn Ser Cys Ser Asp
165          170          175
Ala Arg Val Met Trp Asp Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly
```

(2) INFORMATION FOR SEQ ID NO:625:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 1498752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

	(x1)	SEQUENCE DESCRIPTION: Seq ID: 1078															
Met	Ile	Gln	Gln	Ala	Met	Met	Gln	Gln	His	Pro	Ser	Leu	Tyr	His	Pro		
1				5					10					15			
Gly	Val	Met	Ala	Pro	Pro	Gln	Met	Glu	Pro	Leu	Pro	Ser	Gly	Asn	Leu		
			20					25					30				
Pro	Pro	Gly	Phe	Asp	Pro	Thr	Thr	Cys	Arg	Ser	Val	Tyr	Ala	Gly	Asn		
		35					40					45					
Ile	His	Thr	Gln	Val	Thr	Glu	Ile	Leu	Leu	Gln	Glu	Ile	Phe	Ala	Ser		
	50					55					60						
Thr	Gly	Pro	Ile	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys	Asp	Lys	Ser	Ser		
65					70					75					80		
Tyr	Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Cys	Ala	Ser	Met	Ala	Ile		
				85				90						95			
Met	Thr	Leu	Asn	Gly	Arg	His	Ile	Phe	Gly	Gln	Pro	Met	Lys	Val	Asn		
			100					105					110				
Trp	Ala	Tyr	Ala	Thr	Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn		
		115				120						125					
Ile	Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp	Ala	Ala	Leu	Phe		
	130					135					140						



```

Asp Ser Phe Ser Ala Phe Asn Ser Cys Ser Asp Ala Arg Val Met Trp
145                               150                               155                               160
Asp Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg
                               165                               170                               175
Asn Gln Gln Asp Ala Gln Thr Ala Ile Asn Glu Met Asn Gly Lys Trp
                               180                               185                               190
Val Ser Ser Arg Gln Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr
                               195                               200                               205
Phe Gly Glu Asp Lys His Ser Ser Asp Glu Lys Ser Val Val Glu Leu
210                               215                               220
Thr Asn Gly Ser Ser Glu Asp Gly Arg Glu Leu Ser Asn Glu Asp Ala
225                               230                               235                               240
Pro Glu Asn Asn Pro Gln Phe Thr Thr Val Tyr Val Gly Asn Leu Ser
                               245                               250                               255
Pro Glu Ile Thr Gln Leu Asp Leu His Arg Leu Phe Tyr Thr Leu Gly
                               260                               265                               270
Ala Gly Val Ile Glu Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly
275                               280                               285
Phe Val Arg Tyr Asn Thr His Asp Glu Ala Ala Leu Ala Ile Gln Met
290                               295                               300
Gly Asn Ala Gln Pro Phe Leu Phe Ser Arg Gln Ile Arg Cys Ser Trp
305                               310                               315                               320
Gly Asn Lys Pro Thr Pro Ser Gly Thr Ala Ser Asn Pro Leu Pro Pro
                               325                               330                               335
Pro Ala Pro Ala Ser Val Pro Ser Leu Ser Ala Met Asp Leu Leu Ala
                               340                               345                               350
Tyr Glu Arg Gln Leu Ala Leu Ala Lys Met His Pro Gln Ala Gln His
355                               360                               365
Ser Leu Arg Gln Ala Gly Leu Gly Val Asn Val Ala Gly Gly Thr Ala
370                               375                               380
Ala Met Tyr Asp Gly Gly Tyr Gln Asn Val Ala Ala Ala His Gln Gln
385                               390                               395                               400
Leu Met Tyr Tyr Gln
                               405

```

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1498753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

```

Met Met Gln Gln His Pro Ser Leu Tyr His Pro Gly Val Met Ala Pro
1                               5                               10                               15
Pro Gln Met Glu Pro Leu Pro Ser Gly Asn Leu Pro Pro Gly Phe Asp
                               20                               25                               30
Pro Thr Thr Cys Arg Ser Val Tyr Ala Gly Asn Ile His Thr Gln Val
35                               40                               45
Thr Glu Ile Leu Leu Gln Glu Ile Phe Ala Ser Thr Gly Pro Ile Glu
50                               55                               60
Ser Cys Lys Leu Ile Arg Lys Asp Lys Ser Ser Tyr Gly Phe Val His
65                               70                               75                               80
Tyr Phe Asp Arg Arg Cys Ala Ser Met Ala Ile Met Thr Leu Asn Gly
85                               90                               95
Arg His Ile Phe Gly Gln Pro Met Lys Val Asn Trp Ala Tyr Ala Thr
100                               105                               110
Gly Gln Arg Glu Asp Thr Ser Ser His Phe Asn Ile Phe Val Gly Asp

```

115	120	125
Leu Ser Pro Glu Val Thr Asp Ala Ala Leu Phe Asp Ser Phe Ser Ala		
130	135	140
Phe Asn Ser Cys Ser Asp Ala Arg Val Met Trp Asp Gln Lys Thr Gly		
145	150	155
Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn Gln Gln Asp Ala		
165	170	175
Gln Thr Ala Ile Asn Glu Met Asn Gly Lys Trp Val Ser Ser Arg Gln		
180	185	190
Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Phe Gly Glu Asp Lys		
195	200	205
His Ser Ser Asp Glu Lys Ser Val Val Glu Leu Thr Asn Gly Ser Ser		
210	215	220
Glu Asp Gly Arg Glu Leu Ser Asn Glu Asp Ala Pro Glu Asn Asn Pro		
225	230	235
Gln Phe Thr Thr Val Tyr Val Gly Asn Leu Ser Pro Glu Ile Thr Gln		
245	250	255
Leu Asp Leu His Arg Leu Phe Tyr Thr Leu Gly Ala Gly Val Ile Glu		
260	265	270
Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe Val Arg Tyr Asn		
275	280	285
Thr His Asp Glu Ala Ala Leu Ala Ile Gln Met Gly Asn Ala Gln Pro		
290	295	300
Phe Leu Phe Ser Arg Gln Ile Arg Cys Ser Trp Gly Asn Lys Pro Thr		
305	310	315
Pro Ser Gly Thr Ala Ser Asn Pro Leu Pro Pro Ala Pro Ala Ser		
325	330	335
Val Pro Ser Leu Ser Ala Met Asp Leu Leu Ala Tyr Glu Arg Gln Leu		
340	345	350
Ala Leu Ala Lys Met His Pro Gln Ala Gln His Ser Leu Arg Gln Ala		
355	360	365
Gly Leu Gly Val Asn Val Ala Gly Gly Thr Ala Ala Met Tyr Asp Gly		
370	375	380
Gly Tyr Gln Asn Val Ala Ala Ala His Gln Gln Leu Met Tyr Tyr Gln		
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

gctgcttaga ttttggtttc ttcattgtcg tcgtcggagt gaattagga ttcgagaatg	60
acgatgaact cgcttccgag gagatttggg aagaatcatg gctatttgga tcgagattat	120
cgaaacggaa gacgatctgg ttcagattcc gatgaagaat tgaagggaat gagtcacgaa	180
gagtatagga ggcagaaacg gcttaagatg aggaaatcag ccaagtctctg cttttggggag	240
aacacaccga gtccacctag agatcagaac gaggattccg atgagaacgc cgacgagatt	300
caggacaaga acggcggcga aagagatgat aattcgaaag ggaaagaaaag gaaaggtaaa	360
tctgactcgg aatctgaatc tgatggtttg agatctagga agaggaagag taagagctcg	420
aggtcaaagc gcaggagaaa gagatcttat gacagcgata gtgaatccga agggagttag	480
agtgattcgg aagaggaaga taggagacga aggaggaaga gttcttctaa gaggaagaag	540
agtagaagca gccgtagttt taggaaaaag cgaagtcata ggagaaagac gaaatacagt	600
gactctgatg agagcagcga tgaagatagt aaagctgaga ttagtgcttc ttcgtctggg	660
gaggaagaag ataccaagtc aaagagcaag aggcggaaga aatcttcgga ttctagtcca	720

```

aaacgaagca agggagagaa gacgaagtca gggagtgcac gcgatggtac tgaggaagat      780
tcgaagatgc aagtagacga aacggtaaga acactgagct agaacttgat gaagaagagt      840
tgaagaagtt caaagagatg attgaattaa agaagaaatc ttcagctgtt gatgaagagg      900
aagaagaagg tgatgttggt ccaatgccat tacctaaagc tgaaggtcac atcagttatg      960
gtggtgcttt aagacccggt gaaggagacg ccrttgcvca gtatgttcag caaggtaaac     1020
gtatcccacg tagaggagaa gtgggtctta acgctgaaga gattcagaag tttgaggatc     1080
ttggttatgt gatgagtga agtaggcac aaaggatgaa tgctattcgt attagaaaag     1140
aaaaccaggt ttacagtgtc gaagacaaac gggcattggc catgtttaac tacgaggaga     1200
aggcgaagcg cgaggctaag gttatgtctg atctgcagcg gcttgtgcag cgccatatgg     1260
gagaagaggt ggggccaaat catgaccctt tcgggtgctgg aaagactgaa gaagatgatg     1320
attgattttg cttggccttc tgcttctgtt atgtgggtac tcatcttatg ctttatcttg     1380
ttgaatgttc cttatttgca tcatagatac tgctgtttgc tacttgcccg ttaatgagct     1440
tcgtagttta tgctttaatc tactatgtat ccgttaatga gcttcatagt ttatgcgtta     1500
atctgctatg tatcacatga ttgtgtttgt gtgtcaaaga taatagattc tg

```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

```

Met Thr Met Asn Ser Leu Pro Arg Arg Phe Gly Lys Asn His Gly Tyr
1      5      10      15
Leu Asp Arg Asp Tyr Arg Asn Gly Arg Ser Gly Ser Asp Ser Asp
20      25      30
Glu Glu Leu Lys Gly Leu Ser His Glu Glu Tyr Arg Arg Gln Lys Arg
35      40      45
Leu Lys Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro
50      55      60
Ser Pro Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu
65      70      75      80
Ile Gln Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys
85      90      95
Glu Arg Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg
100     105     110
Ser Arg Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys
115     120     125
Arg Ser Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser
130     135     140
Glu Glu Glu Asp Arg Arg Arg Arg Lys Ser Ser Ser Lys Arg Lys
145     150     155     160
Lys Ser Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg
165     170     175
Lys Thr Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys
180     185     190
Ala Glu Ile Ser Ala Ser Ser Ser Gly Glu Glu Glu Asp Thr Lys Ser
195     200     205
Lys Ser Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Ser Lys Arg Ser
210     215     220
Lys Gly Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu
225     230     235     240
Asp Ser Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser
245     250

```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..252
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```
Met Asn Ser Leu Pro Arg Arg Phe Gly Lys Asn His Gly Tyr Leu Asp
1          5          10          15
Arg Asp Tyr Arg Asn Gly Arg Arg Ser Gly Ser Asp Ser Asp Glu Glu
          20          25          30
Leu Lys Gly Leu Ser His Glu Glu Tyr Arg Arg Gln Lys Arg Leu Lys
          35          40          45
Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro Ser Pro
          50          55          60
Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu Ile Gln
          65          70          75          80
Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys Glu Arg
          85          90          95
Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg Ser Arg
          100          105          110
Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys Arg Ser
          115          120          125
Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser Glu Glu
          130          135          140
Glu Asp Arg Arg Arg Arg Arg Lys Ser Ser Ser Lys Arg Lys Lys Ser
          145          150          155          160
Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg Lys Thr
          165          170          175
Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys Ala Glu
          180          185          190
Ile Ser Ala Ser Ser Ser Gly Glu Glu Glu Asp Thr Lys Ser Lys Ser
          195          200          205
Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Ser Lys Arg Ser Lys Gly
          210          215          220
Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu Asp Ser
          225          230          235          240
Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser
          245          250
```

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 204 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..204
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

```
Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro Ser Pro
1          5          10          15
Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu Ile Gln
          20          25          30
Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys Glu Arg
          35          40          45
Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg Ser Arg
          50          55          60
```

Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys Arg Ser  
65 70 75 80  
Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser Glu Glu  
85 90 95  
Glu Asp Arg Arg Arg Arg Arg Lys Ser Ser Ser Lys Arg Lys Lys Ser  
100 105 110  
Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg Lys Thr  
115 120 125  
Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys Ala Glu  
130 135 140  
Ile Ser Ala Ser Ser Ser Gly Glu Glu Glu Asp Thr Lys Ser Lys Ser  
145 150 155 160  
Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Ser Lys Arg Ser Lys Gly  
165 170 175  
Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu Asp Ser  
180 185 190  
Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

aatctttttt	tttttgctta	ttattttttt	gactttgatc	tcccatcagt	tcattcttctt	60
cttctttcttc	tgatcaacca	tggtctgtgc	tataagtgtc	gcagtctctt	taccttcctc	120
caagtcattcc	tctctcctca	ccaaaatctc	ctctgtatcc	cctcaaagga	ttttcctcaa	180
gaagagcaca	gtgtgttaca	gaagagttgt	gtcagtgaag	gctcagggtga	caacagatac	240
taccgaggca	ccaccagtta	aagtagtcaa	ggagtctaag	aaacaggaag	aagggattgt	300
tgtcaacaaa	ttcaaacctt	agaaccctta	cactggctgc	tgctttttga	acaccaagat	360
caccggtgat	gacgtctccg	gtgagacttg	gcacattgtc	ttcaccaccg	aaggtgaggt	420
tccgtataga	gaaggacaat	cgataggagt	gattccagag	ggaatagaca	agaacgggaa	480
gccgcacaag	ctcaggcttt	actctatcgc	gagtagtgcc	attgggtgact	ttggagactc	540
caagaccgtt	tctctctgtg	tcaagagact	agttttacaca	aatgatggcg	gagagattgt	600
taaggggggtc	tgtctcaact	tcttgtgtga	cttgaagccg	ggtgatgaag	ctaagatcac	660
tggacctgtt	ggcaaggaaa	tgcttatgcc	aaaagacccc	aatgccacca	tcattcatgct	720
tggaacagga	actggaatag	ctccattcag	atcattttttg	tggaaaatgt	tcttttgagga	780
gcacgaggac	tacaagttca	atgggtttggc	gtggcttttc	ttgggtgtac	ccagaagcag	840
ctcactgcta	tacaaggagg	agtttgagaa	gatgaaggag	aagaacccag	acaacttcag	900
gctggacttt	gcggtgagca	gagagcagac	gaacgagaag	ggagagaaaa	gtacattca	960
gacaagaatg	gcagagtatg	cagaaagagc	tgtggggagt	gctgaagaaa	gacaacacct	1020
ttgttttacat	gtgtggtctt	aagggtatgg	agaagggtat	cgatgacatt	atggtctcgc	1080
ttgtctgctaa	agatgggatac	gattgggttg	agtacaagaa	gcaattgaag	aggagtgaac	1140
agtggaaatgt	tgaagtctac	taaggaagct	tctgagggag	taattatata	atgtagataa	1200
aaagcttcag	atgcattgtg	aaatcttcat	atctgcttct	tttttctttc	tcaaggattt	1260
tcaatcaaaa	catcc					

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1498759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

Met	Ala	Ala	Ala	Ile	Ser	Ala	Ala	Val	Ser	Leu	Pro	Ser	Ser	Lys	Ser
1				5				10						15	
Ser	Ser	Leu	Leu	Thr	Lys	Ile	Ser	Ser	Val	Ser	Pro	Gln	Arg	Ile	Phe
			20					25					30		
Leu	Lys	Lys	Ser	Thr	Val	Cys	Tyr	Arg	Arg	Val	Val	Ser	Val	Lys	Ala
			35					40				45			
Gln	Val	Thr	Thr	Asp	Thr	Thr	Glu	Ala	Pro	Pro	Val	Lys	Val	Val	Lys
	50					55					60				
Glu	Ser	Lys	Lys	Gln	Glu	Glu	Gly	Ile	Val	Val	Asn	Lys	Phe	Lys	Pro
65				70					75					80	
Lys	Asn	Pro	Tyr	Thr	Gly	Arg	Cys	Leu	Leu	Asn	Thr	Lys	Ile	Thr	Gly
			85					90					95		
Asp	Asp	Ala	Pro	Gly	Glu	Thr	Trp	His	Ile	Val	Phe	Thr	Thr	Glu	Gly
			100					105					110		
Glu	Val	Pro	Tyr	Arg	Glu	Gly	Gln	Ser	Ile	Gly	Val	Ile	Pro	Glu	Gly
		115					120					125			
Ile	Asp	Lys	Asn	Gly	Lys	Pro	His	Lys	Leu	Arg	Leu	Tyr	Ser	Ile	Ala
	130					135					140				
Ser	Ser	Ala	Ile	Gly	Asp	Phe	Gly	Asp	Ser	Lys	Thr	Val	Ser	Leu	Cys
145				150						155				160	
Val	Lys	Arg	Leu	Val	Tyr	Thr	Asn	Asp	Gly	Gly	Glu	Ile	Val	Lys	Gly
			165						170					175	
Val	Cys	Ser	Asn	Phe	Leu	Cys	Asp	Leu	Lys	Pro	Gly	Asp	Glu	Ala	Lys
			180					185					190		
Ile	Thr	Gly	Pro	Val	Gly	Lys	Glu	Met	Leu	Met	Pro	Lys	Asp	Pro	Asn
	195						200					205			
Ala	Thr	Ile	Ile	Met	Leu	Gly	Thr	Gly	Thr	Gly	Ile	Ala	Pro	Phe	Arg
	210					215					220				
Ser	Phe	Leu	Trp	Lys	Met	Phe	Phe	Glu	Glu	His	Glu	Asp	Tyr	Lys	Phe
225				230						235				240	
Asn	Gly	Leu	Ala	Trp	Leu	Phe	Leu	Gly	Val	Pro	Arg	Ser	Ser	Ser	Leu
			245					250						255	
Leu	Tyr	Lys	Glu	Glu	Phe	Glu	Lys	Met	Lys	Glu	Lys	Asn	Pro	Asp	Asn
		260					265					270			
Phe	Arg	Leu	Asp	Phe	Ala	Val	Ser	Arg	Glu	Gln	Thr	Asn	Glu	Lys	Gly
	275					280						285			
Glu	Lys	Met	Tyr	Ile	Gln	Thr	Arg	Met	Ala	Glu	Tyr	Ala	Glu	Arg	Ala
	290					295				300					
Val	Gly	Val	Ala	Glu	Glu	Arg	Gln	His	Leu	Cys	Leu	His	Val	Trp	Ser
305				310					315					320	

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1498760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

atatacttttc	tctgtttaca	ttctcgtttc	cgaggagaaa	agtctcgatc	ttctggatct	60
ggggtttggg	ttggtttggg	gttgactcgg	ttttgactcg	ggacaagtcg	tctcgtgaga	120
tggatgtctc	tcgtttatta	gtatctcttt	gagagtctgt	ctttctgggt	tcaatagatt	180
cttatagttt	cgcttagaaa	cacgcacaaa	aagatgtcgt	tgaagcatca	tcacagagga	240

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ttagagctct ctgcttcgaa gagttttgtc tcaaagaaat ggactttatt tctctgtatc 300
ggttttcttct ggcaggaat tctcttctcc gacagaatgt ggccagagcc tgaatccaat 360
gttgatataca gggacacagt agcatcagat gaacggctgc ggtagagtc tgaggactgt 420
gattcatcaa aaaagggttt taaagcgtga atcgaaagac atccttgagg atgtttacaa 480
gagtccagat gcaattcaaa cgcttgataa aacgatttca aagctggaaa cagaactggc 540
cgatgcaaga gctgcgcaag aatctatcat gaatggttca ccagtttctg atgactttaa 600
gctccctgaa actgtcacta aaagaaagta tctgatgggt gttgggtgta atactgcgtt 660
tagcagcaga aagcgcaggg attcagtcctg tgctacttgg atgcctcccg gtgaggagag 720
aaagaagctc gaggaagaga aagggatcgt gatgcgggtt gtgataggcc atagttctac 780
tcccgggtgga attcttgata gagcgattca ggctgaagaa agtaaacadg gagacttctt 840
gaggctggat catgttgaag gttatctcga gctgtcagca aagactaaaa cttactttac 900
cacggctttt gcaatgtggg atgcagactt ctacgtcaaa gtcgatgatg atgtgcatgt 960
aaatatagcc acgcttgagg cagaattagc aagataccgg atgaagcccc gagtgtacat 1020
tggttgcatg aaatctggac ctgttcttgc tcagaaagga gtgagatata atgaaccgca 1080
atactggaaa tttggagaag agggtaacaa atacttccgc catgccacag gtcagctcta 1140
tgcaatatcc agggagttgg cgtcttacat atcgataaac caaaacgtac ttcacaaata 1200
tgtaatgaa gatgtctctt taggatcatg gtttcttgga ttagatgtgg agcatgtaga 1260
tgaccgtagg ctatgttgtg gtacaacaga ttgtgagtgg aaggcgcagg cgggcaacat 1320
ctgtgttgcc tcgttcgatt ggagctgcag tgggatttgt agatcagcgg ataggatgaa 1380
ggatgttcat cgtaggtgtg gagaagggtg aaaggccctt ctggctgcat ctttctgaaa 1440
cacaataact aaagaaacac attgaggaag aagagtacag agacaaatcc gctcgacagt 1500
ctacacttgg tagtatagac acacagtcac actctctcta tatatgtatg tatgtatgta 1560
tgtatgtatc ttgtgaactg agatgagaag ggtgcttttt gccctccttt cttgtttctt 1620
tatgcttttc tcaattctct gaaggtcttg agttctttgc acacagaaaa tgcagatttt 1680
agctgcaaag gcggactcca tgagtgcacc ttcagagtca tttcattgag gcgttttctc 1740
tgccttttga gcttttcttc ttcatttctt tttggatttt gcctattttg ttcatttttt 1800
cctttgccat gattgtggtg aaacatgggt tgtttatgtg tgtacttgaa acgc

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1498761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

```

Met Asn Gly Ser Pro Val Ser Asp Asp Phe Lys Leu Pro Glu Thr Val
1          5          10          15
Thr Lys Arg Lys Tyr Leu Met Val Val Gly Val Asn Thr Ala Phe Ser
20          25          30
Ser Arg Lys Arg Arg Asp Ser Val Arg Ala Thr Trp Met Pro Pro Gly
35          40          45
Glu Glu Arg Lys Lys Leu Glu Glu Lys Gly Ile Val Met Arg Phe
50          55          60
Val Ile Gly His Ser Ser Thr Pro Gly Gly Ile Leu Asp Arg Ala Ile
65          70          75          80
Gln Ala Glu Glu Ser Lys His Gly Asp Phe Leu Arg Leu Asp His Val
85          90          95
Glu Gly Tyr Leu Glu Leu Ser Ala Lys Thr Lys Thr Tyr Phe Thr Thr
100          105          110
Ala Phe Ala Met Trp Asp Ala Asp Phe Tyr Val Lys Val Asp Asp Asp
115          120          125
Val His Val Asn Ile Ala Thr Leu Gly Ala Glu Leu Ala Arg Tyr Arg
130          135          140
Met Lys Pro Arg Val Tyr Ile Gly Cys Met Lys Ser Gly Pro Val Leu
145          150          155          160
Ala Gln Lys Gly Val Arg Tyr His Glu Pro Glu Tyr Trp Lys Phe Gly
165          170          175

```

Glu Glu Gly Asn Lys Tyr Phe Arg His Ala Thr Gly Gln Leu Tyr Ala  
180 185 190  
Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn Gln Asn Val Leu  
195 200 205  
His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser Trp Phe Leu Gly  
210 215 220  
Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys Cys Gly Thr Thr  
225 230 235 240  
Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys Val Ala Ser Phe  
245 250 255  
Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp Arg Met Lys Asp  
260 265 270  
Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser  
275 280 285  
Phe

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1498762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met Val Val Gly Val Asn Thr Ala Phe Ser Ser Arg Lys Arg Arg Asp  
1 5 10 15  
Ser Val Arg Ala Thr Trp Met Pro Pro Gly Glu Glu Arg Lys Lys Leu  
20 25 30  
Glu Glu Glu Lys Gly Ile Val Met Arg Phe Val Ile Gly His Ser Ser  
35 40 45  
Thr Pro Gly Gly Ile Leu Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys  
50 55 60  
His Gly Asp Phe Leu Arg Leu Asp His Val Glu Gly Tyr Leu Glu Leu  
65 70 75 80  
Ser Ala Lys Thr Lys Thr Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp  
85 90 95  
Ala Asp Phe Tyr Val Lys Val Asp Asp Asp Val His Val Asn Ile Ala  
100 105 110  
Thr Leu Gly Ala Glu Leu Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr  
115 120 125  
Ile Gly Cys Met Lys Ser Gly Pro Val Leu Ala Gln Lys Gly Val Arg  
130 135 140  
Tyr His Glu Pro Glu Tyr Trp Lys Phe Gly Glu Glu Gly Asn Lys Tyr  
145 150 155 160  
Phe Arg His Ala Thr Gly Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala  
165 170 175  
Ser Tyr Ile Ser Ile Asn Gln Asn Val Leu His Lys Tyr Val Asn Glu  
180 185 190  
Asp Val Ser Leu Gly Ser Trp Phe Leu Gly Leu Asp Val Glu His Val  
195 200 205  
Asp Asp Arg Arg Leu Cys Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala  
210 215 220  
Gln Ala Gly Asn Ile Cys Val Ala Ser Phe Asp Trp Ser Cys Ser Gly  
225 230 235 240  
Ile Cys Arg Ser Ala Asp Arg Met Lys Asp Val His Arg Arg Cys Gly  
245 250 255  
Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser Phe



260 265  
(2) INFORMATION FOR SEQ ID NO:636:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..245  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498763  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:  
Met Pro Pro Gly Ile Glu Arg Lys Lys Leu Glu Glu Glu Lys Gly Ile  
1 5 10 15  
Val Met Arg Phe Val Ile Gly His Ser Ser Thr Pro Gly Gly Ile Leu  
20 25 30  
Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys His Gly Asp Phe Leu Arg  
35 40 45  
Leu Asp His Val Glu Gly Tyr Leu Glu Leu Ser Ala Lys Thr Lys Thr  
50 55 60  
Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp Ala Asp Phe Tyr Val Lys  
65 70 75 80  
Val Asp Asp Asp Val His Val Asn Ile Ala Thr Leu Gly Ala Glu Leu  
85 90 95  
Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr Ile Gly Cys Met Lys Ser  
100 105 110  
Gly Pro Val Leu Ala Gln Lys Gly Val Arg Tyr His Glu Pro Glu Tyr  
115 120 125  
Trp Lys Phe Gly Glu Glu Gly Asn Lys Tyr Phe Arg His Ala Thr Gly  
130 135 140  
Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn  
145 150 155 160  
Gln Asn Val Leu His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser  
165 170 175  
Trp Phe Leu Gly Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys  
180 185 190  
Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys  
195 200 205  
Val Ala Ser Phe Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp  
210 215 220  
Arg Met Lys Asp Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu  
225 230 235 240  
Leu Ala Ala Ser Phe  
245

(2) INFORMATION FOR SEQ ID NO:637:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 865 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..865  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498764  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:  
accataaaaaaa aaactcaaga gagactttgt ggccatggca gcctctctcc aatccaccgc 60  
tacattcctc cagtcggcga agatcgccac cgctccttct cgcggaagt ctcacctccg 120  
atcgactcaa gccgtcggca aatcttttgg gctcgaaact tcctcggctc gcctcacttg 180  
ctccttcacag tctgacttta aggacttcac cggtaaattgc tccgacgctg tcaaaaatcgc 240

```
cggattcgcct cttgccacct ctgctctcgt cgtctcggga gcaagtgcgg agggagctcc 300
aaagagattg acctatgacg agatcgaagg acccttcgag gttgcttcag acggaagcgt 360
caatttcaag gaagaagatg gaatcgacta tgctgcagtc acagtccaac ttccaggagg 420
tgaacgtgtg ccatttcctt tcacagtcaa acagcttgac tcctcaggca aaccagacag 480
cttcaccgga aaattcttgg ttccatcgta ccgtggctct tccttcttgg acccaaaggg 540
ccgtggtgga tccacaggat atgacaacgc cgtggcattg ccagctggag gcagaggaga 600
cgaggaggag cttgtaaagg agaacgtgaa gaacactgcc gcttcagtgg gagagatcac 660
tctgaaagtg acaaagagca agccggagac aggagaggtg atcggagtgt tcgagagtct 720
tcagccgtcg gatactgact tgggtgctaa ggtaccaaag gatgtgaaga tccaaggggt 780
gtggtatggt caacttgagt gatcatgtta ttatatatttc cgttgattgt gtttgatgat 840
aatgataaca tcttttgatg ctttc
```

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..266

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

```
Pro Lys Lys Lys Leu Lys Arg Asp Phe Val Ala Met Ala Ala Ser Leu
1      5      10      15
Gln Ser Thr Ala Thr Phe Leu Gln Ser Ala Lys Ile Ala Thr Ala Pro
      20      25      30
Ser Arg Gly Ser Ser His Leu Arg Ser Thr Gln Ala Val Gly Lys Ser
      35      40      45
Phe Gly Leu Glu Thr Ser Ser Ala Arg Leu Thr Cys Ser Phe Gln Ser
      50      55      60
Asp Phe Lys Asp Phe Thr Gly Lys Cys Ser Asp Ala Val Lys Ile Ala
      65      70      75      80
Gly Phe Ala Leu Ala Thr Ser Ala Leu Val Val Ser Gly Ala Ser Ala
      85      90      95
Glu Gly Ala Pro Lys Arg Leu Thr Tyr Asp Glu Ile Glu Gly Pro Phe
      100     105     110
Glu Val Ala Ser Asp Gly Ser Val Asn Phe Lys Glu Glu Asp Gly Ile
      115     120     125
Asp Tyr Ala Ala Val Thr Val Gln Leu Pro Gly Gly Glu Arg Val Pro
      130     135     140
Phe Leu Phe Thr Val Lys Gln Leu Asp Ser Ser Gly Lys Pro Asp Ser
      145     150     155     160
Phe Thr Gly Lys Phe Leu Val Pro Ser Tyr Arg Gly Ser Ser Phe Leu
      165     170     175
Asp Pro Lys Gly Arg Gly Gly Ser Thr Gly Tyr Asp Asn Ala Val Ala
      180     185     190
Leu Pro Ala Gly Gly Arg Gly Asp Glu Glu Glu Leu Val Lys Glu Asn
      195     200     205
Val Lys Asn Thr Ala Ala Ser Val Gly Glu Ile Thr Leu Lys Val Thr
      210     215     220
Lys Ser Lys Pro Glu Thr Gly Glu Val Ile Gly Val Phe Glu Ser Leu
      225     230     235     240
Gln Pro Ser Asp Thr Asp Leu Gly Ala Lys Val Pro Lys Asp Val Lys
      245     250     255
Ile Gln Gly Val Trp Tyr Gly Gln Leu Glu
      260     265
```

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..255  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498766  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:  
Met Ala Ala Ser Leu Gln Ser Thr Ala Thr Phe Leu Gln Ser Ala Lys  
1                  5                  10                  15  
Ile Ala Thr Ala Pro Ser Arg Gly Ser Ser His Leu Arg Ser Thr Gln  
          20                  25                  30  
Ala Val Gly Lys Ser Phe Gly Leu Glu Thr Ser Ser Ala Arg Leu Thr  
          35                  40                  45  
Cys Ser Phe Gln Ser Asp Phe Lys Asp Phe Thr Gly Lys Cys Ser Asp  
          50                  55                  60  
Ala Val Lys Ile Ala Gly Phe Ala Leu Ala Thr Ser Ala Leu Val Val  
65                  70                  75                  80  
Ser Gly Ala Ser Ala Glu Gly Ala Pro Lys Arg Leu Thr Tyr Asp Glu  
          85                  90                  95  
Ile Glu Gly Pro Phe Glu Val Ala Ser Asp Gly Ser Val Asn Phe Lys  
          100                 105                 110  
Glu Glu Asp Gly Ile Asp Tyr Ala Ala Val Thr Val Gln Leu Pro Gly  
          115                 120                 125  
Gly Glu Arg Val Pro Phe Leu Phe Thr Val Lys Gln Leu Asp Ser Ser  
          130                 135                 140  
Gly Lys Pro Asp Ser Phe Thr Gly Lys Phe Leu Val Pro Ser Tyr Arg  
145                 150                 155                 160  
Gly Ser Ser Phe Leu Asp Pro Lys Gly Arg Gly Gly Ser Thr Gly Tyr  
          165                 170                 175  
Asp Asn Ala Val Ala Leu Pro Ala Gly Gly Arg Gly Asp Glu Glu Glu  
          180                 185                 190  
Leu Val Lys Glu Asn Val Lys Asn Thr Ala Ala Ser Val Gly Glu Ile  
          195                 200                 205  
Thr Leu Lys Val Thr Lys Ser Lys Pro Glu Thr Gly Glu Val Ile Gly  
210                 215                 220  
Val Phe Glu Ser Leu Gln Pro Ser Asp Thr Asp Leu Gly Ala Lys Val  
225                 230                 235                 240  
Pro Lys Asp Val Lys Ile Gln Gly Val Trp Tyr Gly Gln Leu Glu  
          245                 250                 255

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

aaggaatcga aaaccagaa gaggactcag tgaacaaatt tcttcagggt aaatttcctc	60
actattctac tgtgtttttg tctcagaat cctcgaaaat cgtaaatattg ttttcgtat	120
gctcctaaaa tctgggcaat tcattagatt tcgttgcgta gataaactta agcttgatgt	180
attcctttggt acaatgtaat tctgtttagt tctataactt ggaatcactc taagtgtaat	240
gtatattgat gcgaagtcaa atgttgctga atttttgctc tcctgcattt ttccccaatt	300
ttttctgagc cagtattgtg aaaaattgga gtctgagaaa actgaaaagt ttaatgtatt	360
ctcatttaat cagtgttcat agattcacta gttgtttgac cagggcttag gcttaatcat	420
tcttgtagaca cttgggtttc ttttaaactc gttttgatgt tcagttttct ttggaagcta	480
tatacccata aacttaaaat gaataaagat ggaagcttta gctgatataa tttgggtggt	540

```
tctttctttt ttccttggtg tgaagctgtt tcaaaatgtc tcggaggtat gatagtcgca 600
ccacgatctt ctccaccgaa ggtcgtctct accagggtga atatgctatg gaagctattg 660
gcaatgctgg ttctgccatt ggaatcttgg caaaagacgg agtggtgttg gttggtgaga 720
agaaagtcac ttctaaaactt cttcaaacct cttcatccat ggagaaaatg tacaagatcg 780
atgaccatgt ggcttgtgca gttgctggta taatgtctga tgccaacatt ctgattaaca 840
ctgctcgagt tcaagctcag cgttacacct ttatgtacca agagccaatg cccgttttagc 900
agctggttca gtctctttgt gacaccaagc aaggatacac ccagtttggt ggtctccgcc 960
cgtttgaggt ttccttttctt ttgacaggct gggacaggaa ccacgggttt cagctgtata 1020
tgagtgacct aagtggaaac tatggtggat ggcaagctgc agctggttga gcaaataatc 1080
aagcggctca gtctattctt aagcaagact ataaggatga tgcaacgagg gaagaagtgg 1140
ttcagctcgc tatcaaggtt ttgagcaaga cgatggacag ctcgagcttt acagctgaaa 1200
aactcgagct tgctgagttg tatctgactc cttcaaaaatg tgtaagtac catgttctact 1260
cgcctgactc gctcactaag ctcttggtta agcatggtgt gactcaacca gccgcagaaa 1320
cttcctaagc tagaaactgg tgacagtttt acctgaccgg cctggttact gtagatgtcc 1380
atltgctttc tttccctttg gagatatcgt atcagaatca atttaccact ctgattatgt 1440
catgtgattc atltgggttg actatctttt atcttgagat tgatcttctt ctagtctaaa 1500
gtaaagttag acttttagagg ttttattcaa taaatgaatg agcaatcacc aacgggcccc 1560
ttagaaagcc cataacattc attgattgag gtaacgggtt ttaatggctc aaattaacga 1620
agaatcagaa tctctttaag tttcaccacg tcgatttaac ggtcaagagt gtctgtttat 1680
taacagaaca gtaaaaatgt taccgctcaa agcgtatatc ttgagcgcca aatggaattt 1740
cattggtaca atgccagaa gttctgggcc agaactggcc tcattgtaag agatttttta 1800
ggagatttat gcagatctgg aaaaacaagt ttttctctct tggattatct acaaaaatatt 1860
atltacttaa gtatgtgtca gttagacaat gccctgaatc caaggaattg tatcgaccgg 1920
gattgaagag accattcttg catcgtctct tctttttgca gcatcgcgat tgtatgaaac 1980
attgatggcc agatctttct tctataagtc aatcaaccgg ccaccggaat taccctaaaa 2040
acatagaaaa tatgttgaag tatattgaga tattagtcac cgactatgac taagtgtcac 2100
aaacttttgt gtgataggat tcaatcaatc caatggatct tagt
```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

```
Met Ser Arg Tyr Asp Ser Arg Thr Thr Ile Phe Ser Pro Glu Gly
1           5           10           15
Arg Leu Tyr Gln Val Glu Tyr Ala Met Glu Ala Ile Gly Asn Ala Gly
20           25           30
Ser Ala Ile Gly Ile Leu Ala Lys Asp Gly Val Val Leu Val Gly Glu
35           40           45
Lys Lys Val Thr Ser Lys Leu Leu Gln Thr Ser Ser Ser Met Glu Lys
50           55           60
Met Tyr Lys Ile Asp Asp His Val Ala Cys Ala Val Ala Gly Ile Met
65           70           75           80
Ser Asp Ala Asn Ile Leu Ile Asn Thr Ala Arg Val Gln Ala Gln Arg
85           90           95
Tyr Thr Phe Met Tyr Gln Glu Pro Met Pro Val
100          105
```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

Met	Glu	Ala	Ile	Gly	Asn	Ala	Gly	Ser	Ala	Ile	Gly	Ile	Leu	Ala	Lys
1				5				10					15		
Asp	Gly	Val	Val	Leu	Val	Gly	Glu	Lys	Lys	Val	Thr	Ser	Lys	Leu	Leu
			20					25					30		
Gln	Thr	Ser	Ser	Ser	Met	Glu	Lys	Met	Tyr	Lys	Ile	Asp	Asp	His	Val
		35					40					45			
Ala	Cys	Ala	Val	Ala	Gly	Ile	Met	Ser	Asp	Ala	Asn	Ile	Leu	Ile	Asn
	50					55					60				
Thr	Ala	Arg	Val	Gln	Ala	Gln	Arg	Tyr	Thr	Phe	Met	Tyr	Gln	Glu	Pro
65					70					75				80	
Met	Pro	Val													

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Met	Ser	Asp	Pro	Ser	Gly	Asn	Tyr	Gly	Gly	Trp	Gln	Ala	Ala	Ala	Val
1				5				10						15	
Gly	Ala	Asn	Asn	Gln	Ala	Ala	Gln	Ser	Ile	Leu	Lys	Gln	Asp	Tyr	Lys
			20					25					30		
Asp	Asp	Ala	Thr	Arg	Glu	Glu	Val	Val	Gln	Leu	Ala	Ile	Lys	Val	Leu
		35					40					45			
Ser	Lys	Thr	Met	Asp	Ser	Thr	Ser	Phe	Thr	Ala	Glu	Lys	Leu	Glu	Leu
	50					55					60				
Ala	Glu	Leu	Tyr	Leu	Thr	Pro	Ser	Lys	Cys	Val	Lys	Tyr	His	Val	His
65				70						75				80	
Ser	Pro	Asp	Ser	Leu	Thr	Lys	Leu	Leu	Val	Lys	His	Gly	Val	Thr	Gln
			85					90						95	
Pro	Ala	Ala	Glu	Thr	Ser										

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1245
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

attgcttttg	ctctgtatag	tcactgattt	agggtttttc	gaatctgaac	ttcttctttt	60
ttgagtttcc	aaagcaatgg	cggcgctcgca	agataagttg	gataagatga	aacttaggca	120
agattaccgg	aatttatggc	actccgatct	catgggcacc	gtcaccgccg	acactcccta	180
ttgctgcac	tcgtgtctgt	gtggaccttg	tgtgtcatat	atgcttcgga	gaagagcact	240
ttacaatgac	atgtcaaggt	atacttgctg	tgctggatat	atgccctgta	gtggaaggtg	300
tggagaaagc	aaatgtcctc	aactttgcct	tgccactgag	gtcttctctt	gcttcggaaa	360
ctctgtggcc	tctaccgct	ttcttctgca	ggatgaattc	aacatccaga	caacacaatg	420

```
cgacaattgc ataattggat ttatgttctg cctcagccaa gttgcttgca tattctctat 480
agttgcttgc attgttggta gtgatgaact ttccgaggct tctcagatac tctcttgctg 540
tgctgatatg gtctactgca cggctctgcg atgtatgcag acacaacaca aacttgagat 600
ggacaaaaga gatggagtgt ttggatcgca gccaatgggt gtgccaccag ctcagcagat 660
gtctcgtttt gatcaacctg tccctcctcc agtcggatac cctcagtcgt atccaccgcc 720
tgctcaaggc taccctcctg catcttacct gcctcccggt tatcctcagc attaagaaat 780
ttaaccagta tcttcatttt atgtgtcaga atagggacac ccgcaatgac aacccgaggc 840
tgtatagagt ctgatttcga gacaatggcg gattttctga taaaggcggc tcagataaca 900
agtgcggttg agagagagca tggaaaagtca cacaaggagt ttgtgaaaag tttatgcacc 960
aacaaagaca tagctgagct tagaaaccga gtcgaagcat ttgctttgca gtatgagatg 1020
cctgcttctc ttattcgaat tgaatgaaag aaaactccac acaacagctt tatttacagt 1080
tgaattttat cttatctctg ggtcaatttt tttttttttt tttggagttc tatcttgtaa 1140
attagagtaa atatataatt atattgggat tgatttgcac tatttttttc catttgtaatt 1200
ctgtaaacad tttgataaat gggaatgatt actacaaatt tactt
```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

```
Met Ala Ala Ser Gln Asp Lys Leu Asp Lys Met Lys Leu Arg Gln Asp
1          5          10          15
Tyr Arg Asn Leu Trp His Ser Asp Leu Met Gly Thr Val Thr Ala Asp
          20          25          30
Thr Pro Tyr Cys Cys Ile Ser Cys Leu Cys Gly Pro Cys Val Ser Tyr
          35          40          45
Met Leu Arg Arg Arg Ala Leu Tyr Asn Asp Met Ser Arg Tyr Thr Cys
          50          55          60
Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg Cys Gly Glu Ser Lys Cys
65          70          75          80
Pro Gln Leu Cys Leu Ala Thr Glu Val Phe Leu Cys Phe Gly Asn Ser
          85          90          95
Val Ala Ser Thr Arg Phe Leu Leu Gln Asp Glu Phe Asn Ile Gln Thr
          100          105          110
Thr Gln Cys Asp Asn Cys Ile Ile Gly Phe Met Phe Cys Leu Ser Gln
          115          120          125
Val Ala Cys Ile Phe Ser Ile Val Ala Cys Ile Val Gly Ser Asp Glu
          130          135          140
Leu Ser Glu Ala Ser Gln Ile Leu Ser Cys Cys Ala Asp Met Val Tyr
145          150          155          160
Cys Thr Val Cys Ala Cys Met Gln Thr Gln His Lys Leu Glu Met Asp
          165          170          175
Lys Arg Asp Gly Val Phe Gly Ser Gln Pro Met Gly Val Pro Pro Ala
          180          185          190
Gln Gln Met Ser Arg Phe Asp Gln Pro Val Pro Pro Pro Val Gly Tyr
          195          200          205
Pro Gln Ser Tyr Pro Pro Pro Ala Gln Gly Tyr Pro Pro Ala Ser Tyr
210          215          220
Pro Pro Pro Gly Tyr Pro Gln His
225          230
```

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..222  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498777  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

Met	Lys	Leu	Arg	Gln	Asp	Tyr	Arg	Asn	Leu	Trp	His	Ser	Asp	Leu	Met
1				5					10					15	
Gly	Thr	Val	Thr	Ala	Asp	Thr	Pro	Tyr	Cys	Cys	Ile	Ser	Cys	Leu	Cys
			20					25					30		
Gly	Pro	Cys	Val	Ser	Tyr	Met	Leu	Arg	Arg	Arg	Ala	Leu	Tyr	Asn	Asp
		35					40					45			
Met	Ser	Arg	Tyr	Thr	Cys	Cys	Ala	Gly	Tyr	Met	Pro	Cys	Ser	Gly	Arg
	50					55					60				
Cys	Gly	Glu	Ser	Lys	Cys	Pro	Gln	Leu	Cys	Leu	Ala	Thr	Glu	Val	Phe
65					70					75					80
Leu	Cys	Phe	Gly	Asn	Ser	Val	Ala	Ser	Thr	Arg	Phe	Leu	Leu	Gln	Asp
				85					90					95	
Glu	Phe	Asn	Ile	Gln	Thr	Thr	Gln	Cys	Asp	Asn	Cys	Ile	Ile	Gly	Phe
		100						105					110		
Met	Phe	Cys	Leu	Ser	Gln	Val	Ala	Cys	Ile	Phe	Ser	Ile	Val	Ala	Cys
		115					120					125			
Ile	Val	Gly	Ser	Asp	Glu	Leu	Ser	Glu	Ala	Ser	Gln	Ile	Leu	Ser	Cys
	130					135						140			
Cys	Ala	Asp	Met	Val	Tyr	Cys	Thr	Val	Cys	Ala	Cys	Met	Gln	Thr	Gln
145					150					155					160
His	Lys	Leu	Glu	Met	Asp	Lys	Arg	Asp	Gly	Val	Phe	Gly	Ser	Gln	Pro
				165					170					175	
Met	Gly	Val	Pro	Pro	Ala	Gln	Gln	Met	Ser	Arg	Phe	Asp	Gln	Pro	Val
			180					185					190		
Pro	Pro	Pro	Val	Gly	Tyr	Pro	Gln	Ser	Tyr	Pro	Pro	Pro	Ala	Gln	Gly
		195					200						205		
Tyr	Pro	Pro	Ala	Ser	Tyr	Pro	Pro	Pro	Gly	Tyr	Pro	Gln	His		
	210					215						220			

(2) INFORMATION FOR SEQ ID NO:647:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 207 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..207  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498778  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

Met	Gly	Thr	Val	Thr	Ala	Asp	Thr	Pro	Tyr	Cys	Cys	Ile	Ser	Cys	Leu
1					5					10				15	
Cys	Gly	Pro	Cys	Val	Ser	Tyr	Met	Leu	Arg	Arg	Arg	Ala	Leu	Tyr	Asn
			20					25					30		
Asp	Met	Ser	Arg	Tyr	Thr	Cys	Cys	Ala	Gly	Tyr	Met	Pro	Cys	Ser	Gly
		35					40					45			
Arg	Cys	Gly	Glu	Ser	Lys	Cys	Pro	Gln	Leu	Cys	Leu	Ala	Thr	Glu	Val
	50					55					60				
Phe	Leu	Cys	Phe	Gly	Asn	Ser	Val	Ala	Ser	Thr	Arg	Phe	Leu	Leu	Gln
65					70					75					80
Asp	Glu	Phe	Asn	Ile	Gln	Thr	Thr	Gln	Cys	Asp	Asn	Cys	Ile	Ile	Gly
			85					90					95		
Phe	Met	Phe	Cys	Leu	Ser	Gln	Val	Ala	Cys	Ile	Phe	Ser	Ile	Val	Ala
			100					105					110		

Cys Ile Val Gly Ser Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Ser  
115 120 125  
Cys Cys Ala Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr  
130 135 140  
Gln His Lys Leu Glu Met Asp Lys Arg Asp Gly Val Phe Gly Ser Gln  
145 150 155 160  
Pro Met Gly Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Pro  
165 170 175  
Val Pro Pro Pro Val Gly Tyr Pro Gln Ser Tyr Pro Pro Pro Ala Gln  
180 185 190  
Gly Tyr Pro Pro Ala Ser Tyr Pro Pro Gly Tyr Pro Gln His  
195 200 205

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

aataggtcag agagaacatt tcttattggt ttagtttgac gtctggtctc tgttttgcwt	60
ctttctaatac aacccatagc tttcattctt tttcttcttt cagcagtggt ttcaagaaaa	120
tgctagtaaat actttttgtg tctgtcaatt tcaggagaaa aggcattttc tttgtcgcca	180
tcgatttgaa cgggcccta tctgaacaag ggccatttga tgttgttttg cataagttgt	240
tgggaaaaga gtgggaagag gttattgagg attaccaaca aaaacacca gaagtgactg	300
tgcttgatcc tccaggatca atacagcgta tatataatcg acaatcgatg cttcagggta	360
tggcagattt gaaactgtca gattgcagtg gcagcctttt tgttccaaag caaatgggtg	420
tcttgaaaga ttcagcagct agtgctgatg cagttgtgga agctggtctc aaatttccac	480
tagttgcaag ccgctctgga tcgatgggac tgcaaagtca catcaattgt acttggtcta	540
tgacaggcgc tcgcttgagc agcttgatcc gccttttagtc cttcaagagt ttgttaatca	600
tgggtggagtt atgttcaagg tatttgtggt ggggtgatgt ataaaagtca tgagacgggt	660
ttctctacca aatgtgagta attgtgaaaa agccaaagtt gatggcgtct tccaattccc	720
aaggggtttca tcagctgctg cttcagctga taacgcagac ttggaccctc gtgttgctga	780
gctacctcca aagcctttcc tcgaggcgct tgtgaaagag ctaagaagct tattgggact	840
tcggcttttc aacatagaca tgatcagggg acatgggagc aaaaacgtgt tttatgttat	900
tgacatcaac tattttcctg gttacggaaa actgccagac tacgagcaag tctttgtaga	960
tttcttccaa aatctggcgc aggtcaaata taagaagaga caacattgta aatgaaagaa	1020
aatggcggca gtttttagat ggtctactaa gaagcgacaa ataataaaat gtctaattat	1080
ggatttgtag agaatttagc tctcccttat ggaagcagta tcagataaac aagttttgat	1140
tactgatttt gaattttcag tgaaataaac gtctcttcat cc	

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

Met Leu Val Ile Leu Phe Val Ser Val Asn Phe Arg Arg Lys Gly Ile  
1 5 10 15  
Phe Phe Val Ala Ile Asp Leu Asn Arg Pro Leu Ser Glu Gln Gly Pro  
20 25 30  
Phe Asp Val Val Leu His Lys Leu Leu Gly Lys Glu Trp Glu Glu Val



35 40 45  
Ile Glu Asp Tyr Gln Gln Lys His Pro Glu Val Thr Val Leu Asp Pro  
50 55 60  
Pro Gly Ser Ile Gln Arg Ile Tyr Asn Arg Gln Ser Met Leu Gln Gly  
65 70 75 80  
Met Ala Asp Leu Lys Leu Ser Asp Cys Ser Gly Ser Leu Phe Val Pro  
85 90 95  
Lys Gln Met Val Val Leu Lys Asp Ser Ala Ala Ser Ala Asp Ala Val  
100 105 110  
Val Glu Ala Gly Leu Lys Phe Pro Leu Val Ala Ser Arg Ser Gly Ser  
115 120 125  
Met Gly Leu Gln Ser His Ile Asn Cys Thr Trp Leu Met Thr Gly Ala  
130 135 140  
Arg Leu Gln Ser Leu Ile Arg Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1498781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

Met Phe Lys Val Phe Val Val Gly Asp Val Ile Lys Val Met Arg Arg  
1 5 10 15  
Phe Ser Leu Pro Asn Val Ser Asn Cys Glu Lys Ala Lys Val Asp Gly  
20 25 30  
Val Phe Gln Phe Pro Arg Val Ser Ser Ala Ala Ala Ser Ala Asp Asn  
35 40 45  
Ala Asp Leu Asp Pro Arg Val Ala Glu Leu Pro Pro Lys Pro Phe Leu  
50 55 60  
Glu Ala Leu Val Lys Glu Leu Arg Ser Leu Leu Gly Leu Arg Leu Phe  
65 70 75 80  
Asn Ile Asp Met Ile Arg Glu His Gly Ser Lys Asn Val Phe Tyr Val  
85 90 95  
Ile Asp Ile Asn Tyr Phe Pro Gly Tyr Gly Lys Leu Pro Asp Tyr Glu  
100 105 110  
Gln Val Phe Val Asp Phe Phe Gln Asn Leu Ala Gln Val Lys Tyr Lys  
115 120 125  
Lys Arg Gln His Cys Lys  
130

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1498782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

Met Arg Arg Phe Ser Leu Pro Asn Val Ser Asn Cys Glu Lys Ala Lys  
1 5 10 15  
Val Asp Gly Val Phe Gln Phe Pro Arg Val Ser Ser Ala Ala Ser  
20 25 30

Ala Asp Asn Ala Asp Leu Asp Pro Arg Val Ala Glu Leu Pro Pro Lys  
35 40 45  
Pro Phe Leu Glu Ala Leu Val Lys Glu Leu Arg Ser Leu Leu Gly Leu  
50 55 60  
Arg Leu Phe Asn Ile Asp Met Ile Arg Glu His Gly Ser Lys Asn Val  
65 70 75 80  
Phe Tyr Val Ile Asp Ile Asn Tyr Phe Pro Gly Tyr Gly Lys Leu Pro  
85 90 95  
Asp Tyr Glu Gln Val Phe Val Asp Phe Phe Gln Asn Leu Ala Gln Val  
100 105 110  
Lys Tyr Lys Lys Arg Gln His Cys Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..733
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

acwtctttca	aggaaatagt	aagtaaatac	agtagagaag	taagagaagt	gggattttaa	60
atagaggaat	taatatcaga	gagcttaggt	ttagaaaaag	attacatgaa	gaaagtgctt	120
ggtgaacaag	gtcaacacat	ggcagtaaac	tattatcctc	catgtcctga	acctgagctc	180
acttacggtt	tacctgctca	taccgaccca	aacgccctaa	ccattcttct	tcaagacact	240
actgtttgcg	gtctccagat	cttgatcgac	ggtcagtggg	tcgccgttaa	tccacatcct	300
gatgcttttg	tcataacat	aggtgaccag	ttacaggcat	taagtaatgg	agtatacaaa	360
agtgtttggc	gtcgcgctgt	aacaaacaca	gaaaatccga	gactatcggt	cgcacgtttt	420
ctgtgcccag	ctgactgtgc	tgatcatgagc	ccggccaagc	ccttggtgga	agctgaggac	480
gatgaaacga	aaccagtcta	caaagatttc	acttatgcag	agtattacaa	gaagttttgg	540
agtaggaatc	tggaaccaaga	acatttcctc	gagaattttc	taaacaacta	agatacatat	600
atctttggcc	tttgtgtttg	tctagtaggc	atatatatac	aagtcaataa	cagcattgat	660
gttcgattct	acatttcctac	caacattttg	ttctagacgt	atgataatag	taggaatcat	720
gatcatatgt	ctt					

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

Xaa	Ser	Phe	Lys	Glu	Ile	Val	Ser	Lys	Tyr	Ser	Arg	Glu	Val	Arg	Glu
1			5					10					15		
Val	Gly	Phe	Lys	Ile	Glu	Glu	Leu	Ile	Ser	Glu	Ser	Leu	Gly	Leu	Glu
			20					25					30		
Lys	Asp	Tyr	Met	Lys	Lys	Val	Leu	Gly	Glu	Gln	Gly	Gln	His	Met	Ala
			35				40					45			
Val	Asn	Tyr	Tyr	Pro	Pro	Cys	Pro	Glu	Pro	Glu	Leu	Thr	Tyr	Gly	Leu
			50				55					60			
Pro	Ala	His	Thr	Asp	Pro	Asn	Ala	Leu	Thr	Ile	Leu	Leu	Gln	Asp	Thr
			65				70				75			80	
Thr	Val	Cys	Gly	Leu	Gln	Ile	Leu	Ile	Asp	Gly	Gln	Trp	Phe	Ala	Val
			85					90						95	

Asn Pro His Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln Leu Gln  
100 105 110  
Ala Leu Ser Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala Val Thr  
115 120 125  
Asn Thr Glu Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys Pro Ala  
130 135 140  
Asp Cys Ala Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala Glu Asp  
145 150 155 160  
Asp Glu Thr Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu Tyr Tyr  
165 170 175  
Lys Lys Phe Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu Glu Asn  
180 185 190  
Phe Leu Asn Asn  
195

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Met Lys Lys Val Leu Gly Glu Gln Gly Gln His Met Ala Val Asn Tyr  
1 5 10 15  
Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr Gly Leu Pro Ala His  
20 25 30  
Thr Asp Pro Asn Ala Leu Thr Ile Leu Leu Gln Asp Thr Thr Val Cys  
35 40 45  
Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe Ala Val Asn Pro His  
50 55 60  
Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln Leu Gln Ala Leu Ser  
65 70 75 80  
Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala Val Thr Asn Thr Glu  
85 90 95  
Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys Pro Ala Asp Cys Ala  
100 105 110  
Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala Glu Asp Asp Glu Thr  
115 120 125  
Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu Tyr Tyr Lys Lys Phe  
130 135 140  
Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu Glu Asn Phe Leu Asn  
145 150 155 160  
Asn

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

Met Ala Val Asn Tyr Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr

1 5 10 15  
Gly Leu Pro Ala His Thr Asp Pro Asn Ala Leu Thr Ile Leu Gln  
20 25 30  
Asp Thr Thr Val Cys Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe  
35 40 45  
Ala Val Asn Pro His Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln  
50 55 60  
Leu Gln Ala Leu Ser Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala  
65 70 75 80  
Val Thr Asn Thr Glu Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys  
85 90 95  
Pro Ala Asp Cys Ala Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala  
100 105 110  
Glu Asp Asp Glu Thr Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu  
115 120 125  
Tyr Tyr Lys Lys Phe Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu  
130 135 140  
Glu Asn Phe Leu Asn Asn  
145 150

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

attaagacgg gatgttgtaa ttaaacacct accaacagac aaaatcaaaa gataggaagc	60
cacgtatgca tatatttagg tgaagctttt gataaaacaa agcgttgggc tcttccaaat	120
atcaaaacaa gttttttttg tttgttggt tataattcac ctgagaaaaa caatatcaat	180
cggctcgttt tctctcctca gtgtttcttc agtagtcctg cgagatcgta taagagattc	240
gaaaccctaa tctatcaatt tgatcctgtc cattctctgt tattgtttga gaattgtgca	300
atccgatggg gacgatgcac cggagtgggt ctcccagaag gacaaatgaa aatgcgaagc	360
ttatcataac gacaatcggt ggagtgggtg ttggtttttt tgttggtatc acattaccat	420
taggttcctt tagaaagatt agcttacctt caggccttat gtcactctct gatgtagcca	480
tgtcagatgg gaaattgttt tctggtggca gatcacctga agatattggt tcaagaaagt	540
ctcctaagat atatgttcca accaatccgc atggtgcaga actacttcct cctgggatta	600
tagtggcaga aacagatttc tacttgccgc gattatgggg tgaacctagt gaagatttga	660
agaagaagcc aaagtatctc gtaactttta cagttggatt tgagcagaga aacaacatta	720
atgcagctgt taagaagttt tctgaagatt tccaaatatt gttattccat tatgatggcc	780
gaacaactga gtgggaccag tttgagtggg ctaaaaatgc aatacatatc agtgcaaaaa	840
agcaaacaaa atggtgggat gcaaagagat ttttgcattc tgatgttgtc tcagcttatg	900
agtatatatt tatatgggat gaagatcttg gagtcgagca cttcaatgca gatagggtgaa	960
ttacttgtct gaaattgtag ttgcagatca gtgacaatct ttacaatttt tattttaaat	1020
tttcaggtag gttgagttag ttaagaagca tggtttggag atttctcaac caggcttaga	1080
gccaaacaac ggacttacat gggaaatgac aaagaggaga ggtgaccgag atgtccacaa	1140
agaaactaag gaaaaaccag gatggtgcag tgatccacat ttacctccat gtgctgcgtt	1200
tgttgagatt atggcacctg tattttctag agaagcatgg cgatgtgtat ggcatatgat	1260
tcagaatgat cttgttcatg gatggggtct cgattttgct ctcagacgat gcgttgagcc	1320
tgtcatgag aagattggtg tggtagattc acagtggatt atccatcaag tgattccttc	1380
ccttggaagt caggggtgag cggaggaggg gaaatctcca tggcaagggg tgagggagag	1440
atgcagaaac gaatggacga tgtccagaa tcgcgtggca gaagctgata aagcatacat	1500
ggaacaacac aaggtaaaag aataatttgg gcctcttctt actctgtctc tgtaaataaa	1560
gcttacgttt ccctgatcaa gtgagtgtga ggagagagat ctatgtagtc ccctatttag	1620
tttaaaacat ctcagatata tctacattat tagcttttta cctaataatat ttcttc	

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..217  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498790  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

Met	Gly	Thr	Met	His	Arg	Ser	Gly	Ala	Pro	Arg	Arg	Thr	Asn	Glu	Asn
1				5					10					15	
Ala	Lys	Leu	Ile	Ile	Thr	Thr	Ile	Val	Gly	Val	Val	Phe	Gly	Phe	Phe
			20					25					30		
Val	Gly	Ile	Thr	Leu	Pro	Leu	Gly	Ser	Phe	Arg	Lys	Ile	Ser	Leu	Pro
			35				40					45			
Ser	Gly	Leu	Met	Ser	Ser	Leu	Asp	Val	Ala	Met	Ser	Asp	Gly	Lys	Leu
			50			55					60				
Phe	Ser	Gly	Gly	Arg	Ser	Pro	Glu	Asp	Ile	Gly	Ser	Arg	Lys	Ser	Pro
65				70						75				80	
Lys	Ile	Tyr	Val	Pro	Thr	Asn	Pro	His	Gly	Ala	Glu	Leu	Leu	Pro	Pro
				85					90					95	
Gly	Ile	Ile	Val	Ala	Glu	Thr	Asp	Phe	Tyr	Leu	Arg	Arg	Leu	Trp	Gly
			100					105					110		
Glu	Pro	Ser	Glu	Asp	Leu	Lys	Lys	Lys	Pro	Lys	Tyr	Leu	Val	Thr	Phe
			115				120					125			
Thr	Val	Gly	Phe	Glu	Gln	Arg	Asn	Asn	Ile	Asn	Ala	Ala	Val	Lys	Lys
			130			135					140				
Phe	Ser	Glu	Asp	Phe	Gln	Ile	Leu	Leu	Phe	His	Tyr	Asp	Gly	Arg	Thr
145				150						155				160	
Thr	Glu	Trp	Asp	Gln	Phe	Glu	Trp	Ser	Lys	Asn	Ala	Ile	His	Ile	Ser
			165						170					175	
Ala	Lys	Lys	Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro
			180					185					190		
Asp	Val	Val	Ser	Ala	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu
			195			200						205			
Gly	Val	Glu	His	Phe	Asn	Ala	Asp	Arg							
			210			215									

(2) INFORMATION FOR SEQ ID NO:658:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 214 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..214  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498791  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

Met	His	Arg	Ser	Gly	Ala	Pro	Arg	Arg	Thr	Asn	Glu	Asn	Ala	Lys	Leu
1				5					10					15	
Ile	Ile	Thr	Thr	Ile	Val	Gly	Val	Val	Phe	Gly	Phe	Phe	Val	Gly	Ile
			20					25					30		
Thr	Leu	Pro	Leu	Gly	Ser	Phe	Arg	Lys	Ile	Ser	Leu	Pro	Ser	Gly	Leu
			35				40					45			
Met	Ser	Ser	Leu	Asp	Val	Ala	Met	Ser	Asp	Gly	Lys	Leu	Phe	Ser	Gly
			50			55				60					
Gly	Arg	Ser	Pro	Glu	Asp	Ile	Gly	Ser	Arg	Lys	Ser	Pro	Lys	Ile	Tyr
65				70					75					80	
Val	Pro	Thr	Asn	Pro	His	Gly	Ala	Glu	Leu	Leu	Pro	Pro	Gly	Ile	Ile

	85		90		95										
Val	Ala	Glu	Thr	Asp	Phe	Tyr	Leu	Arg	Arg	Leu	Trp	Gly	Glu	Pro	Ser
	100							105					110		
Glu	Asp	Leu	Lys	Lys	Lys	Pro	Lys	Tyr	Leu	Val	Thr	Phe	Thr	Val	Gly
	115						120					125			
Phe	Glu	Gln	Arg	Asn	Asn	Ile	Asn	Ala	Ala	Val	Lys	Lys	Phe	Ser	Glu
	130					135				140					
Asp	Phe	Gln	Ile	Leu	Leu	Phe	His	Tyr	Asp	Gly	Arg	Thr	Thr	Glu	Trp
145					150				155					160	
Asp	Gln	Phe	Glu	Trp	Ser	Lys	Asn	Ala	Ile	His	Ile	Ser	Ala	Lys	Lys
			165						170				175		
Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Val	Val
			180					185				190			
Ser	Ala	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu	Gly	Val	Glu
		195					200					205			
His	Phe	Asn	Ala	Asp	Arg										
	210														

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1498792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Met	Ser	Ser	Leu	Asp	Val	Ala	Met	Ser	Asp	Gly	Lys	Leu	Phe	Ser	Gly
1			5						10					15	
Gly	Arg	Ser	Pro	Glu	Asp	Ile	Gly	Ser	Arg	Lys	Ser	Pro	Lys	Ile	Tyr
			20					25				30			
Val	Pro	Thr	Asn	Pro	His	Gly	Ala	Glu	Leu	Leu	Pro	Pro	Gly	Ile	Ile
			35				40				45				
Val	Ala	Glu	Thr	Asp	Phe	Tyr	Leu	Arg	Arg	Leu	Trp	Gly	Glu	Pro	Ser
	50				55					60					
Glu	Asp	Leu	Lys	Lys	Lys	Pro	Lys	Tyr	Leu	Val	Thr	Phe	Thr	Val	Gly
65				70					75					80	
Phe	Glu	Gln	Arg	Asn	Asn	Ile	Asn	Ala	Ala	Val	Lys	Lys	Phe	Ser	Glu
			85					90					95		
Asp	Phe	Gln	Ile	Leu	Leu	Phe	His	Tyr	Asp	Gly	Arg	Thr	Thr	Glu	Trp
		100						105				110			
Asp	Gln	Phe	Glu	Trp	Ser	Lys	Asn	Ala	Ile	His	Ile	Ser	Ala	Lys	Lys
	115					120						125			
Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Val	Val
	130					135				140					
Ser	Ala	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu	Gly	Val	Glu
145				150					155					160	
His	Phe	Asn	Ala	Asp	Arg										
			165												

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1373 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1373

(D) OTHER INFORMATION: / Ceres Seq. ID 1498801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

atgctttgtc	tttagtttaa	cgcgcgcac	ctctctctct	ggctcggagaa	atctccagat	60
ttggtcattt	ctccaatcct	ctcgggaacc	taatttaacc	aaacctctcc	tccttcagat	120
tcatcttcct	cctaatactc	ctaaaagctc	aaacctttct	ctcaatcaat	tctaaacaat	180
ggcaacagaa	gcaacaacca	aattcccaga	atccgatctc	cgtccaatcc	cacaaccacc	240
ggattttcat	ccagcaatca	tgcgttccagc	tcaaaacaca	actcttaaat	tctggcaact	300
aatggctgcc	ggttcaatcg	ctgggtcagt	cgaacacatg	gctatgtttc	cagtagatac	360
agtcaaaacc	catatgcaag	ctcttcgttc	atgtccgatt	aaaccaatcg	gaatccgtca	420
agctttccgt	tcaattatca	aaaccgatgg	acctctcgct	ttatatagag	gtatttgggc	480
tatgggactt	ggtgctggac	cagctcacgc	tgtttatttc	tcattctatg	aagtctctaa	540
gaagttttta	tccggtggaa	accctaataa	ctctgctgca	cacgctatct	ccggtgtttt	600
cgctactata	tctagtgtatg	ctgtgtttac	tccaatggat	atgggttaagc	aaaggttgca	660
aattgggaat	ggaacttata	aaggagtgtg	ggattgtatc	aagagagtaa	cgcgtgagga	720
agggtttggg	gctttttacg	cttcgtatag	aactactgtg	ttgatgaatg	ctccgtttac	780
cgctgtgcat	ttcactactt	atgaggcggg	taagagaggt	ttgagggaga	tgtttcctga	840
gcatgctggt	ggagtagagg	atgaggaagg	ttgggtgatt	tatgctactg	ctggagctgc	900
ggctgggtgg	ttagcggctg	ctgtaactac	tccgcttgat	gttggttaaga	cgcagttgca	960
atgtcagggt	gtgtgtggtt	gtgaccgttt	caagagcagt	tcaataagcg	atgtgttccg	1020
tacaatagt	aagaaagacg	gttatagagg	acttgctaga	ggatggctac	caagaatgct	1080
cttccatgct	ccagcagctg	cgatttgctg	gtccacttat	gaaacagtca	aatctttctt	1140
tcaagatctc	aatggtgaag	caaacgcagc	ttgaaaagac	acaaacatac	atgctgttgg	1200
cataattttac	ttgcctgatt	caggtcattg	attcttcata	gagctagcta	ctgggttggtt	1260
agtattaaca	ctagctctta	gagaagatct	ctgtttgtat	aattttattg	ttttcttcac	1320
gcaataatgt	tgtcagatta	gagttacaac	aacccaag	ccttttttct	ggt	

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1498802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

Met	Ala	Thr	Glu	Ala	Thr	Thr	Lys	Phe	Pro	Glu	Ser	Asp	Leu	Arg	Pro
1				5					10					15	
Ile	Pro	Gln	Pro	Pro	Asp	Phe	His	Pro	Ala	Ile	Ile	Val	Pro	Ala	Gln
			20					25					30		
Asn	Thr	Thr	Leu	Lys	Phe	Trp	Gln	Leu	Met	Val	Ala	Gly	Ser	Ile	Ala
			35				40					45			
Gly	Ser	Val	Glu	His	Met	Ala	Met	Phe	Pro	Val	Asp	Thr	Val	Lys	Thr
	50				55						60				
His	Met	Gln	Ala	Leu	Arg	Ser	Cys	Pro	Ile	Lys	Pro	Ile	Gly	Ile	Arg
65				70					75					80	
Gln	Ala	Phe	Arg	Ser	Ile	Ile	Lys	Thr	Asp	Gly	Pro	Ser	Ala	Leu	Tyr
			85					90					95		
Arg	Gly	Ile	Trp	Ala	Met	Gly	Leu	Gly	Ala	Gly	Pro	Ala	His	Ala	Val
		100					105					110			
Tyr	Phe	Ser	Phe	Tyr	Glu	Val	Ser	Lys	Lys	Phe	Leu	Ser	Gly	Gly	Asn
	115					120					125				
Pro	Asn	Asn	Ser	Ala	Ala	His	Ala	Ile	Ser	Gly	Val	Phe	Ala	Thr	Ile
	130					135					140				
Ser	Ser	Asp	Ala	Val	Phe	Thr	Pro	Met	Asp	Met	Val	Lys	Gln	Arg	Leu
145				150					155					160	
Gln	Ile	Gly	Asn	Gly	Thr	Tyr	Lys	Gly	Val	Trp	Asp	Cys	Ile	Lys	Arg
			165					170					175		
Val	Thr	Arg	Glu	Gly	Phe	Gly	Ala	Phe	Tyr	Ala	Ser	Tyr	Arg	Thr	
		180					185					190			

Thr	Val	Leu	Met	Asn	Ala	Pro	Phe	Thr	Ala	Val	His	Phe	Thr	Thr	Tyr
	195						200					205			
Glu	Ala	Val	Lys	Arg	Gly	Leu	Arg	Glu	Met	Phe	Pro	Glu	His	Ala	Val
	210					215					220				
Gly	Val	Glu	Asp	Glu	Glu	Gly	Trp	Leu	Ile	Tyr	Ala	Thr	Ala	Gly	Ala
225					230					235					240
Ala	Ala	Gly	Gly	Leu	Ala	Ala	Ala	Val	Thr	Thr	Pro	Leu	Asp	Val	Val
				245					250					255	
Lys	Thr	Gln	Leu	Gln	Cys	Gln	Gly	Val	Cys	Gly	Cys	Asp	Arg	Phe	Lys
		260						265					270		
Ser	Ser	Ser	Ile	Ser	Asp	Val	Phe	Arg	Thr	Ile	Val	Lys	Lys	Asp	Gly
		275					280					285			
Tyr	Arg	Gly	Leu	Ala	Arg	Gly	Trp	Leu	Pro	Arg	Met	Leu	Phe	His	Ala
	290					295					300				
Pro	Ala	Ala	Ala	Ile	Cys	Trp	Ser	Thr	Tyr	Glu	Thr	Val	Lys	Ser	Phe
305					310					315					320
Phe	Gln	Asp	Leu	Asn	Gly	Glu	Ala	Asn	Ala	Ala					
				325					330						

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met	Val	Ala	Gly	Ser	Ile	Ala	Gly	Ser	Val	Glu	His	Met	Ala	Met	Phe
1				5					10				15		
Pro	Val	Asp	Thr	Val	Lys	Thr	His	Met	Gln	Ala	Leu	Arg	Ser	Cys	Pro
		20						25					30		
Ile	Lys	Pro	Ile	Gly	Ile	Arg	Gln	Ala	Phe	Arg	Ser	Ile	Ile	Lys	Thr
		35				40						45			
Asp	Gly	Pro	Ser	Ala	Leu	Tyr	Arg	Gly	Ile	Trp	Ala	Met	Gly	Leu	Gly
	50					55				60					
Ala	Gly	Pro	Ala	His	Ala	Val	Tyr	Phe	Ser	Phe	Tyr	Glu	Val	Ser	Lys
65				70					75					80	
Lys	Phe	Leu	Ser	Gly	Gly	Asn	Pro	Asn	Asn	Ser	Ala	Ala	His	Ala	Ile
			85					90					95		
Ser	Gly	Val	Phe	Ala	Thr	Ile	Ser	Ser	Asp	Ala	Val	Phe	Thr	Pro	Met
	100						105					110			
Asp	Met	Val	Lys	Gln	Arg	Leu	Gln	Ile	Gly	Asn	Gly	Thr	Tyr	Lys	Gly
	115					120						125			
Val	Trp	Asp	Cys	Ile	Lys	Arg	Val	Thr	Arg	Glu	Glu	Gly	Phe	Gly	Ala
	130					135				140					
Phe	Tyr	Ala	Ser	Tyr	Arg	Thr	Thr	Val	Leu	Met	Asn	Ala	Pro	Phe	Thr
145					150				155					160	
Ala	Val	His	Phe	Thr	Thr	Tyr	Glu	Ala	Val	Lys	Arg	Gly	Leu	Arg	Glu
			165					170					175		
Met	Phe	Pro	Glu	His	Ala	Val	Gly	Val	Glu	Asp	Glu	Glu	Gly	Trp	Leu
	180						185					190			
Ile	Tyr	Ala	Thr	Ala	Gly	Ala	Ala	Ala	Gly	Gly	Leu	Ala	Ala	Ala	Val
	195					200					205				
Thr	Thr	Pro	Leu	Asp	Val	Val	Lys	Thr	Gln	Leu	Gln	Cys	Gln	Gly	Val
	210					215					220				
Cys	Gly	Cys	Asp	Arg	Phe	Lys	Ser	Ser	Ser	Ile	Ser	Asp	Val	Phe	Arg
225					230					235					240
Thr	Ile	Val	Lys	Lys	Asp	Gly	Tyr	Arg	Gly	Leu	Ala	Arg	Gly	Trp	Leu



			245					250					255		
Pro	Arg	Met	Leu	Phe	His	Ala	Pro	Ala	Ala	Ile	Cys	Trp	Ser	Thr	
			260					265				270			
Tyr	Glu	Thr	Val	Lys	Ser	Phe	Phe	Gln	Asp	Leu	Asn	Gly	Glu	Ala	Asn
			275					280				285			
Ala	Ala														
			290												

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1498804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met	Ala	Met	Phe	Pro	Val	Asp	Thr	Val	Lys	Thr	His	Met	Gln	Ala	Leu
1				5					10					15	
Arg	Ser	Cys	Pro	Ile	Lys	Pro	Ile	Gly	Ile	Arg	Gln	Ala	Phe	Arg	Ser
			20					25					30		
Ile	Ile	Lys	Thr	Asp	Gly	Pro	Ser	Ala	Leu	Tyr	Arg	Gly	Ile	Trp	Ala
		35				40						45			
Met	Gly	Leu	Gly	Ala	Gly	Pro	Ala	His	Ala	Val	Tyr	Phe	Ser	Phe	Tyr
	50					55					60				
Glu	Val	Ser	Lys	Lys	Phe	Leu	Ser	Gly	Gly	Asn	Pro	Asn	Asn	Ser	Ala
65					70					75					80
Ala	His	Ala	Ile	Ser	Gly	Val	Phe	Ala	Thr	Ile	Ser	Ser	Asp	Ala	Val
				85					90					95	
Phe	Thr	Pro	Met	Asp	Met	Val	Lys	Gln	Arg	Leu	Gln	Ile	Gly	Asn	Gly
			100					105					110		
Thr	Tyr	Lys	Gly	Val	Trp	Asp	Cys	Ile	Lys	Arg	Val	Thr	Arg	Glu	Glu
		115				120						125			
Gly	Phe	Gly	Ala	Phe	Tyr	Ala	Ser	Tyr	Arg	Thr	Thr	Val	Leu	Met	Asn
	130					135						140			
Ala	Pro	Phe	Thr	Ala	Val	His	Phe	Thr	Thr	Tyr	Glu	Ala	Val	Lys	Arg
145					150					155					160
Gly	Leu	Arg	Glu	Met	Phe	Pro	Glu	His	Ala	Val	Gly	Val	Glu	Asp	Glu
			165						170					175	
Glu	Gly	Trp	Leu	Ile	Tyr	Ala	Thr	Ala	Gly	Ala	Ala	Ala	Gly	Gly	Leu
			180					185					190		
Ala	Ala	Ala	Val	Thr	Thr	Pro	Leu	Asp	Val	Val	Lys	Thr	Gln	Leu	Gln
		195					200					205			
Cys	Gln	Gly	Val	Cys	Gly	Cys	Asp	Arg	Phe	Lys	Ser	Ser	Ser	Ile	Ser
	210					215					220				
Asp	Val	Phe	Arg	Thr	Ile	Val	Lys	Lys	Asp	Gly	Tyr	Arg	Gly	Leu	Ala
225				230						235					240
Arg	Gly	Trp	Leu	Pro	Arg	Met	Leu	Phe	His	Ala	Pro	Ala	Ala	Ala	Ile
			245						250					255	
Cys	Trp	Ser	Thr	Tyr	Glu	Thr	Val	Lys	Ser	Phe	Phe	Gln	Asp	Leu	Asn
			260					265					270		
Gly	Glu	Ala	Asn	Ala	Ala										
			275												

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```
accatccact ctactcaaca tggactcctc caaactctca tctctctctc tttgectctt      60
cctcatttgc attatctatc tcccccaaca ttctctcgca tgcggtcttt gcaacccacg      120
gaaggggcgga aagcactccc ctaagctacc agttcctccg gtgaccgtcc ctaagctacc      180
agttcctccg gtgaccgtcc ctaagctacc agtccctccg gtgaccgtcc ctaagctacc      240
cgttcctcct gtgaccatcc ctaagctacc cgttccacca gtgactgtac ctaagctacc      300
cgttcctcct gtgaccgtcc ccaagctacc cgttcctcca gtgaccgtcc ccaagctacc      360
cgttcctcca gtgacagtcc ctaagctacc cgttcccccg gtaactgtac ctaagctacc      420
cgttcctcca gtgaccgtcc ctaagctacc ccttcctccg atttcagggc taccataacc      480
tccagtggta ggtcccaatc tgccattgcc acctttgcca attgtaggtc ctattcttcc      540
accgggaaca accccaccag ccacaggagg gaaggactgt cctccaccgc cagggagcgt      600
aaagccacca tcagggggcg ggaaggcgac atgtccaata gacacgctga agttagggtg      660
ttgcgtcgac ttgttgggag gtttagtaaa gatagggtct ggggatccag cagttaacaa      720
atgttgtccg ttacttaaaag gcctcgttga aatcgaagcc gcggcttgtc tctgcactac      780
cctcaagctc aaagctcttg acctcaatct ttatgtccct gatgctcttc agcttctcct      840
tacctgtggc aaaaatccac ctccgggcta cacttggtcc atatgataaa ctcaactccac      900
ttataaagga tgctttggag aaaaaagtga gaagagaatg gcagagctcc aatctttcct      960
gtcttgggtt accaaatata tcatatcaaa tcctatccct ttgattcttt cctctatcgt     1020
tcccttatgc ttgtatcatt aattaatgtg tgcttttttag attaatagatt cttctcttgt     1080
attaaagtat gatttgaaat cttttttttt tctctatctc tttttattga attgattgaa     1140
ctgcgttcat gatactgtca aaaagagaga aaaagagtac aatttt
```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1498809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

```
Pro Ser Thr Leu Leu Asn Met Asp Ser Ser Lys Leu Ser Ser Leu Ser
1          5          10          15
Leu Cys Leu Phe Leu Ile Cys Ile Ile Tyr Leu Pro Gln His Ser Leu
20          25          30
Ala Cys Gly Ser Cys Asn Pro Arg Lys Gly Gly Lys His Ser Pro Lys
35          40          45
Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val
50          55          60
Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro
65          70          75          80
Val Pro Pro Val Thr Ile Pro Lys Leu Pro Val Pro Pro Val Thr Val
85          90          95
Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro
100         105         110
Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys
115         120         125
Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val
130         135         140
Thr Val Pro Lys Leu Pro Leu Pro Pro Ile Ser Gly Leu Pro Ile Pro
145         150         155         160
Pro Val Val Gly Pro Asn Leu Pro Leu Pro Pro Leu Pro Ile Val Gly
165         170         175
Pro Ile Leu Pro Pro Gly Thr Thr Pro Pro Ala Thr Gly Gly Lys Asp
```

Met	Asp	Ser	Ser	Lys	Leu	Ser	Ser	Leu	Ser	Leu	Cys	Leu	Phe	Leu	Ile
1				5				10						15	
Cys	Ile	Ile	Tyr	Leu	Pro	Gln	His	Ser	Leu	Ala	Cys	Gly	Ser	Cys	Asn
			20					25					30		
Pro	Arg	Lys	Gly	Gly	Lys	His	Ser	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val
			35				40					45			
Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro
	50					55					60				
Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Ile
65				70						75				80	
Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro
				85				90						95	
Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys
			100					105					110		
Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val
			115				120					125			
Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro
						135					140				
Leu	Pro	Pro	Ile	Ser	Gly	Leu	Pro	Ile	Pro	Pro	Val	Val	Gly	Pro	Asn
145				150						155				160	
Leu	Pro	Leu	Pro	Pro	Leu	Pro	Ile	Val	Gly	Pro	Ile	Leu	Pro	Pro	Gly
				165					170					175	
Thr	Thr	Pro	Pro	Ala	Thr	Gly	Gly	Lys	Asp	Cys	Pro	Pro	Pro	Pro	Gly
			180					185					190		
Ser	Val	Lys	Pro	Pro	Ser	Gly	Gly	Gly	Lys	Ala	Thr	Cys	Pro	Ile	Asp
			195				200					205			
Thr	Leu	Lys	Leu	Gly	Ala	Cys	Val	Asp	Leu	Leu	Gly	Gly	Leu	Val	Lys
						215					220				
Ile	Gly	Leu	Gly	Asp	Pro	Ala	Val	Asn	Lys	Cys	Cys	Pro	Leu	Leu	Lys
225				230						235				240	
Gly	Leu	Val	Glu	Ile	Glu	Ala	Ala	Ala	Cys	Leu	Cys	Thr	Thr	Leu	Lys
				245					250					255	
Leu	Lys	Ala	Leu	Asp	Leu	Asn	Leu	Tyr	Val	Pro	Asp	Ala	Leu	Gln	Leu
			260					265					270		

Leu Leu Thr Cys Gly Lys Asn Pro Pro Pro Gly Tyr Thr Cys Ser Ile  
275 280 285

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1777
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

gaagacgaag	aagaagaaga	agaagaagaa	agcttgagac	tttctctctg	tgtgcaattt	60
cgaaatcgat	aaagacttca	actttcgggt	ctaacaatga	caatttcctg	atagtttgat	120
tttgtccacc	tctttcaccg	attacctgat	ttcatcgctg	gcgttagtca	tcaaatggga	180
gctcgttgct	caaagttctc	attctgcttg	ttcccttctc	acttcaaata	cgcttcagtt	240
ctcgagtcct	ctgatatcga	gaatggagga	aaagtgtggc	cgacttttaa	ggaattcaaa	300
ttggagcagc	tgaaatctgc	gaccggaggt	ttctcttcag	acaacattgt	atcagaacac	360
ggcgagaaag	ctccaaacgt	tgtctacaga	ggaaggcttg	atgatggctg	tttgattgct	420
gtcaaacgat	tcaatcgctt	tgcttgggct	gatcatcgac	agttcctgga	tgaagctaaa	480
gctgttggga	gcttgaggag	tgatagatta	gcaaatctga	ttggatgttg	ctttgaagga	540
gaagagagat	tactagttgc	tgagtttatg	cctcatgaaa	cgcttgcaaa	gcattctttc	600
caactgggaga	ataatccgat	gaaatgggag	atgagattaa	gagttgcatt	gtgttttagca	660
caagcatttg	aatattgtag	taataaaggg	gagagctttg	tatcatgata	tcaatgctta	720
cagggttttg	tttgacaagg	atgggaatcc	caggttgtct	tgttttggac	tcatgaaaaa	780
tagcagagat	gggaagagtt	atagcacaaa	cttggcattt	actcctccag	agtatttgct	840
aacgggtaga	gttacaccag	agagtgttgt	attcagtttt	ggaaccgttt	tgctcgatct	900
catgagtggg	aaacatattc	caccgagtca	tgcgcttgac	ctaatacagag	gcaagaactg	960
tgcaatgtta	atggattctg	ctctcgaggg	tcattttctc	aacgaagacg	gaactgagct	1020
agtacgctta	gccacacggt	gtctgcagta	tgaagctcga	gaaagaccaa	atgtgaaatc	1080
tctcgtgact	tcacttgctc	cactccagaa	ggaatctgat	gtagcttcct	acgttccttat	1140
gggtataccc	catgaaaccg	aggctgaaga	agagtctccg	ctttctttga	caccctttgg	1200
tgatgcatgc	ttaagagtgg	atcttacagc	catcacaggaa	atactcagta	agattgggata	1260
caaggatgat	gaaggaattg	ccaatgagct	ctcgtttcaa	atgtggacca	atcagatgca	1320
ggaatctctc	aattcgaaga	agcaaggcga	cttagctttc	cgttccaaag	atttttacaac	1380
cgcggtcgat	tgctacactc	agttcataga	tgggggaaca	atgggtgcac	caacagtaca	1440
cgcacggcgg	tgcttgctcat	atctgatgaa	cgacaacgca	caagaggctc	tgacagatgc	1500
attgcagaca	caggttgtgt	ctccggattg	gccaaccgcc	ttgtatctgc	aagcggcctg	1560
cttgttcaag	ctgggtatgg	aagccgatgc	tcagcaagct	cttaaggatg	ggactacatt	1620
ggaagctaag	aagagtaaca	agcgcgtgata	aaatagcgtt	ttcaaaagct	tttgatatatg	1680
ctttatatttg	tttcctttct	ctctatttcc	atctatatgc	gcatacatat	acatatgcgg	1740
gtgtattttat	tatatatgtg	catatacttt	tgatgcc			

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

Met	Lys	Asn	Ser	Arg	Asp	Gly	Lys	Ser	Tyr	Ser	Thr	Asn	Leu	Ala	Phe
1															
Thr	Pro	Pro	Glu	Tyr	Leu	Arg	Thr	Gly	Arg	Val	Thr	Pro	Glu	Ser	Val

Val	Phe	Ser	20	Gly	Thr	Val	Leu	25	Leu	Asp	Leu	Met	Ser	30	Gly	Lys	His
			35					40						45			
Ile	Pro	Pro	Ser	His	Ala	Leu	Asp	Leu	Ile	Arg	Gly	Lys	Asn	Cys	Ala		
			50					55					60				
Met	Leu	Met	Asp	Ser	Ala	Leu	Glu	Gly	His	Phe	Ser	Asn	Glu	Asp	Gly		
65					70					75					80		
Thr	Glu	Leu	Val	Arg	Leu	Ala	Thr	Arg	Cys	Leu	Gln	Tyr	Glu	Ala	Arg		
				85					90					95			
Glu	Arg	Pro	Asn	Val	Lys	Ser	Leu	Val	Thr	Ser	Leu	Val	Thr	Leu	Gln		
			100					105					110				
Lys	Glu	Ser	Asp	Val	Ala	Ser	Tyr	Val	Leu	Met	Gly	Ile	Pro	His	Glu		
			115					120					125				
Thr	Glu	Ala	Glu	Glu	Glu	Ser	Pro	Leu	Ser	Leu	Thr	Pro	Phe	Gly	Asp		
			130					135				140					
Ala	Cys	Leu	Arg	Val	Asp	Leu	Thr	Ala	Ile	Gln	Glu	Ile	Leu	Ser	Lys		
145					150					155					160		
Ile	Gly	Tyr	Lys	Asp	Asp	Glu	Gly	Ile	Ala	Asn	Glu	Leu	Ser	Phe	Gln		
				165						170					175		
Met	Trp	Thr	Asn	Gln	Met	Gln	Glu	Ser	Leu	Asn	Ser	Lys	Lys	Gln	Gly		
			180					185						190			
Asp	Leu	Ala	Phe	Arg	Ser	Lys	Asp	Phe	Thr	Thr	Ala	Val	Asp	Cys	Tyr		
			195					200					205				
Thr	Gln	Phe	Ile	Asp	Gly	Gly	Thr	Met	Val	Ser	Pro	Thr	Val	His	Ala		
			210					215				220					
Arg	Arg	Cys	Leu	Ser	Tyr	Leu	Met	Asn	Asp	Asn	Ala	Gln	Glu	Ala	Leu		
225					230					235					240		
Thr	Asp	Ala	Leu	Gln	Thr	Gln	Val	Val	Ser	Pro	Asp	Trp	Pro	Thr	Ala		
				245						250				255			
Leu	Tyr	Leu	Gln	Ala	Ala	Cys	Leu	Phe	Lys	Leu	Gly	Met	Glu	Ala	Asp		
			260					265					270				
Ala	Gln	Gln	Ala	Leu	Lys	Asp	Gly	Thr	Thr	Leu	Glu	Ala	Lys	Lys	Ser		
			275					280					285				
Asn	Lys	Arg															
			290														

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..248

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

Met	Ser	Gly	Lys	His	Ile	Pro	Pro	Ser	His	Ala	Leu	Asp	Leu	Ile	Arg
1				5					10					15	
Gly	Lys	Asn	Cys	Ala	Met	Leu	Met	Asp	Ser	Ala	Leu	Glu	Gly	His	Phe
			20					25					30		
Ser	Asn	Glu	Asp	Gly	Thr	Glu	Leu	Val	Arg	Leu	Ala	Thr	Arg	Cys	Leu
			35				40					45			
Gln	Tyr	Glu	Ala	Arg	Glu	Arg	Pro	Asn	Val	Lys	Ser	Leu	Val	Thr	Ser
			50			55				60					
Leu	Val	Thr	Leu	Gln	Lys	Glu	Ser	Asp	Val	Ala	Ser	Tyr	Val	Leu	Met
65				70					75					80	
Gly	Ile	Pro	His	Glu	Thr	Glu	Ala	Glu	Glu	Glu	Ser	Pro	Leu	Ser	Leu
			85					90					95		
Thr	Pro	Phe	Gly	Asp	Ala	Cys	Leu	Arg	Val	Asp	Leu	Thr	Ala	Ile	Gln
			100					105					110		

Glu Ile Leu Ser Lys Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn  
115 120 125  
Glu Leu Ser Phe Gln Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn  
130 135 140  
Ser Lys Lys Gln Gly Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr  
145 150 155 160  
Ala Val Asp Cys Tyr Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser  
165 170 175  
Pro Thr Val His Ala Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn  
180 185 190  
Ala Gln Glu Ala Leu Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro  
195 200 205  
Asp Trp Pro Thr Ala Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu  
210 215 220  
Gly Met Glu Ala Asp Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu  
225 230 235 240  
Glu Ala Lys Lys Ser Asn Lys Arg  
245

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1498814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met Leu Met Asp Ser Ala Leu Glu Gly His Phe Ser Asn Glu Asp Gly  
1 5 10 15  
Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu Gln Tyr Glu Ala Arg  
20 25 30  
Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser Leu Val Thr Leu Gln  
35 40 45  
Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met Gly Ile Pro His Glu  
50 55 60  
Thr Glu Ala Glu Glu Glu Ser Pro Leu Ser Leu Thr Pro Phe Gly Asp  
65 70 75 80  
Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln Glu Ile Leu Ser Lys  
85 90 95  
Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn Glu Leu Ser Phe Gln  
100 105 110  
Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn Ser Lys Lys Gln Gly  
115 120 125  
Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr Ala Val Asp Cys Tyr  
130 135 140  
Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser Pro Thr Val His Ala  
145 150 155 160  
Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn Ala Gln Glu Ala Leu  
165 170 175  
Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro Asp Trp Pro Thr Ala  
180 185 190  
Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu Gly Met Glu Ala Asp  
195 200 205  
Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu Glu Ala Lys Lys Ser  
210 215 220  
Asn Lys Arg  
225

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1368 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1368  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498815  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```
aaaataagct tatcattctt acaaaaatat ttctgggttt ctgatattgt tcttgttctc      60
ttgaatcttt attacttgaa aaacatataa agtgatggcg gttgtggttg aagaagggtgt      120
ggtgttgaat catggagggtg aagagcttgt ggatttgcca cctggtttca ggtttcatcc      180
aacagacgaa gagatcataa catgttacct taaggagaag gttttaaaca gccgattcac      240
ggctgtggcc atgggagaag ctgatctcaa caagtgtgag ccttgggatt tgccaatagg      300
gcaaagatgg gggagaaaga gttctacttc ttctgtcaaa gggacaggaa gtatccgact      360
gggatgagga cgaaccgtgc gacggagtca ggatactgga aagccaccgg gaaggataag      420
gagatcttca aaggcaaagg ttgtctcggt gggatgaaga aaacacttgt gttttataga      480
ggaagagctc caaaagggtga aaagactaat tgggtcatgc atgaatatcg tcttgaaggc      540
aaatatctgt attacaatct cccaaaatct gcaaggggacg aatgggtcgt gtgtagggtt      600
tttcacaaga acaatccttc taccacaacc caaccaatga cgagaatacc cgttgaagat      660
ttcacaagga tggattctct agagaacatt gatcatctcc tagacttctc atctcttcct      720
cctotcatag acccgagttt catgagtcaa accgaacaac caaacttcaa acccatcaac      780
cctccaactt acgatatctc atcaccaatc caaccccatc atttcaattc ttaccaatca      840
atctttaacc accagggttt tggttctgct tcgggctcta cgtacaacaa caacaacgag      900
atgatcaaga tggagcaatc acttgtagt gtatctcaag aaacatgcct aagctcagat      960
gtgaacgcga acatgactac aaccacggag gtatcttcgg gtcctgtaat gaaacaagaa     1020
atggggatga tgggaatggt gaatggtagc aagtcgtatg aagatctatg tgacttgagg     1080
ggggacttgt gggacttcta attaatcatt tgactgtggt gaaagagtat atttgttggg     1140
atttaaatca tgttagttaa tacatataca tataggattt actagaggct taatcctagt     1200
taactatttt cacttcattg atattattta attagttgat tgtttaatta gtttatactt     1260
tatagtgtgg ttaaaaaaga aaagaaagga ttgtgataat ttgggatttt agtgcataag     1320
ttatatctca atgtaaactg tatttgtata catataatta gtcttctc
```

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 264 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..264  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

```
Met Gly Glu Lys Glu Phe Tyr Phe Phe Cys Gln Arg Asp Arg Lys Tyr
1      5      10      15
Pro Thr Gly Met Arg Thr Asn Arg Ala Thr Glu Ser Gly Tyr Trp Lys
20     25     30
Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys Gly Lys Gly Cys Leu Val
35     40     45
Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly
50     55     60
Glu Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr
65     70     75     80
Ser Tyr Tyr Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys
85     90     95
Arg Val Phe His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr
100    105    110
Arg Ile Pro Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile
```

115	120	125
Asp His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser		
130	135	140
Phe Met Ser Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro		
145	150	155
Thr Tyr Asp Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr		
165	170	175
Gln Ser Ile Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr		
180	185	190
Tyr Asn Asn Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser		
195	200	205
Val Ser Gln Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr		
210	215	220
Thr Thr Thr Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly		
225	230	235
Met Met Gly Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp		
245	250	255
Leu Arg Gly Asp Leu Trp Asp Phe		
260		

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1498817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

Met Arg Thr Asn Arg Ala Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly	
1	5
Lys Asp Lys Glu Ile Phe Lys Gly Lys Gly Cys Leu Val Gly Met Lys	
20	25
Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr	
35	40
Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr	
50	55
Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys Arg Val Phe	
65	70
His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr Arg Ile Pro	
85	90
Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile Asp His Leu	
100	105
Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser Phe Met Ser	
115	120
Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp	
130	135
Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr Gln Ser Ile	
145	150
Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn	
165	170
Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser Val Ser Gln	
180	185
Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr Thr Thr Thr	
195	200
Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly Met Met Gly	
210	215
Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp Leu Arg Gly	
225	230
	235
	240



Asp Leu Trp Asp Phe  
245

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```
Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Glu
1          5          10          15
Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Ser
          20          25          30
Tyr Tyr Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys Arg
          35          40          45
Val Phe His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr Arg
          50          55          60
Ile Pro Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile Asp
65          70          75          80
His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser Phe
          85          90          95
Met Ser Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro Thr
          100          105          110
Tyr Asp Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr Gln
          115          120          125
Ser Ile Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr Tyr
          130          135          140
Asn Asn Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser Val
145          150          155          160
Ser Gln Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr Thr
          165          170          175
Thr Thr Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly Met
          180          185          190
Met Gly Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp Leu
          195          200          205
Arg Gly Asp Leu Trp Asp Phe
210          215
```

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1898
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

```
aaaaaattaa gtgatcatca cttctcctcc ttatcgaga gtttcagttt tagagcaaca      60
atgtctctat ttctgaagcc ctctctcttc ctatacgaca ccactcttag tcttctctta      120
cttctgttca atggatggag tcttgaggat acagcagcag cccaaaagag gcgtgaagca      180
gacaaaaatg ctgcagaaac tgaatggatc caactccaat acttgtggac caaaacaagg      240
agtgtgttac tacttcccggt tttcaaggggt ttggtgggta tgtgtttgggt tctatccatt      300
atagtgttct tcgagagttt ttacatgaac tttgtgatac tcttcgtcaa gttattttaa      360
cgtaaaccctt ataaagtgtg caaatgggag gccatgcaag aagatgttga ggttggaccct      420
```

```

gataactacc caatggttct tatccaaata ccaatgtaca atgaaaaaga ggtctttcaa 480
ttatctatag cagcaatatg tagtttggtc tggccatcga gccgtctagt agttcaagtt 540
gtagatgatt ctacggatcc ggccgtaagg gaaggtgtgg acgtagagat tgcaaaatgg 600
caaagccaag gcataaacat aaggtgtgaa aggagagata acaggaacgg ctacaaagcc 660
ggagctatga aagaagctct tacgcagagc tacgtcaagc aatgcgactt cgtagcagtc 720
ttcgaatgctg atttccaacc cgagcccgat tatctcatcc gcgctgtccc tttccttgtc 780
cacaaccctg acgttgctct agttcaagcc cgatggatat ttgttaacgc gaacaaatgc 840
ttgatgacga ggatgcaaga gatgtctctc aactatcatt tcaaagtggg acaagaatca 900
gggtcgacta gacatgcttt cttcggggtt aatggaaccg cgggtgtatg gagaatatcg 960
gcaatggaag cagcaggagg atggaaatca aggaccacag tagaggacat ggacttggct 1020
gttcgtgttg gtcttcattg ctggaaattt gtctacctta acgacctcac ggtgagaaac 1080
gagcttccaa gcaaatttaa ggccctacaga ttccagcaac ataggtggtc ctgtggaccg 1140
gcgaatctat tttagaaaaat gacgatggag atcatttttca ataagagagt atcaatttgg 1200
aagaagtttt atgtgatcta cagctttttc ttcgtaagga aagtggcggg acacttcttg 1260
acattcttct tctactgtat aattgtgcc acaagtgtct tcttccctga aatccacatc 1320
ccatcttggg ctaccattta cgttccctct ttgatcagta tcttccacac cctggcaact 1380
ccaagatcct tctacctcgt gatattttgg gtcttggtcg agaatgtaat ggctatgcat 1440
cgaaccaaag gtacgtgcat tggcctactt gaaggaggaa gagtaaacga atgggttgtg 1500
accgaaaaac taggagatgc tttgaagagt aagctactct ctcggttagt ccaaagaaaa 1560
tcttggttatt aaagagtga tccaaggaa gtgatggtg ggtatatacat attagatgt 1620
gcactctatg gcctgatcta tgggcacaca tggttacatt tctatctttt tcttcaggcc 1680
acagcctttt tcgtctccgg ttttggtttt gtcggaacgg cctaagaacc ttccctgccc 1740
attattttta gtcaccaa atattctcca tgttttagtt cttatttaca cttttattta 1800
ttttgacacc attgtacggg ttggacccca tatcatcatg ttgtataagt ataacgaata 1860
atgatttttt gtttggttga atgtatgcgt cactcggg

```

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1498824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

```

Lys Lys Leu Ser Asp His His Phe Ser Ser Phe Ile Glu Ser Phe Ser
1      5      10      15
Phe Arg Ala Thr Met Ser Leu Phe Leu Lys Pro Phe Leu Phe Leu Tyr
20      25      30
Asp Thr Thr Leu Ser Leu Leu Leu Leu Leu Phe Asn Gly Trp Ser Leu
35      40      45
Glu Asp Thr Ala Ala Ala Gln Lys Arg Arg Glu Ala Asp Lys Asn Ala
50      55      60
Ala Glu Thr Glu Trp Ile Gln Leu Gln Tyr Leu Trp Thr Lys Thr Arg
65      70      75      80
Ser Val Val Leu Leu Pro Val Phe Lys Gly Leu Val Val Met Cys Leu
85      90      95
Val Leu Ser Ile Ile Val Phe Phe Glu Ser Phe Tyr Met Asn Phe Val
100     105     110
Ile Leu Phe Val Lys Leu Phe Lys Arg Lys Pro His Lys Val Tyr Lys
115     120     125
Trp Glu Ala Met Gln Glu Asp Val Glu Val Gly Pro Asp Asn Tyr Pro
130     135     140
Met Val Leu Ile Gln Ile Pro Met Tyr Asn Glu Lys Glu Val Phe Gln
145     150     155     160
Leu Ser Ile Ala Ala Ile Cys Ser Leu Val Trp Pro Ser Ser Arg Leu
165     170     175
Val Val Gln Val Val Asp Asp Ser Thr Asp Pro Ala Val Arg Glu Gly
180     185     190

```

```

Val Asp Val Glu Ile Ala Lys Trp Gln Ser Gln Gly Ile Asn Ile Arg
    195                200                205
Cys Glu Arg Arg Asp Asn Arg Asn Gly Tyr Lys Ala Gly Ala Met Lys
    210                215                220
Glu Ala Leu Thr Gln Ser Tyr Val Lys Gln Cys Asp Phe Val Ala Val
    225                230                235                240
Phe Asp Ala Asp Phe Gln Pro Glu Pro Asp Tyr Leu Ile Arg Ala Val
    245                250                255
Pro Phe Leu Val His Asn Pro Asp Val Ala Leu Val Gln Ala Arg Trp
    260                265                270
Ile Phe Val Asn Ala Asn Lys Cys Leu Met Thr Arg Met Gln Glu Met
    275                280                285
Ser Leu Asn Tyr His Phe Lys Val Glu Gln Glu Ser Gly Ser Thr Arg
    290                295                300
His Ala Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Ser
    305                310                315                320
Ala Met Glu Ala Ala Gly Gly Trp Lys Ser Arg Thr Thr Val Glu Asp
    325                330                335
Met Asp Leu Ala Val Arg Val Gly Leu His Gly Trp Lys Phe Val Tyr
    340                345                350
Leu Asn Asp Leu Thr Val Arg Asn Glu Leu Pro Ser Lys Phe Lys Ala
    355                360                365
Tyr Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala Asn Leu Phe
    370                375                380
Arg Lys Met Thr Met Glu Ile Ile Phe Asn Lys Arg Val Ser Ile Trp
    385                390                395                400
Lys Lys Phe Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Val Ala
    405                410                415
Val His Phe Leu Thr Phe Phe Phe Tyr Cys Ile Ile Val Pro Thr Ser
    420                425                430
Val Phe Phe Pro Glu Ile His Ile Pro Ser Trp Ser Thr Ile Tyr Val
    435                440                445
Pro Ser Leu Ile Ser Ile Phe His Thr Leu Ala Thr Pro Arg Ser Phe
    450                455                460
Tyr Leu Val Ile Phe Trp Val Leu Phe Glu Asn Val Met Ala Met His
    465                470                475                480
Arg Thr Lys Gly Thr Cys Ile Gly Leu Leu Glu Gly Gly Arg Val Asn
    485                490                495
Glu Trp Val Val Thr Glu Lys Leu Gly Asp Ala Leu Lys Ser Lys Leu
    500                505                510
Leu Ser Arg Val Val Gln Arg Lys Ser Cys Tyr Gln Arg Val Asn Ser
    515                520                525
Lys Glu Val Met Val Gly Val Tyr Ile Leu Gly Cys Ala Leu Tyr Gly
    530                535                540
Leu Ile Tyr Gly His Thr Trp Leu His Phe Tyr Leu Phe Leu Gln Ala
    545                550                555                560
Thr Ala Phe Phe Val Ser Gly Phe Gly Phe Val Gly Thr Ala
    565                570

```

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..554
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Met Ser Leu Phe Leu Lys Pro Phe Leu Phe Leu Tyr Asp Thr Thr Leu

1		5		10		15
Ser	Leu	Leu	Leu	Leu	Phe	Asn
		20		25		30
Ala	Ala	Gln	Lys	Arg	Arg	Glu
		35		40		45
Trp	Ile	Gln	Leu	Gln	Tyr	Leu
		50		55		60
Leu	Pro	Val	Phe	Lys	Gly	Leu
65				70		75
Ile	Val	Phe	Phe	Glu	Ser	Phe
			85			90
Lys	Leu	Phe	Lys	Arg	Lys	Pro
			100			105
Gln	Glu	Asp	Val	Glu	Val	Gly
		115				120
Gln	Ile	Pro	Met	Tyr	Asn	Glu
		130				135
Ala	Ile	Cys	Ser	Leu	Val	Trp
145				150		155
Val	Asp	Asp	Ser	Thr	Asp	Pro
			165			170
Ile	Ala	Lys	Trp	Gln	Ser	Gln
			180			185
Asp	Asn	Arg	Asn	Gly	Tyr	Lys
			195			200
Gln	Ser	Tyr	Val	Lys	Gln	Cys
			210			215
Phe	Gln	Pro	Glu	Pro	Asp	Tyr
225				230		235
His	Asn	Pro	Asp	Val	Ala	Leu
			245			250
Ala	Asn	Lys	Cys	Leu	Met	Thr
			260			265
His	Phe	Lys	Val	Glu	Gln	Glu
			275			280
Gly	Phe	Asn	Gly	Thr	Ala	Gly
			290			295
Ala	Gly	Gly	Trp	Lys	Ser	Arg
305				310		315
Val	Arg	Val	Gly	Leu	His	Gly
			325			330
Thr	Val	Arg	Asn	Glu	Leu	Pro
			340			345
Gln	His	Arg	Trp	Ser	Cys	Gly
			355			360
Met	Glu	Ile	Ile	Phe	Asn	Lys
			370			375
Val	Ile	Tyr	Ser	Phe	Phe	Phe
385				390		395
Thr	Phe	Phe	Phe	Tyr	Cys	Ile
			405			410
Glu	Ile	His	Ile	Pro	Ser	Trp
			420			425
Ser	Ile	Phe	His	Thr	Leu	Ala
			435			440
Phe	Trp	Val	Leu	Phe	Glu	Asn
			450			455
Thr	Cys	Ile	Gly	Leu	Leu	Glu
465				470		475
Thr	Glu	Lys	Leu	Gly	Asp	Ala
			485			490

Val Gln Arg Lys Ser Cys Tyr Gln Arg Val Asn Ser Lys Glu Val Met  
500 505 510  
Val Gly Val Tyr Ile Leu Gly Cys Ala Leu Tyr Gly Leu Ile Tyr Gly  
515 520 525  
His Thr Trp Leu His Phe Tyr Leu Phe Leu Gln Ala Thr Ala Phe Phe  
530 535 540  
Val Ser Gly Phe Gly Phe Val Gly Thr Ala  
545 550

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1498826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Cys Leu Val Leu Ser Ile Ile Val Phe Phe Glu Ser Phe Tyr Met  
1 5 10 15  
Asn Phe Val Ile Leu Phe Val Lys Leu Phe Lys Arg Lys Pro His Lys  
20 25 30  
Val Tyr Lys Trp Glu Ala Met Gln Glu Asp Val Glu Val Gly Pro Asp  
35 40 45  
Asn Tyr Pro Met Val Leu Ile Gln Ile Pro Met Tyr Asn Glu Lys Glu  
50 55 60  
Val Phe Gln Leu Ser Ile Ala Ala Ile Cys Ser Leu Val Trp Pro Ser  
65 70 75 80  
Ser Arg Leu Val Val Gln Val Val Asp Asp Ser Thr Asp Pro Ala Val  
85 90 95  
Arg Glu Gly Val Asp Val Glu Ile Ala Lys Trp Gln Ser Gln Gly Ile  
100 105 110  
Asn Ile Arg Cys Glu Arg Arg Asp Asn Arg Asn Gly Tyr Lys Ala Gly  
115 120 125  
Ala Met Lys Glu Ala Leu Thr Gln Ser Tyr Val Lys Gln Cys Asp Phe  
130 135 140  
Val Ala Val Phe Asp Ala Asp Phe Gln Pro Glu Pro Asp Tyr Leu Ile  
145 150 155 160  
Arg Ala Val Pro Phe Leu Val His Asn Pro Asp Val Ala Leu Val Gln  
165 170 175  
Ala Arg Trp Ile Phe Val Asn Ala Asn Lys Cys Leu Met Thr Arg Met  
180 185 190  
Gln Glu Met Ser Leu Asn Tyr His Phe Lys Val Glu Gln Glu Ser Gly  
195 200 205  
Ser Thr Arg His Ala Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp  
210 215 220  
Arg Ile Ser Ala Met Glu Ala Ala Gly Gly Trp Lys Ser Arg Thr Thr  
225 230 235 240  
Val Glu Asp Met Asp Leu Ala Val Arg Val Gly Leu His Gly Trp Lys  
245 250 255  
Phe Val Tyr Leu Asn Asp Leu Thr Val Arg Asn Glu Leu Pro Ser Lys  
260 265 270  
Phe Lys Ala Tyr Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala  
275 280 285  
Asn Leu Phe Arg Lys Met Thr Met Glu Ile Ile Phe Asn Lys Arg Val  
290 295 300  
Ser Ile Trp Lys Lys Phe Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg  
305 310 315 320  
Lys Val Ala Val His Phe Leu Thr Phe Phe Phe Tyr Cys Ile Ile Val

Pro	Thr	Ser	Val	Phe	Phe	Pro	Glu	Ile	His	Ile	Pro	Ser	Trp	Ser	Thr
			340					345					350		
Ile	Tyr	Val	Pro	Ser	Leu	Ile	Ser	Ile	Phe	His	Thr	Leu	Ala	Thr	Pro
		355					360					365			
Arg	Ser	Phe	Tyr	Leu	Val	Ile	Phe	Trp	Val	Leu	Phe	Glu	Asn	Val	Met
	370					375				380					
Ala	Met	His	Arg	Thr	Lys	Gly	Thr	Cys	Ile	Gly	Leu	Leu	Glu	Gly	Gly
385					390				395					400	
Arg	Val	Asn	Glu	Trp	Val	Val	Thr	Glu	Lys	Leu	Gly	Asp	Ala	Leu	Lys
			405					410						415	
Ser	Lys	Leu	Leu	Ser	Arg	Val	Val	Gln	Arg	Lys	Ser	Cys	Tyr	Gln	Arg
		420					425					430			
Val	Asn	Ser	Lys	Glu	Val	Met	Val	Gly	Val	Tyr	Ile	Leu	Gly	Cys	Ala
	435						440					445			
Leu	Tyr	Gly	Leu	Ile	Tyr	Gly	His	Thr	Trp	Leu	His	Phe	Tyr	Leu	Phe
	450				455					460					
Leu	Gln	Ala	Thr	Ala	Phe	Phe	Val	Ser	Gly	Phe	Gly	Phe	Val	Gly	Thr
465					470				475					480	
Ala															

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

ttccaaggaa	aaaaaaagtc	tttacccgta	aacatttttt	ctccatcttc	ttgatatcaa	60
caaaacacac	ctcaacaaaa	aaaaaaaaaa	aacttcatct	ctctcagatt	tcgaaattga	120
cccgctcggtg	attcttaatc	tctcctctct	gttcttctcc	gatcaaacct	cattccaaag	180
aaacaaacca	tggatctcca	accagaagag	cttcaattct	tgacaatacc	tcaactactt	240
caagaatcaa	tctcaatcaa	gaaacgatct	ccaagaacct	tctacctcat	aaccctctcc	300
ttcatcttcc	ctctctcctt	cgctatcctc	gctcactcac	tcttactca	accaatctta	360
gccaaactcg	acaaatccga	cccaccaaac	tcagatcggt	cacgtcatga	ttggactggt	420
cttctaattc	tccagttcag	ttacttgatc	ttcctctttg	ccttctctct	tctctcaacc	480
gctgcwgtwg	tcttcaccgt	cgcttctctt	tacaccgg			

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

Met	Asp	Leu	Gln	Pro	Glu	Glu	Leu	Gln	Phe	Leu	Thr	Ile	Pro	Gln	Leu
1			5				10							15	
Leu	Gln	Glu	Ser	Ile	Ser	Ile	Lys	Lys	Arg	Ser	Pro	Arg	Thr	Phe	Tyr
		20					25					30			
Leu	Ile	Thr	Leu	Ser	Phe	Ile	Phe	Pro	Leu	Ser	Phe	Ala	Ile	Leu	Ala
	35					40					45				
His	Ser	Leu	Phe	Thr	Gln	Pro	Ile	Leu	Ala	Lys	Leu	Asp	Lys	Ser	Asp

```

      50              55              60
Pro Pro Asn Ser Asp Arg Ser Arg His Asp Trp Thr Val Leu Leu Ile
65              70              75              80
Phe Gln Phe Ser Tyr Leu Ile Phe Leu Phe Ala Phe Ser Leu Leu Ser
      85              90              95
Thr Ala Xaa Xaa Val Phe Thr Val Ala Ser Leu Tyr Thr
      100              105
```

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

```

aactttcaat ctcagcta atcaagtaac gtggaaagga tttgttccgt caaaggttgg      60
tgattataca gagactgagt tcttgataag ttggattgag cttgttttca attgcggatc      120
tttgagaaaa aagtttgcaa ctttatggct ctggaacaac aacatgtttg tgaaaagcgg      180
cttcaagcca agaccttttc tacccaagag tttcagttga ctctcaattg ggatgattta      240
acttggtccca tttgtttgga tttccctcac aatgggtgtgc ttctccagtg ttcttcttac      300
ggaaacggtt gccgtgcttt tgtctgcaat actgatcacc ttcactctaa ctgtttggat      360
cgtttcatta gcgcctgtgg tactgaatca cctcctgctc ctgatgagcc tcgctctaag      420
gttttagaag agagttgcaa acctgtgtgt ccactgtgta gaggagaagt tactggctgg      480
cttgttgtag aagaagctcg tcttcgtctt gatgagaaaa aacgttgctg tgaggaagac      540
gatgcaggtt tatgggtact ttacttggag cttcgcaaac atgctcagtc agagcatc
```

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

```

Met Ala Leu Glu Gln Gln His Val Cys Glu Lys Arg Leu Gln Ala Lys
1              5              10              15
Thr Phe Ser Thr Gln Glu Phe Gln Leu Thr Leu Asn Trp Asp Asp Leu
      20              25              30
Thr Cys Pro Ile Cys Leu Asp Phe Pro His Asn Gly Val Leu Leu Gln
      35              40              45
Cys Ser Ser Tyr Gly Asn Gly Cys Arg Ala Phe Val Cys Asn Thr Asp
      50              55              60
His Leu His Ser Asn Cys Leu Asp Arg Phe Ile Ser Ala Cys Gly Thr
      65              70              75              80
Glu Ser Pro Pro Ala Pro Asp Glu Pro Arg Ser Lys Val Leu Glu Glu
      85              90              95
Ser Cys Lys Pro Val Cys Pro Leu Cys Arg Gly Glu Val Thr Gly Trp
      100              105              110
Leu Val Val Glu Glu Ala Arg Leu Arg Leu Asp Glu Lys Lys Arg Cys
      115              120              125
Cys Glu Glu Asp Asp Ala Gly Leu Trp Val Leu Tyr Leu Glu Leu Arg
      130              135              140
Lys His Ala Gln Ser Glu His
145              150
```

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

aatttaaatt tctcttttcta tctactataa aaagtgactc tctaagaact ccaaagatta	60
gaacattgaa ttgaattagc catggagaag aatacttctc aaaccatctt ctccaacttt	120
tttcttctcc ttctcctttc ttcatgtgtc tctgctcagc tccggacagg tttctaccag	180
aactcatgtc cgaacgtgga aaccattgta cgtaacgctg tccgtcagaa attccagcag	240
acttttcgtta ccgctccggc cactcttcgc ctcttcttcc acgattgctt cgttcgtgga	300
tgtgatgcgt caataatgat agcatcacca tccggagagag accatccaga tgacatgtca	360
ttggccggag acggattcga cacggtggtg aaggcgaaca agccgttgat agcaatccca	420
attgccgcaa caaagtctca tgtgctgaca ttttggtctc cgccactcgt gaagtcgtcg	480
ttttgac	

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Met	Glu	Lys	Asn	Thr	Ser	Gln	Thr	Ile	Phe	Ser	Asn	Phe	Phe	Leu	Leu
1			5					10						15	
Leu	Leu	Leu	Ser	Ser	Cys	Val	Ser	Ala	Gln	Leu	Arg	Thr	Gly	Phe	Tyr
			20					25					30		
Gln	Asn	Ser	Cys	Pro	Asn	Val	Glu	Thr	Ile	Val	Arg	Asn	Ala	Val	Arg
			35				40					45			
Gln	Lys	Phe	Gln	Gln	Thr	Phe	Val	Thr	Ala	Pro	Ala	Thr	Leu	Arg	Leu
			50			55					60				
Phe	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Ala	Ser	Ile	Met	Ile
65					70					75				80	
Ala	Ser	Pro	Ser	Glu	Arg	Asp	His	Pro	Asp	Asp	Met	Ser	Leu	Ala	Gly
				85				90					95		
Asp	Gly	Phe	Asp	Thr	Val	Val	Lys	Ala	Asn	Lys	Pro	Leu	Ile	Ala	Ile
			100				105					110			
Pro	Ile	Ala	Ala	Thr	Lys	Ser	His	Val	Leu	Thr	Phe	Trp	Leu	Ser	Pro
			115				120					125			
Leu	Val	Lys	Ser	Ser	Phe										

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..527



(D) OTHER INFORMATION: / Ceres Seq. ID 1498843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

aaaatccgaa aaagaccaat caatcctttc tccctgaaat ggcggcggct ctgcagacga	60
atatccggac ggtcaagggt cccgctacgt tcagagctgt aagtaaacag tcattggcac	120
ccttttagagt aagatgtgct gttgcttccc ctgggaaaaa acgatacacc atcactctcc	180
ttcccgagaga cggcatcggt cccgaggttg tctccattgc caaaaatgtg cttcagcaag	240
ctggatcttt ggaagggtgtg gaatttaact tccgtgagat gccattgga ggagctgctt	300
tggatttggt cggagtgtcc ttgccggagg agactatctc agctgcaaaa gaatcagatg	360
cagtgttct tggagccatt ggaggttaca aatgggataa caatgaaaaa catctgaggc	420
ctgagaaggg gttacttcag attcgtgcag ctctcaaagt ctttgcaaat ctgagacctg	480
ctacagtctt cccacagtta gtggatgctt ccaccttaaa gagagag	

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

Asn Pro Lys Lys Thr Asn Gln Ser Phe Leu Pro Glu Met Ala Ala Ala	
1 5 10 15	
Leu Gln Thr Asn Ile Arg Thr Val Lys Val Pro Ala Thr Phe Arg Ala	
20 25 30	
Val Ser Lys Gln Ser Leu Ala Pro Phe Arg Val Arg Cys Ala Val Ala	
35 40 45	
Ser Pro Gly Lys Lys Arg Tyr Thr Ile Thr Leu Leu Pro Gly Asp Gly	
50 55 60	
Ile Gly Pro Glu Val Val Ser Ile Ala Lys Asn Val Leu Gln Gln Ala	
65 70 75 80	
Gly Ser Leu Glu Gly Val Glu Phe Asn Phe Arg Glu Met Pro Ile Gly	
85 90 95	
Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro Glu Glu Thr Ile	
100 105 110	
Ser Ala Ala Lys Glu Ser Asp Ala Val Leu Leu Gly Ala Ile Gly Gly	
115 120 125	
Tyr Lys Trp Asp Asn Asn Glu Lys His Leu Arg Pro Glu Lys Gly Leu	
130 135 140	
Leu Gln Ile Arg Ala Ala Leu Lys Val Phe Ala Asn Leu Arg Pro Ala	
145 150 155 160	
Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu Lys Arg Glu	
165 170 175	

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

Met Ala Ala Ala Leu Gln Thr Asn Ile Arg Thr Val Lys Val Pro Ala	
1 5 10 15	
Thr Phe Arg Ala Val Ser Lys Gln Ser Leu Ala Pro Phe Arg Val Arg	
20 25 30	

Cys Ala Val Ala Ser Pro Gly Lys Lys Arg Tyr Thr Ile Thr Leu Leu  
35 40 45  
Pro Gly Asp Gly Ile Gly Pro Glu Val Val Ser Ile Ala Lys Asn Val  
50 55 60  
Leu Gln Gln Ala Gly Ser Leu Glu Gly Val Glu Phe Asn Phe Arg Glu  
65 70 75 80  
Met. Pro Ile Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro  
85 90 95  
Glu Glu Thr Ile Ser Ala Ala Lys Glu Ser Asp Ala Val Leu Leu Gly  
100 105 110  
Ala Ile Gly Gly Tyr Lys Trp Asp Asn Asn Glu Lys His Leu Arg Pro  
115 120 125  
Glu Lys Gly Leu Leu Gln Ile Arg Ala Ala Leu Lys Val Phe Ala Asn  
130 135 140  
Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu  
145 150 155 160  
Lys Arg Glu

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

aaacccaaac atttttccgat tttccccgac tttctccgac gatgcatgg cgatagcgat	60
ggtgattccg gtgacttatg ctccgacgat tgacacgac atttgaggca gtctcctttg	120
tccagatttt ctcttcaac ctctttctct tgcttaccga ccaaattcat catctttgaa	180
actgcttcat ccctttcgct ttggtgattc tgaagactcc gctttatacc cattttgatc	240
tggagaagga tatagatgaa gtgctacagt cgcatactgt ttattcaaat gtttcgaaag	300
gagttcttgc aaaatcgaaa gacttgatga agtcgtttgg atcagatgat catacgaaaa	360
tatgcatcga tattttggag aaaggagagc ttcaagttgc tggaaaagaa agagaatcac	420
agttctcaag ccagtttcgg gatatagcaa cgattgttat gcagaaaact atcaaccctg	480
aaacacaacg accittatacc atcagcatgg tagagcgcct aatgcatgaa attcattttg	540
ctgttgatcc tcatagtaat tccaagaagc aggcaactga tgtcatccgt gagctgcaaa	600
agcacttccc tataaagcgt tctccaatga gactgcgtct tactgttcct gttcaaaatt	660
tcccctcgct tctggagaag ctaaaagaat gggatggtag tgttgctctc aaagacgaat	720
ctggaacaca gatgtccact gtctgcgaga tggaaaccgg cctattccga gagtgtgatt	780
cccattgtgag gagtatccag ggaagactag aaatactcgc tgtatcagtt catgcagaag	840
gtgacacaag catggatcat tacgatgagc atgatgatat ggcattgcaa acccacaagc	900
cgttgttacc tgctgagact gagactaagg atttgaccga tcccgtcgtt gaacttagca	960
agaaaactgca gaagcaagag ataagtacta cagataacat aaagcaagaa ggtggagaag	1020
aaaagaaggg gaccaagtgc agcacttgca acacgttcgt tggagaggct aagcaataca	1080
gagagcactg taagagtgat tggcacaac acaaccttaa gcgtaagact cggaaactcc	1140
ctcctattag tgctgacgaa tgcattgtct agattgacat ggacgactct agagcagatt	1200
tgaagacta ctctttctga aactacaatt ttctcctttt gtgcttttaa ttttgtcaat	1260
gtgttaaata tcgtagtcatt atgtgagtat gaatacacia aacttgtgga atgaaatttt	1320
gcgcaaaact taagagtaaa aacttgtgtt taagag	

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1498847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

Met	Lys	Ser	Phe	Gly	Ser	Asp	Asp	His	Thr	Lys	Ile	Cys	Ile	Asp	Ile
1				5					10					15	
Leu	Glu	Lys	Gly	Glu	Leu	Gln	Val	Ala	Gly	Lys	Glu	Arg	Glu	Ser	Gln
			20					25					30		
Phe	Ser	Ser	Gln	Phe	Arg	Asp	Ile	Ala	Thr	Ile	Val	Met	Gln	Lys	Thr
		35					40					45			
Ile	Asn	Pro	Glu	Thr	Gln	Arg	Pro	Tyr	Thr	Ile	Ser	Met	Val	Glu	Arg
	50					55					60				
Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His	Ser	Asn	Ser	Lys
65					70					75					80
Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys	His	Phe	Pro	Ile
			85					90						95	
Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro	Val	Gln	Asn	Phe
			100					105					110		
Pro	Ser	Leu	Leu	Glu	Lys	Leu	Lys	Glu	Trp	Asp	Gly	Ser	Val	Val	Ser
		115					120					125			
Lys	Asp	Glu	Ser	Gly	Thr	Gln	Met	Ser	Thr	Val	Cys	Glu	Met	Glu	Pro
	130					135					140				
Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser	Ile	Gln	Gly	Arg
145					150					155					160
Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly	Asp	Thr	Ser	Met
			165					170						175	
Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln	Thr	His	Lys	Pro
		180						185					190		
Leu	Leu	Pro	Ala	Glu	Thr	Glu	Thr	Lys	Asp	Leu	Thr	Asp	Pro	Val	Val
		195					200					205			
Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser	Thr	Thr	Asp	Asn
	210					215					220				
Ile	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr	Lys	Cys	Ser	Thr
225					230					235					240
Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg	Glu	His	Cys	Lys
			245						250					255	
Ser	Asp	Trp	His	Lys	His	Asn	Leu	Lys	Arg	Lys	Thr	Arg	Lys	Leu	Pro
		260						265					270		
Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp	Met	Asp	Asp	Ser
		275					280					285			
Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe							
	290					295									

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1498848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met	Gln	Lys	Thr	Ile	Asn	Pro	Glu	Thr	Gln	Arg	Pro	Tyr	Thr	Ile	Ser
1				5					10					15	
Met	Val	Glu	Arg	Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His
		20						25					30		
Ser	Asn	Ser	Lys	Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys
		35				40						45			
His	Phe	Pro	Ile	Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro

50	55	60
Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly		
65	70	75
Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys		80
	85	90
Glu Met Glu Pro Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser		95
	100	105
Ile Gln Gly Arg Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly		110
	115	120
Asp Thr Ser Met Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln		125
	130	135
Thr His Lys Pro Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr		140
145	150	155
Asp Pro Val Val Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser		160
	165	170
Thr Thr Asp Asn Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr		175
	180	185
Lys Cys Ser Thr Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg		190
	195	200
Glu His Cys Lys Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr		205
	210	215
Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp		220
225	230	235
Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr Ser Phe		240
	245	250

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1498849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Met Val Glu Arg Leu Met His Glu Ile His Phe Ala Val Asp Pro His		
1	5	10
Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys		15
	20	25
His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro		30
	35	40
Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly		45
	50	55
Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys		60
65	70	75
Glu Met Glu Pro Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser		80
	85	90
Ile Gln Gly Arg Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly		95
	100	105
Asp Thr Ser Met Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln		110
	115	120
Thr His Lys Pro Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr		125
	130	135
Asp Pro Val Val Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser		140
145	150	155
Thr Thr Asp Asn Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr		160
	165	170
Lys Cys Ser Thr Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg		175
	180	185
		190

Glu His Cys Lys Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr  
195 200 205  
Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp  
210 215 220  
Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr Ser Phe  
225 230 235

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

atatgaacat aacccaatct gaagatcaat cataacctta aaccatctct cataatttta	60
gtattttctat tctcaccacc aaaactcggt gatacatcac accccaactg ttgttactca	120
tgtcctacag atcgatttac cgcactcttc gaccggtact atcatcttcg gtacaatcct	180
ccggttttagg aattggagga ttcaggggac atctcattag ccacttgccc aatgttcggc	240
tattgagctc tgacacgtca tctccggtaa gtgggaataa ccagccagaa aatcctatcc	300
gaacggccga tggtaaagtt atatccactt attgggggtat acctcctact aagatcacta	360
aaccggacgg ttcagcttgg aagtgggaatt gttttcagcc atgggattca taaaaaccgg	420
atgtgtccat tgatgtaact aaacatcata aaccctccaa tttcactgac aaattcgcat	480
attggaccgt tcaaactctg aaaataaccgg ttcaactatt ttttcagagg aagcacatgt	540
gccatgcat gttgctagag acggtggctg cggtgccggg aatggtcggg tggatgcttt	600
tgcacttgaa atctctccgg aggttcgaac atagcggggg atggatcaaa gctttgctcg	660
aagaggctga gaacgagcgt atgcatctca tgactttcat cgaactttca caacccaaat	720
ggtacgaacg agcgattgtg ttcacggtcc aaggcgtttt cttcaacgca tatcttctgg	780
cttatgtaat ttcacccaaa ctgtctcatc gtatcactgg atacttagaa gaagaggctg	840
taaattctta cactgaattt ctcaaagaca ttgatgccgg aaaattcgaa aactcgccag	900
ctccagccat cgcaatcgat tactggcggg tgccataaaga tgcaacgctt agggatgtgg	960
tttatgttat acgagctgac gaagctcacc accgtgatat taaccactat gcttcggata	1020
tacaattcaa aggacatgaa ctcaaggaag ctccggctcc tattggatat cattaagat	1080
tatgtgacaa agtcacaaag ctgtgtatac atctatgaac atatgttgtt gtggatctcc	1140
atgatatttt tattttatgt tttcgattta tttaaaactg ttattcgttt ttattagctc	1200
aatatggata tttaaacctt attattttgt tacgatttat gaacatagta ctactcatgt	1260
gtgtgtaaaa gatcatactg cctggacacg aagcggatat ccggaaaaat tataatattt	1320
gttttttgat tcgtttc	

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

Met Ser Tyr Arg Ser Ile Tyr Arg Thr Leu Arg Pro Val Leu Ser Ser	
1 5 10 15	
Ser Val Gln Ser Ser Gly Leu Gly Ile Gly Gly Phe Arg Gly His Leu	
20 25 30	
Ile Ser His Leu Pro Asn Val Arg Leu Leu Ser Ser Asp Thr Ser Ser	
35 40 45	
Pro Val Ser Gly Asn Asn Gln Pro Glu Asn Pro Ile Arg Thr Ala Asp	
50 55 60	

Gly	Lys	Val	Ile	Ser	Thr	Tyr	Trp	Gly	Ile	Pro	Pro	Thr	Lys	Ile	Thr
65					70				75						80
Lys	Pro	Asp	Gly	Ser	Ala	Trp	Lys	Trp	Asn	Cys	Phe	Gln	Pro	Trp	Asp
				85					90					95	
Ser	Tyr	Lys	Pro	Asp	Val	Ser	Ile	Asp	Val	Thr	Lys	His	His	Lys	Pro
			100					105					110		
Ser	Asn	Phe	Thr	Asp	Lys	Phe	Ala	Tyr	Trp	Thr	Val	Gln	Thr	Leu	Lys
		115					120					125			
Ile	Pro	Val	Gln	Leu	Phe	Phe	Gln	Arg	Lys	His	Met	Cys	His	Ala	Met
	130					135					140				
Leu	Leu	Glu	Thr	Val	Ala	Val	Pro	Gly	Met	Val	Gly	Trp	Met	Leu	
145					150				155					160	
Leu	His	Leu	Lys	Ser	Leu	Arg	Arg	Phe	Glu	His	Ser	Gly	Gly	Trp	Ile
				165					170					175	
Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met	Thr
			180					185					190		
Phe	Ile	Glu	Leu	Ser	Gln	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Ile	Val	Phe
		195					200					205			
Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Ala	Tyr	Val	Ile
	210					215					220				
Ser	Pro	Lys	Leu	Ala	His	Arg	Ile	Thr	Gly	Tyr	Leu	Glu	Glu	Glu	Ala
225					230					235					240
Val	Asn	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Ile	Asp	Ala	Gly	Lys	Phe
				245					250					255	
Glu	Asn	Ser	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu	Pro
			260					265					270		
Lys	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Tyr	Val	Ile	Arg	Ala	Asp	Glu
		275					280					285			
Ala	His	His	Arg	Asp	Ile	Asn	His	Tyr	Ala	Ser	Asp	Ile	Gln	Phe	Lys
	290					295					300				
Gly	His	Glu	Leu	Lys	Glu	Ala	Pro	Ala	Pro	Ile	Gly	Tyr	His		
305					310					315					

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

Met	Cys	His	Ala	Met	Leu	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met
1				5					10					15	
Val	Gly	Trp	Met	Leu	Leu	His	Leu	Lys	Ser	Leu	Arg	Arg	Phe	Glu	His
			20					25					30		
Ser	Gly	Gly	Trp	Ile	Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg
		35					40					45			
Met	His	Leu	Met	Thr	Phe	Ile	Glu	Leu	Ser	Gln	Pro	Lys	Trp	Tyr	Glu
	50					55					60				
Arg	Ala	Ile	Val	Phe	Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe
65					70					75					80
Leu	Ala	Tyr	Val	Ile	Ser	Pro	Lys	Leu	Ala	His	Arg	Ile	Thr	Gly	Tyr
			85					90						95	
Leu	Glu	Glu	Glu	Ala	Val	Asn	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Ile
			100					105					110		
Asp	Ala	Gly	Lys	Phe	Glu	Asn	Ser	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp
		115					120					125			
Tyr	Trp	Arg	Leu	Pro	Lys	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Tyr	Val

130	135	140
Ile Arg Ala Asp Glu Ala His His Arg Asp	Ile Asn His Tyr Ala Ser	
145	150	155
Asp Ile Gln Phe Lys Gly His Glu Leu Lys	Glu Ala Pro Ala Pro Ile	160
	165	170
		175

Gly Tyr His

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

Met	Leu	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met	Val	Gly	Trp	Met
1			5						10					15	
Leu	Leu	His	Leu	Lys	Ser	Leu	Arg	Arg	Phe	Glu	His	Ser	Gly	Gly	Trp
			20					25					30		
Ile	Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met
		35					40					45			
Thr	Phe	Ile	Glu	Leu	Ser	Gln	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Ile	Val
		50				55					60				
Phe	Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Ala	Tyr	Val
65					70					75				80	
Ile	Ser	Pro	Lys	Leu	Ala	His	Arg	Ile	Thr	Gly	Tyr	Leu	Glu	Glu	Glu
			85						90					95	
Ala	Val	Asn	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Ile	Asp	Ala	Gly	Lys
		100							105				110		
Phe	Glu	Asn	Ser	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu
		115					120					125			
Pro	Lys	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Tyr	Val	Ile	Arg	Ala	Asp
		130					135					140			
Glu	Ala	His	His	Arg	Asp	Ile	Asn	His	Tyr	Ala	Ser	Asp	Ile	Gln	Phe
145				150						155				160	
Lys	Gly	His	Glu	Leu	Lys	Glu	Ala	Pro	Ala	Pro	Ile	Gly	Tyr	His	
			165					170						175	

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1159 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1159

(D) OTHER INFORMATION: / Ceres Seq. ID 1498858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

atagtttgggt	acttttagtgt	tgactgtttga	ccgcgacgaa	tccgtcggaa	accggaatca	60
ccatggatttt	tccctccgacg	aagcttgatt	atcatgtaga	catgttcaat	cttcagtctc	120
attccagatt	tctctcctta	tttaaggcgc	aagatggacg	catagctcta	atactagaat	180
caacggtggt	tcatccacaa	gggtgtggcc	agcgcgcaga	caccggttta	attgttttct	240
ccggttcgga	tttgaaattt	tccgttcaag	atgttcgatc	gaaagacgga	attgttctcc	300
attacggagt	tttcgaaggt	tcgaatcctg	aaagtggaa	tgatagtga	aaagggaaag	360
aagtttactt	aactgttgat	gaatcaaggc	gtaaactcaa	ttccaggttg	cactcagctg	420
gacacttgct	agatatgtgt	atgcagaaa	ttgggttagg	acatttgagg	cctggaaaag	480

```
ggtaccattt tctgacggt ccttttgtgg aatacaaagg aagcgtccca caggaggagt 540
ttcaggtgaa gcagaaagag ttggaggcag aagctaacga actgatatcc aaaggaggaa 600
aggtttatgc tgctatatgg ccctatgaag aggcatctgt gctctgtggg ggcagtcttc 660
ctgattatat ttccaagggc agcaactccc ggatcataaa attaggtgac agccccgggt 720
gtccatgtgg tggaacccat gtctccaatt tatctgatat cataagcatg aagatcacac 780
agatgagaac aaagaaagga atgacgaaag ttttctacac cattgcatct tgaaactctt 840
atgggttcca gtttctatac ggtagatata caataagtca aggaaggaa tgatagttag 900
gacgactgtt ttcacaggtt ggcttcaaca gcaagcagct tctcctgtgc ctcaacagcc 960
acaaatcagt atttgtgggt atttatcaat ctcttaaagc actctctcta ttattgataa 1020
gtcgtatatg atatatgata ttgatgtgat attttcttcc actcagcctc ttaattagta 1080
ttaatatatt gactcttggg attgtagaat cgtaccgggc atttggctct agatttttat 1140
tcatgcatcg gtttgattt
```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```
Met Asp Phe Pro Pro Thr Lys Leu Asp Tyr His Val Asp Met Phe Asn
1          5          10          15
Leu Gln Ser His Ser Arg Phe Leu Ser Leu Phe Lys Ala Gln Asp Gly
20          25          30
Arg Ile Ala Leu Ile Leu Glu Ser Thr Val Phe His Pro Gln Gly Gly
35          40          45
Gly Gln Pro Ser Asp Thr Gly Leu Ile Val Phe Ser Gly Ser Asp Leu
50          55          60
Lys Phe Ser Val Gln Asp Val Arg Ser Lys Asp Gly Ile Val Leu His
65          70          75          80
Tyr Gly Val Phe Glu Gly Ser Asn Pro Glu Ser Gly Ile Asp Ser Glu
85          90          95
Lys Gly Lys Glu Val Tyr Leu Thr Val Asp Glu Ser Arg Arg Lys Leu
100          105          110
Asn Ser Arg Leu His Ser Ala Gly His Leu Leu Asp Met Cys Met Gln
115          120          125
Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly Tyr His Phe Pro
130          135          140
Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro Gln Glu Glu Phe
145          150          155          160
Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Ala Asn Glu Leu Ile Ser
165          170          175
Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr Glu Glu Ala Ser
180          185          190
Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser Lys Gly Ser Thr
195          200          205
Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys Pro Cys Gly Gly
210          215          220
Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met Lys Ile Thr Gln
225          230          235          240
Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr Thr Ile Ala Ser
245          250          255
```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..243
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Met	Phe	Asn	Leu	Gln	Ser	His	Ser	Arg	Phe	Leu	Ser	Leu	Phe	Lys	Ala
1			5					10						15	
Gln	Asp	Gly	Arg	Ile	Ala	Leu	Ile	Leu	Glu	Ser	Thr	Val	Phe	His	Pro
			20					25					30		
Gln	Gly	Gly	Gly	Gln	Pro	Ser	Asp	Thr	Gly	Leu	Ile	Val	Phe	Ser	Gly
			35					40					45		
Ser	Asp	Leu	Lys	Phe	Ser	Val	Gln	Asp	Val	Arg	Ser	Lys	Asp	Gly	Ile
			50					55				60			
Val	Leu	His	Tyr	Gly	Val	Phe	Glu	Gly	Ser	Asn	Pro	Glu	Ser	Gly	Ile
65							70				75				80
Asp	Ser	Glu	Lys	Gly	Lys	Glu	Val	Tyr	Leu	Thr	Val	Asp	Glu	Ser	Arg
							85				90				95
Arg	Lys	Leu	Asn	Ser	Arg	Leu	His	Ser	Ala	Gly	His	Leu	Leu	Asp	Met
			100					105						110	
Cys	Met	Gln	Lys	Val	Gly	Leu	Gly	His	Leu	Glu	Pro	Gly	Lys	Gly	Tyr
			115					120					125		
His	Phe	Pro	Asp	Gly	Pro	Phe	Val	Glu	Tyr	Lys	Gly	Ser	Val	Pro	Gln
			130					135				140			
Glu	Glu	Phe	Gln	Val	Lys	Gln	Lys	Glu	Leu	Glu	Ala	Glu	Ala	Asn	Glu
145							150				155				160
Leu	Ile	Ser	Lys	Gly	Gly	Lys	Val	Tyr	Ala	Ala	Ile	Leu	Pro	Tyr	Glu
							165				170				175
Glu	Ala	Ser	Val	Leu	Cys	Gly	Gly	Ser	Leu	Pro	Asp	Tyr	Ile	Ser	Lys
			180					185					190		
Gly	Ser	Thr	Pro	Arg	Ile	Ile	Lys	Leu	Gly	Asp	Ser	Pro	Gly	Cys	Pro
			195				200					205			
Cys	Gly	Gly	Thr	His	Val	Ser	Asn	Leu	Ser	Asp	Ile	Ile	Ser	Met	Lys
			210				215					220			
Ile	Thr	Gln	Met	Arg	Thr	Lys	Lys	Gly	Met	Thr	Lys	Val	Phe	Tyr	Thr
225						230				235					240
Ile	Ala	Ser													

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..132
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

Met	Cys	Met	Gln	Lys	Val	Gly	Leu	Gly	His	Leu	Glu	Pro	Gly	Lys	Gly
1			5					10						15	
Tyr	His	Phe	Pro	Asp	Gly	Pro	Phe	Val	Glu	Tyr	Lys	Gly	Ser	Val	Pro
			20					25					30		
Gln	Glu	Glu	Phe	Gln	Val	Lys	Gln	Lys	Glu	Leu	Glu	Ala	Glu	Ala	Asn
			35					40					45		
Glu	Leu	Ile	Ser	Lys	Gly	Gly	Lys	Val	Tyr	Ala	Ala	Ile	Leu	Pro	Tyr
			50				55					60			

Glu Glu Ala Ser Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser  
65 70 75 80  
Lys Gly Ser Thr Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys  
85 90 95  
Pro Cys Gly Gly Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met  
100 105 110  
Lys Ile Thr Gln Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr  
115 120 125  
Thr Ile Ala Ser  
130

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

cttcttcgta	cgtaattaa	aatctgaaga	aacaaaatcg	tgaaatcgat	ctctttaagc	60
atcatctagg	gttcatcact	gaaatcaaaa	atgcaattaa	atctctacaa	aatctctcag	120
atctaattcc	agatcggtgt	tggtttcttc	tccgtaaaacc	aatcccacat	atgaattaaa	180
gattcgatct	cgaaatcggt	ggcttttgtt	gttggtgcat	tcttcgggtga	tggtcccgac	240
tcggattcta	accagagacg	aagagcttgg	tggtatttca	gacgatgatg	attctccatc	300
gggtaaaaga	tctaaacttg	atcgcttccc	tcttagccgt	tggaactcg	ccgtttctct	360
cgggtgtctt	ctcgtcttct	cctctggact	ctgttgatc	tacatgacca	tgctgtctgc	420
tgaatttggc	aaactcaaac	ttccaagaaa	gcctcgctga	tctccgtttg	ctcaaagata	480
atctagcvaa	ttatgcgrat	gagtatccgg	cgcagttttg	ttttagggtg	ttgtgcaacg	540
tacattttta	tgcagacctt	tatgattcca	gggactatct	tcatgtcact	attagctgga	600
gctctctttg	gagtattcaa	aggtgtgtgc	ttggttggtt	tcaatgcaac	agcaggagct	660
acctcggtgt	tctttttgtc	gaaattgatt	ggtcgaccgt	tgattacttg	gctatggcct	720
gacaaattaa	gattctttca	agcagagatt	agtaagcgta	gagataagct	tctgaactat	780
atgttgtttt	tgaggataac	accaactctg	ccaaatcttt	ttatcaatct	tgcatctcct	840
atagtcgatg	tacctttcca	tgtcttcttt	ttggcgacat	tgattgggtc	cattcctgca	900
gcttatataa	ctgtcagagc	tggccttgct	acttgagat	ctcaaatacg	tgaaagatct	960
gtatgatttc	aagacattgt	cagtgccttt	cctcatcggt	tttatctcta	ttcttccaac	1020
gatactgaaa	agaaagaaga	ttgttgtaata	gccaggggaga	agcatcttta	caatacacat	1080
ggcctaacat	tcaatgccat	acagagaaca	agaatacact	taacttggtt	agaggacaca	1140
acagaacaaa	acttctgatt	cgtttacttg	tcacttgctg	taacgattcg	ttgatagttt	1200
ttttgttgtc	atattttctt	actatttggc	aagtagaggt	tgagaagaaa	ttacagaaat	1260
aatacaattt	ttgtacaag	acgagagacc	atgaaatatt	ttggttct		

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

Met Xaa Met Ser Ile Arg Arg Ser Phe Val Leu Gly Tyr Cys Ala Thr  
1 5 10 15  
Tyr Ile Phe Met Gln Thr Phe Met Ile Pro Gly Thr Ile Phe Met Ser  
20 25 30  
Leu Leu Ala Gly Ala Leu Phe Gly Val Phe Lys Gly Val Val Leu Val

(2) INFORMATION FOR SEQ ID NO:702:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1498876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1498877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met	Gln	Thr	Phe	Met	Ile	Pro	Gly	Thr	Ile	Phe	Met	Ser	Leu	Leu	Ala
1				5					10					15	

Gly Ala Leu Phe Gly Val Phe Lys Gly Val Val Leu Val Val Phe Asn  
20 25 30  
Ala Thr Ala Gly Ala Thr Ser Cys Phe Phe Leu Ser Lys Leu Ile Gly  
35 40 45  
Arg Pro Leu Ile Thr Trp Leu Trp Pro Asp Lys Leu Arg Phe Phe Gln  
50 55 60  
Ala Glu Ile Ser Lys Arg Arg Asp Lys Leu Leu Asn Tyr Met Leu Phe  
65 70 75 80  
Leu Arg Ile Thr Pro Thr Leu Pro Asn Leu Phe Ile Asn Leu Ala Ser  
85 90 95  
Pro Ile Val Asp Val Pro Phe His Val Phe Phe Leu Ala Thr Leu Ile  
100 105 110  
Gly Leu Ile Pro Ala Ala Tyr Ile Thr Val Arg Ala Gly Leu Ala Thr  
115 120 125  
Trp Arg Ser Gln Ile Gly Glu Arg Ser Val  
130 135

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1603
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

ctttttgcga	tcaatcgaaa	gaaaacaaaa	aatggggaaa	gttccgtcgt	cgtttcgtag	60
tataccggcg	atattattgg	tcagaaaaac	aacaccatct	cctccagcgc	cgccgcgaga	120
ttttcgcaac	agaaccgccg	tgggaggaga	ttcagccaaa	cttccccaca	atactcaagc	180
ccctcgcgag	ccctccttga	ggaatccatt	caagtcacca	aatctctcag	acgctaaaag	240
cctcttcaat	tcaatcgccg	ccacttcacg	aatcccactc	gatctcaa	tccacaactc	300
tgttctccaa	tcctatgctt	caatcgccgt	cgtcgacgat	acggtgaaat	tctttcagca	360
tattatgaaa	tcgcagccta	atttcaggcc	gggacgttca	acgttcctta	tcttgctttc	420
acatgcttgt	agagctcctg	attcgctcgt	ttcgaatggt	catagagttc	ttaatctcat	480
ggttaataat	ggtttagagc	ctgatcaagt	aactaccgat	atcgcggtga	ggtctctttg	540
cgaaacgggt	cgggttgatg	aagctaagga	tttgatgaag	gagctcactg	agaaacactc	600
tcctccggat	acataacttt	ataactttct	actgaagcat	ttgtgcaaat	gcaaagatct	660
tcattgttgt	tatgagtttg	ttgatgagat	gagagatgat	ttcgatgtta	agccggatct	720
tgtttagcttc	actatcttga	ttgataatgt	ttgtaactct	aagaacttga	gggaggcaat	780
gtatctagtt	agtaagttag	gtaatgctgg	gtttaagccg	gattgtttcc	tctataaacac	840
gattatgaaa	ggtttttgca	caactgagtaa	agggagttag	gcggttggtg	tgtataagaa	900
aatgaaggaa	gaagggtgtg	agccagatca	gattacttac	aatactttga	tattttggact	960
gtcgaaagct	ggtagagttg	aggaagctag	gatgtatttg	aaaactatgg	ttgatgcggg	1020
gtatgagccg	gatactgcta	cttacacatc	actgatgaat	ggaatgtgta	gaaaagggtga	1080
gtcttttaggt	gcgttgagtt	tgttagaaga	aatggaagca	agagggtgtg	ctccaaatga	1140
ttgtacttat	aatacttttg	ttcatggatt	gtgtaaagca	aggttgatgg	ataaagggat	1200
ggagttatat	gaaatgatga	aatcaagtgg	tgtaaagctt	gagagtaatg	gttatgctac	1260
acttgtgagg	tctctgggta	aaagtggcaa	ggtcgcagag	gcttatgaag	tgtttgatta	1320
tgcagttgat	agcaagagtt	tgtcagatgc	ttctgcgtac	tctacacttg	aaactacctt	1380
gaaatgggtg	aaaaaagcta	agaacaagg	cttggttcca	taaatggtat	cctctagctg	1440
agctttaccg	actttcttct	ttatgcaagt	ccatatttca	tttttgaagt	agtgttactc	1500
caaaagcaat	gaatttggtt	cgaaatatgc	tggttcgattc	ttaagggacc	agcagtgatt	1560
tataatagta	actttgttgg	taatatattg	gtcacttgag	att		

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1498879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

Phe	Leu	Arg	Ser	Ile	Glu	Arg	Lys	Gln	Lys	Met	Gly	Lys	Val	Pro	Ser
1				5					10					15	
Ser	Phe	Arg	Ser	Ile	Pro	Ala	Asn	Leu	Val	Arg	Lys	Thr	Thr	Pro	
			20					25				30			
Ser	Pro	Pro	Ala	Pro	Pro	Arg	Asp	Phe	Arg	Asn	Arg	Thr	Ala	Val	Gly
			35				40					45			
Gly	Asp	Ser	Ala	Lys	Leu	Pro	His	Asn	Thr	Gln	Ala	Pro	Arg	Glu	Pro
	50					55				60					
Ser	Leu	Arg	Asn	Pro	Phe	Lys	Ser	Pro	Asn	Leu	Ser	Asp	Ala	Lys	Ser
65					70				75					80	
Leu	Phe	Asn	Ser	Ile	Ala	Ala	Thr	Ser	Arg	Ile	Pro	Leu	Asp	Leu	Lys
				85					90					95	
Phe	His	Asn	Ser	Val	Leu	Gln	Ser	Tyr	Ala	Ser	Ile	Ala	Val	Val	Asp
			100					105					110		
Asp	Thr	Val	Lys	Phe	Phe	Gln	His	Ile	Met	Lys	Ser	Gln	Pro	Asn	Phe
			115				120					125			
Arg	Pro	Gly	Arg	Ser	Thr	Phe	Leu	Ile	Leu	Leu	Ser	His	Ala	Cys	Arg
	130					135					140				
Ala	Pro	Asp	Ser	Ser	Ile	Ser	Asn	Val	His	Arg	Val	Leu	Asn	Leu	Met
145					150					155				160	
Val	Asn	Asn	Gly	Leu	Glu	Pro	Asp	Gln	Val	Thr	Thr	Asp	Ile	Ala	Val
				165					170					175	
Arg	Ser	Leu	Cys	Glu	Thr	Gly	Arg	Val	Asp	Glu	Ala	Lys	Asp	Leu	Met
			180					185					190		
Lys	Glu	Leu	Thr	Glu	Lys	His	Ser	Pro	Pro	Asp	Thr	Tyr	Thr	Tyr	Asn
	195						200					205			
Phe	Leu	Leu	Lys	His	Leu	Cys	Lys	Cys	Lys	Asp	Leu	His	Val	Val	Tyr
	210					215					220				
Glu	Phe	Val	Asp	Glu	Met	Arg	Asp	Asp	Phe	Asp	Val	Lys	Pro	Asp	Leu
225					230					235				240	
Val	Ser	Phe	Thr	Ile	Leu	Ile	Asp	Asn	Val	Cys	Asn	Ser	Lys	Asn	Leu
				245					250					255	
Arg	Glu	Ala	Met	Tyr	Leu	Val	Ser	Lys	Leu	Gly	Asn	Ala	Gly	Phe	Lys
			260					265					270		
Pro	Asp	Cys	Phe	Leu	Tyr	Asn	Thr	Ile	Met	Lys	Gly	Phe	Cys	Thr	Leu
		275				280						285			
Ser	Lys	Gly	Ser	Glu	Ala	Val	Gly	Val	Tyr	Lys	Lys	Met	Lys	Glu	Glu
	290					295					300				
Gly	Val	Glu	Pro	Asp	Gln	Ile	Thr	Tyr	Asn	Thr	Leu	Ile	Phe	Gly	Leu
305					310					315				320	
Ser	Lys	Ala	Gly	Arg	Val	Glu	Glu	Ala	Arg	Met	Tyr	Leu	Lys	Thr	Met
				325					330					335	
Val	Asp	Ala	Gly	Tyr	Glu	Pro	Asp	Thr	Ala	Thr	Tyr	Thr	Ser	Leu	Met
			340					345					350		
Asn	Gly	Met	Cys	Arg	Lys	Gly	Glu	Ser	Leu	Gly	Ala	Leu	Ser	Leu	Leu
		355				360						365			
Glu	Glu	Met	Glu	Ala	Arg	Gly	Cys	Ala	Pro	Asn	Asp	Cys	Thr	Tyr	Asn
	370					375					380				
Thr	Leu	Leu	His	Gly	Leu	Cys	Lys	Ala	Arg	Leu	Met	Asp	Lys	Gly	Met
385					390					395				400	
Glu	Leu	Tyr	Glu	Met	Met	Lys	Ser	Ser	Gly	Val	Lys	Leu	Glu	Ser	Asn
			405						410					415	
Gly	Tyr	Ala	Thr	Leu	Val	Arg	Ser	Leu	Val	Lys	Ser	Gly	Lys	Val	Ala
			420					425					430		
Glu	Ala	Tyr	Glu	Val	Phe	Asp	Tyr	Ala	Val	Asp	Ser	Lys	Ser	Leu	Ser

435 440 445  
Asp Ala Ser Ala Tyr Ser Thr Leu Glu Thr Thr Leu Lys Trp Leu Lys  
450 455 460  
Lys Ala Lys Glu Gln Gly Leu Val Pro  
465 470

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met Gly Lys Val Pro Ser Ser Phe Arg Ser Ile Pro Ala Asn Leu Leu  
1 5 10 15  
Val Arg Lys Thr Thr Pro Ser Pro Pro Ala Pro Pro Arg Asp Phe Arg  
20 25 30  
Asn Arg Thr Ala Val Gly Gly Asp Ser Ala Lys Leu Pro His Asn Thr  
35 40 45  
Gln Ala Pro Arg Glu Pro Ser Leu Arg Asn Pro Phe Lys Ser Pro Asn  
50 55 60  
Leu Ser Asp Ala Lys Ser Leu Phe Asn Ser Ile Ala Ala Thr Ser Arg  
65 70 75 80  
Ile Pro Leu Asp Leu Lys Phe His Asn Ser Val Leu Gln Ser Tyr Ala  
85 90 95  
Ser Ile Ala Val Val Asp Asp Thr Val Lys Phe Phe Gln His Ile Met  
100 105 110  
Lys Ser Gln Pro Asn Phe Arg Pro Gly Arg Ser Thr Phe Leu Ile Leu  
115 120 125  
Leu Ser His Ala Cys Arg Ala Pro Asp Ser Ser Ile Ser Asn Val His  
130 135 140  
Arg Val Leu Asn Leu Met Val Asn Asn Gly Leu Glu Pro Asp Gln Val  
145 150 155 160  
Thr Thr Asp Ile Ala Val Arg Ser Leu Cys Glu Thr Gly Arg Val Asp  
165 170 175  
Glu Ala Lys Asp Leu Met Lys Glu Leu Thr Glu Lys His Ser Pro Pro  
180 185 190  
Asp Thr Tyr Thr Tyr Asn Phe Leu Leu Lys His Leu Cys Lys Cys Lys  
195 200 205  
Asp Leu His Val Val Tyr Glu Phe Val Asp Glu Met Arg Asp Asp Phe  
210 215 220  
Asp Val Lys Pro Asp Leu Val Ser Phe Thr Ile Leu Ile Asp Asn Val  
225 230 235 240  
Cys Asn Ser Lys Asn Leu Arg Glu Ala Met Tyr Leu Val Ser Lys Leu  
245 250 255  
Gly Asn Ala Gly Phe Lys Pro Asp Cys Phe Leu Tyr Asn Thr Ile Met  
260 265 270  
Lys Gly Phe Cys Thr Leu Ser Lys Gly Ser Glu Ala Val Gly Val Tyr  
275 280 285  
Lys Lys Met Lys Glu Glu Gly Val Glu Pro Asp Gln Ile Thr Tyr Asn  
290 295 300  
Thr Leu Ile Phe Gly Leu Ser Lys Ala Gly Arg Val Glu Glu Ala Arg  
305 310 315 320  
Met Tyr Leu Lys Thr Met Val Asp Ala Gly Tyr Glu Pro Asp Thr Ala  
325 330 335  
Thr Tyr Thr Ser Leu Met Asn Gly Met Cys Arg Lys Gly Glu Ser Leu  
340 345 350

Gly	Ala	Leu	Ser	Leu	Leu	Glu	Glu	Met	Glu	Ala	Arg	Gly	Cys	Ala	Pro
		355						360					365		
Asn	Asp	Cys	Thr	Tyr	Asn	Thr	Leu	Leu	His	Gly	Leu	Cys	Lys	Ala	Arg
		370					375				380				
Leu	Met	Asp	Lys	Gly	Met	Glu	Leu	Tyr	Glu	Met	Met	Lys	Ser	Ser	Gly
	385					390				395					400
Val	Lys	Leu	Glu	Ser	Asn	Gly	Tyr	Ala	Thr	Leu	Val	Arg	Ser	Leu	Val
				405					410					415	
Lys	Ser	Gly	Lys	Val	Ala	Glu	Ala	Tyr	Glu	Val	Phe	Asp	Tyr	Ala	Val
			420					425					430		
Asp	Ser	Lys	Ser	Leu	Ser	Asp	Ala	Ser	Ala	Tyr	Ser	Thr	Leu	Glu	Thr
		435					440					445			
Thr	Leu	Lys	Trp	Leu	Lys	Lys	Ala	Lys	Glu	Gln	Gly	Leu	Val	Pro	
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met	Lys	Ser	Gln	Pro	Asn	Phe	Arg	Pro	Gly	Arg	Ser	Thr	Phe	Leu	Ile
1			5					10						15	
Leu	Leu	Ser	His	Ala	Cys	Arg	Ala	Pro	Asp	Ser	Ser	Ile	Ser	Asn	Val
			20					25					30		
His	Arg	Val	Leu	Asn	Leu	Met	Val	Asn	Asn	Gly	Leu	Glu	Pro	Asp	Gln
		35				40						45			
Val	Thr	Thr	Asp	Ile	Ala	Val	Arg	Ser	Leu	Cys	Glu	Thr	Gly	Arg	Val
	50				55					60					
Asp	Glu	Ala	Lys	Asp	Leu	Met	Lys	Glu	Leu	Thr	Glu	Lys	His	Ser	Pro
	65				70					75				80	
Pro	Asp	Thr	Tyr	Thr	Tyr	Asn	Phe	Leu	Leu	Lys	His	Leu	Cys	Lys	Cys
			85					90					95		
Lys	Asp	Leu	His	Val	Val	Tyr	Glu	Phe	Val	Asp	Glu	Met	Arg	Asp	Asp
		100						105					110		
Phe	Asp	Val	Lys	Pro	Asp	Leu	Val	Ser	Phe	Thr	Ile	Leu	Ile	Asp	Asn
		115				120						125			
Val	Cys	Asn	Ser	Lys	Asn	Leu	Arg	Glu	Ala	Met	Tyr	Leu	Val	Ser	Lys
	130				135					140					
Leu	Gly	Asn	Ala	Gly	Phe	Lys	Pro	Asp	Cys	Phe	Leu	Tyr	Asn	Thr	Ile
	145				150				155					160	
Met	Lys	Gly	Phe	Cys	Thr	Leu	Ser	Lys	Gly	Ser	Glu	Ala	Val	Gly	Val
			165						170					175	
Tyr	Lys	Lys	Met	Lys	Glu	Glu	Gly	Val	Glu	Pro	Asp	Gln	Ile	Thr	Tyr
		180					185						190		
Asn	Thr	Leu	Ile	Phe	Gly	Leu	Ser	Lys	Ala	Gly	Arg	Val	Glu	Glu	Ala
	195					200						205			
Arg	Met	Tyr	Leu	Lys	Thr	Met	Val	Asp	Ala	Gly	Tyr	Glu	Pro	Asp	Thr
	210					215					220				
Ala	Thr	Tyr	Thr	Ser	Leu	Met	Asn	Gly	Met	Cys	Arg	Lys	Gly	Glu	Ser
	225				230				235					240	
Leu	Gly	Ala	Leu	Ser	Leu	Leu	Glu	Glu	Met	Glu	Ala	Arg	Gly	Cys	Ala
			245					250					255		
Pro	Asn	Asp	Cys	Thr	Tyr	Asn	Thr	Leu	Leu	His	Gly	Leu	Cys	Lys	Ala
		260				265						270			
Arg	Leu	Met	Asp	Lys	Gly	Met	Glu	Leu	Tyr	Glu	Met	Met	Lys	Ser	Ser

	275					280						285							
Gly	Val	Lys	Leu	Glu	Ser	Asn	Gly	Tyr	Ala	Thr	Leu	Val	Arg	Ser	Leu				
	290					295						300							
Val	Lys	Ser	Gly	Lys	Val	Ala	Glu	Ala	Tyr	Glu	Val	Phe	Asp	Tyr	Ala				
305					310					315					320				
Val	Asp	Ser	Lys	Ser	Leu	Ser	Asp	Ala	Ser	Ala	Tyr	Ser	Thr	Leu	Glu				
				325					330					335					
Thr	Thr	Leu	Lys	Trp	Leu	Lys	Lys	Ala	Lys	Glu	Gln	Gly	Leu	Val	Pro				
			340					345					350						

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..823
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

taacttctgc	aaaaaaaaatca	atcccgatcc	cgatcaagtt	ttattttccg	attcgcttcc	60
aagttcaatt	caatttcaac	cctaattttg	tttgaaaga	ttaagccatg	ggaggtcacg	120
gtggtttgaa	tattcttcca	cagaagaggt	ggaacgttta	caacttgac	agtccgaaaag	180
gatgaagaag	ctgcggttag	agaagagcag	atcaaacgcg	aggacgctag	aaaaagagat	240
gctgaatctc	gtctcgaagt	gcttcgtaac	gtccgtggtt	tagccctct	caccggaggc	300
agagaagggt	aaggatgaga	cgggtggtgt	ggcggcggct	gttgtaaat	ccacggatgt	360
tgttggtgag	agtgttgaat	cggaaaatgt	atagattggg	atatggagtt	gctggtaaaag	420
gtgtgaagcg	tccttgagaa	acgtaacgat	gaaaatgata	gtgttcgagg	tgagggtgat	480
gatggtggat	gtggtggtta	tgaagctaag	aagaagaaga	tgagtgggaa	gaagagctta	540
aaggagttga	agagggagag	ggttgagaag	gaaagagaga	gagccctttt	catgaaacag	600
agccagagag	cgggtggttt	ttcccggagg	tgagtttttg	gatgaaatta	tacgttattt	660
gcattgggtt	tgtacaagtt	agtagttaac	tgttgttact	tgattcatat	ccaaagtatt	720
ggtttattaa	cgctactcga	tgcttagtgc	tgatagaacc	atgtacatag	tttgagtggt	780
gatagatagt	ttatcagggg	aatcaatagt	ttatcaggtc	ctc		

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Thr	Ser	Ala	Lys	Lys	Ser	Ile	Pro	Ile	Pro	Ile	Lys	Phe	Tyr	Phe	Pro
1			5					10					15		
Ile	Arg	Phe	Gln	Val	Gln	Phe	Asn	Phe	Asn	Pro	Asn	Phe	Val	Trp	Lys
			20				25					30			
Asp															

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..40  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498884  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:  
Met Arg Arg Trp Trp Trp Arg Arg Leu Leu Leu Asn Pro Arg Met Leu  
1                    5                    10                    15  
Leu Trp Arg Val Leu Asn Arg Lys Met Tyr Arg Leu Gly Tyr Gly Val  
                    20                    25                    30  
Ala Gly Lys Gly Val Lys Arg Pro  
                    35                    40

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..37
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Met Ser Gly Lys Lys Ser Leu Lys Glu Leu Lys Arg Glu Arg Val Glu  
1                    5                    10                    15  
Lys Glu Arg Glu Arg Ala Leu Phe Met Lys Gln Ser Gln Arg Ala Gly  
                    20                    25                    30  
Gly Phe Ser Arg Arg  
                    35

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

aaactaagaa	acacccaaga	aaacaaacaa	acttttttaa	aaatgtccgt	ttcaacacat	60
caccaccacg	tggctcctct	cccttacatg	tcaaaaggcc	acatcatccc	tctcctccaa	120
ttcggtcgtc	tcctcctccg	tcaccaccgc	aaagaaccaa	ccatcacccg	caccgttttc	180
accactccca	agaaccaacc	tttcatctca	gacttcctct	cggacacgcc	ggagatcaaa	240
gtcatctctc	tccctttccc	ggaaaacatc	accggaatcc	ctcccggcgt	cgagaacacc	300
gaaaggctcc	catccatgtc	acttttcgtc	cccttcacac	gcgccacgaa	gcttctccaa	360
cctttcttgc	aagaaacact	caagactcct	ccaaaagttt	cgttcatggt	ctctgatgga	420
ttcctctggt	ggacatcgga	gtctgcagct	aagttcaaca	ttccaagatt	tgtctcctac	480
ggcatgaact	cttactccgc	cgctgtctcc	atctctgttt	tcaaacacga	actctttacc	540
gaaccggaaa	gtaaatctga	taccgaaccg	gtcactgtac	cagactttcc	atggatcaag	600
atcaagaagt	gtgatttoga	ccatggcact	accgagccgg	aagaatcagg	tgcagccctc	660
gaactatcta	tggaccaaat	caagtcgacc	accacaagcc	atgggttttt	agtcaatagc	720
ttctacgagc	tcgagtcagc	atttgttgat	tacaacaaca	actctggtga	taaaccaaaag	780
tcgtggtgtg	ttgggccact	gtgtttgaca	gatacctcta	aacaggggag	tgctaaaccg	840
gcttggattc	attggttgga	tcagaagcga	gaggaagggc	gtccgggttt	gtacgtggcg	900
tttggaacgc	aggcagagat	atcgaacaag	cagcttatgg	aactagcttt	cggcttgga	960
gattcaaagg	tgaactttct	gtgggtcaca	agaaaagatg	tggaggagat	tattggagaa	1020
ggattcaacg	atagaataag	agagagtggg	atgatagtga	gagattgggt	ggaccaatgg	1080
gagatattgt	cacatgaaag	tgtcaaaagga	tttttgagcc	attgtgggtg	gaactcagca	1140

caagagagca tatgtgtcgg ggtcccattg ttggcttggc cgatgatggc cgagcaaccg 1200  
ctcaatgcga agatggttgt ggaggagata aaggtgggag taagagttga aacggaagat 1260  
gggagtgtaa aaggttttgt gacaagagag gaactaagtg gaaagattaa agaactgatg 1320  
gaaggagaaa cggggaaaac cgcaagaaag aatgtgaaag aatactcgaa aatggcaaaa 1380  
gcggcttttg tcgaaggac tggttcgtca tggaagaatt tagatatgat tcttaaggac 1440  
ttatgtaaga gtagagattc aaacggtgct agtgagtaga gtgattaaga attgaataac 1500  
tgaaccggtc tacgttt

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1498887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Met	Ser	Val	Ser	Thr	His	His	His	His	Val	Val	Leu	Phe	Pro	Tyr	Met
1			5						10					15	
Ser	Lys	Gly	His	Ile	Ile	Pro	Leu	Leu	Gln	Phe	Gly	Arg	Leu	Leu	Leu
			20					25					30		
Arg	His	His	Arg	Lys	Glu	Pro	Thr	Ile	Thr	Val	Thr	Val	Phe	Thr	Thr
			35				40					45			
Pro	Lys	Asn	Gln	Pro	Phe	Ile	Ser	Asp	Phe	Leu	Ser	Asp	Thr	Pro	Glu
	50					55					60				
Ile	Lys	Val	Ile	Ser	Leu	Pro	Phe	Pro	Glu	Asn	Ile	Thr	Gly	Ile	Pro
65					70					75					80
Pro	Gly	Val	Glu	Asn	Thr	Glu	Arg	Leu	Pro	Ser	Met	Ser	Leu	Phe	Val
				85					90					95	
Pro	Phe	Thr	Arg	Ala	Thr	Lys	Leu	Leu	Gln	Pro	Phe	Phe	Glu	Glu	Thr
			100					105					110		
Leu	Lys	Thr	Leu	Pro	Lys	Val	Ser	Phe	Met	Val	Ser	Asp	Gly	Phe	Leu
			115				120					125			
Trp	Trp	Thr	Ser	Glu	Ser	Ala	Lys	Phe	Asn	Ile	Pro	Arg	Phe	Val	
	130					135				140					
Ser	Tyr	Gly	Met	Asn	Ser	Tyr	Ser	Ala	Ala	Val	Ser	Ile	Ser	Val	Phe
145					150					155					160
Lys	His	Glu	Leu	Phe	Thr	Glu	Pro	Glu	Ser	Lys	Ser	Asp	Thr	Glu	Pro
				165					170					175	
Val	Thr	Val	Pro	Asp	Phe	Pro	Trp	Ile	Lys	Ile	Lys	Lys	Cys	Asp	Phe
			180					185					190		
Asp	His	Gly	Thr	Thr	Glu	Pro	Glu	Ser	Gly	Ala	Ala	Leu	Glu	Leu	
	195					200					205				
Ser	Met	Asp	Gln	Ile	Lys	Ser	Thr	Thr	Ser	His	Gly	Phe	Leu	Val	
	210					215				220					
Asn	Ser	Phe	Tyr	Glu	Leu	Glu	Ser	Ala	Phe	Val	Asp	Tyr	Asn	Asn	Asn
225					230					235					240
Ser	Gly	Asp	Lys	Pro	Lys	Ser	Trp	Cys	Val	Gly	Pro	Leu	Cys	Leu	Thr
			245						250					255	
Asp	Pro	Pro	Lys	Gln	Gly	Ser	Ala	Lys	Pro	Ala	Trp	Ile	His	Trp	Leu
			260					265					270		
Asp	Gln	Lys	Arg	Glu	Glu	Gly	Arg	Pro	Val	Leu	Tyr	Val	Ala	Phe	Gly
	275						280					285			
Thr	Gln	Ala	Glu	Ile	Ser	Asn	Lys	Gln	Leu	Met	Glu	Leu	Ala	Phe	Gly
	290					295					300				
Leu	Glu	Asp	Ser	Lys	Val	Asn	Phe	Leu	Trp	Val	Thr	Arg	Lys	Asp	Val
305					310					315					320
Glu	Glu	Ile	Ile	Gly	Glu	Gly	Phe	Asn	Asp	Arg	Ile	Arg	Glu	Ser	Gly
				325					330					335	

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Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu Ile Leu Ser His Glu
      340                      345                      350
Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp Asn Ser Ala Gln Glu
      355                      360                      365
Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp Pro Met Met Ala Glu
      370                      375                      380
Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu Ile Lys Val Gly Val
      385                      390                      395                      400
Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly Phe Val Thr Arg Glu
      405                      410                      415
Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu Gly Glu Thr Gly Lys
      420                      425                      430
Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys Met Ala Lys Ala Ala
      435                      440                      445
Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn Leu Asp Met Ile Leu
      450                      455                      460
Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly Ala Ser Glu
      465                      470                      475

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(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

```

Met Ser Lys Gly His Ile Ile Pro Leu Leu Gln Phe Gly Arg Leu Leu
1           5           10           15
Leu Arg His His Arg Lys Glu Pro Thr Ile Thr Val Thr Val Phe Thr
      20           25           30
Thr Pro Lys Asn Gln Pro Phe Ile Ser Asp Phe Leu Ser Asp Thr Pro
      35           40           45
Glu Ile Lys Val Ile Ser Leu Pro Phe Pro Glu Asn Ile Thr Gly Ile
      50           55           60
Pro Pro Gly Val Glu Asn Thr Glu Arg Leu Pro Ser Met Ser Leu Phe
      65           70           75           80
Val Pro Phe Thr Arg Ala Thr Lys Leu Leu Gln Pro Phe Phe Glu Glu
      85           90           95
Thr Leu Lys Thr Leu Pro Lys Val Ser Phe Met Val Ser Asp Gly Phe
      100          105          110
Leu Trp Trp Thr Ser Glu Ser Ala Ala Lys Phe Asn Ile Pro Arg Phe
      115          120          125
Val Ser Tyr Gly Met Asn Ser Tyr Ser Ala Ala Val Ser Ile Ser Val
      130          135          140
Phe Lys His Glu Leu Phe Thr Glu Pro Glu Ser Lys Ser Asp Thr Glu
      145          150          155          160
Pro Val Thr Val Pro Asp Phe Pro Trp Ile Lys Ile Lys Lys Cys Asp
      165          170          175
Phe Asp His Gly Thr Thr Glu Pro Glu Ser Gly Ala Ala Leu Glu
      180          185          190
Leu Ser Met Asp Gln Ile Lys Ser Thr Thr Thr Ser His Gly Phe Leu
      195          200          205
Val Asn Ser Phe Tyr Glu Leu Glu Ser Ala Phe Val Asp Tyr Asn Asn
      210          215          220
Asn Ser Gly Asp Lys Pro Lys Ser Trp Cys Val Gly Pro Leu Cys Leu
      225          230          235          240
Thr Asp Pro Pro Lys Gln Gly Ser Ala Lys Pro Ala Trp Ile His Trp

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Leu	Asp	Gln	Lys	Arg	Glu	Glu	Gly	Arg	Pro	Val	Leu	Tyr	Val	Ala	Phe
			245						250					255	
			260					265					270		
Gly	Thr	Gln	Ala	Glu	Ile	Ser	Asn	Lys	Gln	Leu	Met	Glu	Leu	Ala	Phe
		275					280					285			
Gly	Leu	Glu	Asp	Ser	Lys	Val	Asn	Phe	Leu	Trp	Val	Thr	Arg	Lys	Asp
	290					295				300					
Val	Glu	Glu	Ile	Ile	Gly	Glu	Gly	Phe	Asn	Asp	Arg	Ile	Arg	Glu	Ser
305					310					315					320
Gly	Met	Ile	Val	Arg	Asp	Trp	Val	Asp	Gln	Trp	Glu	Ile	Leu	Ser	His
			325						330					335	
Glu	Ser	Val	Lys	Gly	Phe	Leu	Ser	His	Cys	Gly	Trp	Asn	Ser	Ala	Gln
		340						345					350		
Glu	Ser	Ile	Cys	Val	Gly	Val	Pro	Leu	Leu	Ala	Trp	Pro	Met	Met	Ala
		355					360					365			
Glu	Gln	Pro	Leu	Asn	Ala	Lys	Met	Val	Val	Glu	Glu	Ile	Lys	Val	Gly
		370				375					380				
Val	Arg	Val	Glu	Thr	Glu	Asp	Gly	Ser	Val	Lys	Gly	Phe	Val	Thr	Arg
385					390					395					400
Glu	Glu	Leu	Ser	Gly	Lys	Ile	Lys	Glu	Leu	Met	Glu	Gly	Glu	Thr	Gly
			405						410					415	
Lys	Thr	Ala	Arg	Lys	Asn	Val	Lys	Glu	Tyr	Ser	Lys	Met	Ala	Lys	Ala
		420						425					430		
Ala	Leu	Val	Glu	Gly	Thr	Gly	Ser	Ser	Trp	Lys	Asn	Leu	Asp	Met	Ile
		435					440					445			
Leu	Lys	Asp	Leu	Cys	Lys	Ser	Arg	Asp	Ser	Asn	Gly	Ala	Ser	Glu	
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met	Ser	Leu	Phe	Val	Pro	Phe	Thr	Arg	Ala	Thr	Lys	Leu	Leu	Gln	Pro
1				5					10					15	
Phe	Phe	Glu	Glu	Thr	Leu	Lys	Thr	Leu	Pro	Lys	Val	Ser	Phe	Met	Val
		20						25					30		
Ser	Asp	Gly	Phe	Leu	Trp	Trp	Thr	Ser	Glu	Ser	Ala	Ala	Lys	Phe	Asn
	35					40					45				
Ile	Pro	Arg	Phe	Val	Ser	Tyr	Gly	Met	Asn	Ser	Tyr	Ser	Ala	Ala	Val
	50					55				60					
Ser	Ile	Ser	Val	Phe	Lys	His	Glu	Leu	Phe	Thr	Glu	Pro	Glu	Ser	Lys
65				70					75					80	
Ser	Asp	Thr	Glu	Pro	Val	Thr	Val	Pro	Asp	Phe	Pro	Trp	Ile	Lys	Ile
			85					90					95		
Lys	Lys	Cys	Asp	Phe	Asp	His	Gly	Thr	Thr	Glu	Pro	Glu	Glu	Ser	Gly
		100					105						110		
Ala	Ala	Leu	Glu	Leu	Ser	Met	Asp	Gln	Ile	Lys	Ser	Thr	Thr	Thr	Ser
		115				120						125			
His	Gly	Phe	Leu	Val	Asn	Ser	Phe	Tyr	Glu	Leu	Glu	Ser	Ala	Phe	Val
	130					135					140				
Asp	Tyr	Asn	Asn	Asn	Ser	Gly	Asp	Lys	Pro	Lys	Ser	Trp	Cys	Val	Gly
145					150					155				160	
Pro	Leu	Cys	Leu	Thr	Asp	Pro	Pro	Lys	Gln	Gly	Ser	Ala	Lys	Pro	Ala
			165						170					175	

Trp Ile His Trp Leu Asp Gln Lys Arg Glu Glu Gly Arg Pro Val Leu  
180 185 190  
Tyr Val Ala Phe Gly Thr Gln Ala Glu Ile Ser Asn Lys Gln Leu Met  
195 200 205  
Glu Leu Ala Phe Gly Leu Glu Asp Ser Lys Val Asn Phe Leu Trp Val  
210 215 220  
Thr Arg Lys Asp Val Glu Glu Ile Ile Gly Glu Gly Phe Asn Asp Arg  
225 230 235 240  
Ile Arg Glu Ser Gly Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu  
245 250 255  
Ile Leu Ser His Glu Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp  
260 265 270  
Asn Ser Ala Gln Glu Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp  
275 280 285  
Pro Met Met Ala Glu Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu  
290 295 300  
Ile Lys Val Gly Val Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly  
305 310 315 320  
Phe Val Thr Arg Glu Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu  
325 330 335  
Gly Glu Thr Gly Lys Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys  
340 345 350  
Met Ala Lys Ala Ala Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn  
355 360 365  
Leu Asp Met Ile Leu Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly  
370 375 380  
Ala Ser Glu  
385

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1689
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

atttggtctt	ttatcttgtc	tttgtctgat	cagtagtcac	tacatttggt	tctttcacaa	60
tctttctttt	ttgcttcata	ttgaactgca	agaccaatcc	atgaatgcaa	atataaaata	120
ttgtcttacg	gttaaccatc	tctaagtgtt	tgctagtcac	gaattgtgaa	attgtttcgc	180
ttcaaacata	gaattagttg	atttggaat	gtagacatga	atgcttatct	aaatacaata	240
aactgtgttc	ttgtttcagt	tgtgtatcag	agatgagacc	ttgactggta	atttcaatgg	300
agcataatta	aatgctaata	atacttattt	tctggttaat	gcaggagggt	tgagagtgtg	360
aagaaacccat	ttacgccacc	caggggaagt	catgttcaag	tcttgcactc	catgccacct	420
caaaagatcg	agatcttcaa	atctatggaa	aactgggccc	aggagaacct	tctgattcac	480
ctcaaggatg	tggagaagtc	ttggcaaccc	caggatttct	tgccctgacc	tgcatcagat	540
gggtttgaag	atcaggtaag	agagttaaga	gagagggcta	gagagctccc	tgatgattac	600
tttgtttgtt	tgggtgggga	catgatcaca	gaagaagcac	ttccgacct	tcaaactatg	660
ttgaacactt	tggatggagt	tagggatgaa	acaggtgcta	gtcctacttc	atgggctatt	720
tggaccagag	cttggaactgc	agaagaaaac	cgacatggcg	atcttctgaa	taaatacctt	780
tacttgctctg	gtcgtgttga	catgaggcag	atcgaaaaga	ccattcagta	cttgattgga	840
tctggaatgg	atccgcggac	agagaataac	ccctaccttg	gcttcatcta	tacgtcattc	900
caagaaagag	cgacattcat	ctctcacgga	aacacagccc	gccaaagcaa	agagcacggg	960
gacatcaaac	tagcccaaat	atgtggcaca	atagctgcag	acgagaagcg	tcatgaaaca	1020
gcataacca	agatagttga	aaagctcttt	gagattgac	ctgatgggtac	tgatcatggc	1080
tttgagaca	tgatgagaaa	gaaaatctca	atgcctgctc	acttgatgta	tgatggggcg	1140
aacgacaacc	tctttgacaa	cttctcttcc	gtggctcaga	ggctcgggtg	ttacaccgcc	1200
aaagactatg	cagacattct	tgagtttctg	gttggttaggt	ggaaaatcca	ggacttaacc	1260

```
gggcttttcag gtgaaggaaa caaagcacaa gactatttat gcgggttggc tccaaggatc 1320
aagagatttg atgagagagc tcaagcaaga gcccaagaaag gacccaagat tcctttcagt 1380
tggatacacg acagagaagt gcagctctaa aaggacaaag aaaaaaacia aaacctatcc 1440
tcccggttcc tcatttcacg tgtctgctct taaaattggg gtagattact atgggtttct 1500
gataatgttg gtgggtctag ttacaaagtt gagatgcagt gatttagtag ctttgttttt 1560
cccagtcact atatgtttgg tctttgggtcc gttagcacac ttgtagtagt taaaacagtt 1620
taagtatggg ctgtgctcag tcttcctctt ctctgtggag ttttgtttaa gttcaggtta 1680
gttttgttt
```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```
Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Met Glu Asn Trp Ala
1      5      10      15
Glu Glu Asn Leu Leu Ile His Leu Lys Asp Val Glu Lys Ser Trp Gln
20      25      30
Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Asp Gly Phe Glu Asp Gln
35      40      45
Val Arg Glu Leu Arg Glu Arg Ala Arg Glu Leu Pro Asp Asp Tyr Phe
50      55      60
Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
65      70      75      80
Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
85      90      95
Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu
100      105      110
Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg
115      120      125
Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser
130      135      140
Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr
145      150      155      160
Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
165      170      175
Arg Gln Ala Lys Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly
180      185      190
Thr Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
195      200      205
Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Met Ala Phe
210      215      220
Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Tyr
225      230      235      240
Asp Gly Arg Asn Asp Asn Leu Phe Asp Asn Phe Ser Ser Val Ala Gln
245      250      255
Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe
260      265      270
Leu Val Gly Arg Trp Lys Ile Gln Asp Leu Thr Gly Leu Ser Gly Glu
275      280      285
Gly Asn Lys Ala Gln Asp Tyr Leu Cys Gly Leu Ala Pro Arg Ile Lys
290      295      300
Arg Leu Asp Glu Arg Ala Gln Ala Arg Ala Lys Lys Gly Pro Lys Ile
305      310      315      320
Pro Phe Ser Trp Ile His Asp Arg Glu Val Gln Leu
```

325

330

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met	Glu	Asn	Trp	Ala	Glu	Glu	Asn	Leu	Leu	Ile	His	Leu	Lys	Asp	Val
1				5				10						15	
Glu	Lys	Ser	Trp	Gln	Pro	Gln	Asp	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Asp
			20					25					30		
Gly	Phe	Glu	Asp	Gln	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ala	Arg	Glu	Leu
		35					40					45			
Pro	Asp	Asp	Tyr	Phe	Val	Val	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu
		50				55					60				
Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg
65					70					75				80	
Asp	Glu	Thr	Gly	Ala	Ser	Pro	Thr	Ser	Trp	Ala	Ile	Trp	Thr	Arg	Ala
				85					90					95	
Trp	Thr	Ala	Glu	Glu	Asn	Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Leu
		100						105					110		
Tyr	Leu	Ser	Gly	Arg	Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln
		115				120						125			
Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr
		130				135					140				
Leu	Gly	Phe	Ile	Tyr	Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser
145					150					155				160	
His	Gly	Asn	Thr	Ala	Arg	Gln	Ala	Lys	Glu	His	Gly	Asp	Ile	Lys	Leu
				165					170					175	
Ala	Gln	Ile	Cys	Gly	Thr	Ile	Ala	Ala	Asp	Glu	Lys	Arg	His	Glu	Thr
		180						185					190		
Ala	Tyr	Thr	Lys	Ile	Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly
		195					200					205			
Thr	Val	Met	Ala	Phe	Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro
		210				215						220			
Ala	His	Leu	Met	Tyr	Asp	Gly	Arg	Asn	Asp	Asn	Leu	Phe	Asp	Asn	Phe
225					230					235				240	
Ser	Ser	Val	Ala	Gln	Arg	Leu	Gly	Val	Tyr	Thr	Ala	Lys	Asp	Tyr	Ala
				245					250					255	
Asp	Ile	Leu	Glu	Phe	Leu	Val	Gly	Arg	Trp	Lys	Ile	Gln	Asp	Leu	Thr
		260					265						270		
Gly	Leu	Ser	Gly	Glu	Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Gly	Leu
		275					280					285			
Ala	Pro	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Arg	Ala	Gln	Ala	Arg	Ala	Lys
		290				295					300				
Lys	Gly	Pro	Lys	Ile	Pro	Phe	Ser	Trp	Ile	His	Asp	Arg	Glu	Val	Gln
305					310					315					320
Leu															

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..262  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498893  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

```
Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr
1           5           10           15
Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Trp Ala
20           25           30
Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu
35           40           45
Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Gln Ile
50           55           60
Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro Arg Thr
65           70           75           80
Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg
85           90           95
Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys Glu His
100          105          110
Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu
115          120          125
Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu
130          135          140
Ile Asp Pro Asp Gly Thr Val Met Ala Phe Ala Asp Met Met Arg Lys
145          150          155          160
Lys Ile Ser Met Pro Ala His Leu Met Tyr Asp Gly Arg Asn Asp Asn
165          170          175
Leu Phe Asp Asn Phe Ser Ser Val Ala Gln Arg Leu Gly Val Tyr Thr
180          185          190
Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp Lys
195          200          205
Ile Gln Asp Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp
210          215          220
Tyr Leu Cys Gly Leu Ala Pro Arg Ile Lys Arg Leu Asp Glu Arg Ala
225          230          235          240
Gln Ala Arg Ala Lys Lys Gly Pro Lys Ile Pro Phe Ser Trp Ile His
245          250          255
Asp Arg Glu Val Gln Leu
260
```

(2) INFORMATION FOR SEQ ID NO:720:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1029 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1029  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```
aacaaagtgt gttcttaa at tatcttctct gataaccaa aaagccctat tttccgagat      60
gaatacccta gaagaagtag atgaatccac tcatatcttc aacgctttga tgagtcta at      120
gaggaaattt ttgttcagag ttctatgcgt cgggtccaatc cctactaaca tttcattcat      180
catggatgga aaccgcaggt tgcctaagaa acacaatctt ataggcctag atgcaggaca      240
tagagctggt ttcatatccg tgaaatatat tcttcaatac tgcaaagaga ttggtgtacc      300
gtacgtcaca ctccacgcgt ttggtatgga taatttcaag agaggacctg aagaagtcaa      360
gtgtgtgatg gatcta atgc ttgagaaagt cgagctcgcg atcgatcaag ctgtatcagg      420
gaatatgaac ggcgtgagaa taatctttgc cgggtgatttg gattcggtta acgagcattt      480
tagagctgcg acaaagaaac tgatggagct tacggaggag aatagagatc tgattgtggt      540
```



```
ggtttgcgtt gcttacagca caagtctcga gattgttcac gctgttcgaa aatcttgtgt 600
tagaaaaatgt acgaatggag atgatcttgt acttttggag ttgagtgatg ttgaagagtg 660
tatgtataca tcgattgtgc cggttccgga tcttgtgata agaaccggag gaggagatcg 720
gctgagtaac ttcattgacgt ggcaaaacttc gaggtctctt cttcacagaa cggaggctct 780
ttggccggag ttagggctctt ggcatttgggt ttgggcaatt cttaaattcc aaagaatgca 840
agattacttg acgaagaaga aaaagctcga ttagatagtt tctaaagtta aaccctgcag 900
gaaagaactt ttaactcttt attacgttta atttacgtgt ttctatgact ggaaacgaga 960
aagctcaca gcaaatcttt tttattatgt attggatccg tataacaaac acgaatatac 1020
aaaacatcg
```

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

```
Thr Lys Cys Val Leu Lys Leu Ser Ser Leu Ile Thr Lys Lys Ala Leu
1          5          10          15
Phe Ser Glu Met Asn Thr Leu Glu Glu Val Asp Glu Ser Thr His Ile
20          25          30
Phe Asn Ala Leu Met Ser Leu Met Arg Lys Phe Leu Phe Arg Val Leu
35          40          45
Cys Val Gly Pro Ile Pro Thr Asn Ile Ser Phe Ile Met Asp Gly Asn
50          55          60
Arg Arg Phe Ala Lys Lys His Asn Leu Ile Gly Leu Asp Ala Gly His
65          70          75          80
Arg Ala Gly Phe Ile Ser Val Lys Tyr Ile Leu Gln Tyr Cys Lys Glu
85          90          95
Ile Gly Val Pro Tyr Val Thr Leu His Ala Phe Gly Met Asp Asn Phe
100          105          110
Lys Arg Gly Pro Glu Glu Val Lys Cys Val Met Asp Leu Met Leu Glu
115          120          125
Lys Val Glu Leu Ala Ile Asp Gln Ala Val Ser Gly Asn Met Asn Gly
130          135          140
Val Arg Ile Ile Phe Ala Gly Asp Leu Asp Ser Leu Asn Glu His Phe
145          150          155          160
Arg Ala Ala Thr Lys Lys Leu Met Glu Leu Thr Glu Glu Asn Arg Asp
165          170          175
Leu Ile Val Val Val Cys Val Ala Tyr Ser Thr Ser Leu Glu Ile Val
180          185          190
His Ala Val Arg Lys Ser Cys Val Arg Lys Cys Thr Asn Gly Asp Asp
195          200          205
Leu Val Leu Leu Glu Leu Ser Asp Val Glu Glu Cys Met Tyr Thr Ser
210          215          220
Ile Val Pro Val Pro Asp Leu Val Ile Arg Thr Gly Gly Gly Asp Arg
225          230          235          240
Leu Ser Asn Phe Met Thr Trp Gln Thr Ser Arg Ser Leu Leu His Arg
245          250          255
Thr Glu Ala Leu Trp Pro Glu Leu Gly Leu Trp His Leu Val Trp Ala
260          265          270
Ile Leu Lys Phe Gln Arg Met Gln Asp Tyr Leu Thr Lys Lys Lys Lys
275          280          285
Leu Asp
290
```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..271  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498907  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Met	Asn	Thr	Leu	Glu	Glu	Val	Asp	Glu	Ser	Thr	His	Ile	Phe	Asn	Ala
1				5					10					15	
Leu	Met	Ser	Leu	Met	Arg	Lys	Phe	Leu	Phe	Arg	Val	Leu	Cys	Val	Gly
			20					25					30		
Pro	Ile	Pro	Thr	Asn	Ile	Ser	Phe	Ile	Met	Asp	Gly	Asn	Arg	Arg	Phe
			35				40					45			
Ala	Lys	Lys	His	Asn	Leu	Ile	Gly	Leu	Asp	Ala	Gly	His	Arg	Ala	Gly
	50					55				60					
Phe	Ile	Ser	Val	Lys	Tyr	Ile	Leu	Gln	Tyr	Cys	Lys	Glu	Ile	Gly	Val
65				70					75					80	
Pro	Tyr	Val	Thr	Leu	His	Ala	Phe	Gly	Met	Asp	Asn	Phe	Lys	Arg	Gly
				85				90						95	
Pro	Glu	Glu	Val	Lys	Cys	Val	Met	Asp	Leu	Met	Leu	Glu	Lys	Val	Glu
			100					105					110		
Leu	Ala	Ile	Asp	Gln	Ala	Val	Ser	Gly	Asn	Met	Asn	Gly	Val	Arg	Ile
			115					120				125			
Ile	Phe	Ala	Gly	Asp	Leu	Asp	Ser	Leu	Asn	Glu	His	Phe	Arg	Ala	Ala
	130					135					140				
Thr	Lys	Lys	Leu	Met	Glu	Leu	Thr	Glu	Glu	Asn	Arg	Asp	Leu	Ile	Val
145					150					155				160	
Val	Val	Cys	Val	Ala	Tyr	Ser	Thr	Ser	Leu	Glu	Ile	Val	His	Ala	Val
				165					170					175	
Arg	Lys	Ser	Cys	Val	Arg	Lys	Cys	Thr	Asn	Gly	Asp	Asp	Leu	Val	Leu
			180					185					190		
Leu	Glu	Leu	Ser	Asp	Val	Glu	Glu	Cys	Met	Tyr	Thr	Ser	Ile	Val	Pro
	195					200						205			
Val	Pro	Asp	Leu	Val	Ile	Arg	Thr	Gly	Gly	Gly	Asp	Arg	Leu	Ser	Asn
	210					215					220				
Phe	Met	Thr	Trp	Gln	Thr	Ser	Arg	Ser	Leu	Leu	His	Arg	Thr	Glu	Ala
225				230						235				240	
Leu	Trp	Pro	Glu	Leu	Gly	Leu	Trp	His	Leu	Val	Trp	Ala	Ile	Leu	Lys
				245					250					255	
Phe	Gln	Arg	Met	Gln	Asp	Tyr	Leu	Thr	Lys	Lys	Lys	Lys	Leu	Asp	
			260					265						270	

(2) INFORMATION FOR SEQ ID NO:723:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 254 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..254  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498908  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Met	Ser	Leu	Met	Arg	Lys	Phe	Leu	Phe	Arg	Val	Leu	Cys	Val	Gly	Pro
1				5					10				15		
Ile	Pro	Thr	Asn	Ile	Ser	Phe	Ile	Met	Asp	Gly	Asn	Arg	Arg	Phe	Ala
			20					25				30			
Lys	Lys	His	Asn	Leu	Ile	Gly	Leu	Asp	Ala	Gly	His	Arg	Ala	Gly	Phe

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1						
aaggaacac	ttaaccaagc	aaacaacaaa	tggctcttc	aatcgcttct	cttccttca	60
ttctcattct	cataccgact	tttctcagtt	cggttttcgc	cgtttcacca	ctcaaaactg	120
atacgttaaa	accggggcag	cagctcagag	actgggagca	gttgatctct	gcggatggta	180
tcttcaactct	cggattcttt	acacctaaag	actcatctac	ttccgaactc	gggtcagctg	240
gtcttagata	tcttggtatt	tggcctcaaa	gtattccaat	aaatctagtt	tgggtgggta	300
acccaaccga	atcagttttc	gattcatctg	gttctctatc	cattgcacac	aatggggttc	360
taaagataac	acaggcaaac	gctattccaa	tcttggtgaa	ccaaagacca	gccgcgcagc	420
tttcattggt	cgggaattgt	tctgccattt	tactcgatac	cggaacttt	gtggtccgag	480
agatcaggcc	aggaggagtt	ccgggtcgtg	ttctatggca	aagctttgac	catcccacaa	540
acacattact	tcccgggatg	aagattgggt	ttaacctaa	aaccaagaaa	gaagtatcag	600
ttacgtcttg	gataactgac	caagtcccag	tcccaggagc	attcagacta	ggagagacct	660
atcaggagct	aaccagttac	tcgtctggcg	ccgcggggaa	atctactggt	ccagtggaat	720
cttgacgaac	aatggaagct	ctcatttgaa	cttagaagta	tccagacact	acattgatta	780
tgaattccaag	ttgcattcaa	ataagtatcat	gaagtaactc	agctactcaa	tcaagaaagc	840
taatagtctg	gtctttttcca	gctggttctt	ggataactcta	ggccaaatca	ctgtaacctt	900
ttctctcagc	agtaacaata	gcagcacctg	gatttccgaa	agcagtgaac	cctgcaagac	960
ggattttaaag	aacagtttcag	caatctgcat	cacggagaag	ccaacggctt	gtaggaaagg	1020
gtcagagtat	ttcgaaccca	gaagaggata	catgatggaa	aataataaccg	gttattattcc	1080
atctttactat	gacgatagtt	tgagcgctgg	tcttagcgac	tgctatggaa	cctgctggag	1140
aaactgttct	tgcatagctt	tccaagcctt	tctgtatgga	tgccaatatt	gggaaaaagg	1200
atacaagttt	gttcctttatg	atagcttcaa	ctccaattta	gtaacttatg	ttcttgattc	1260
tgtaaagtga	tgtgtgggtg	taacttgaac	gagcaattat	gtaaccagac	tagtatcagt	1320

aaaggggttt attaagaaac taaagaatca agcagttc

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Met	Ala	Leu	Ser	Ile	Val	Leu	Leu	Pro	Phe	Ile	Leu	Ile	Leu	Ile	Pro
1			5					10					15		
Thr	Phe	Leu	Ser	Ser	Val	Phe	Ala	Val	Ser	Pro	Leu	Lys	Thr	Asp	Thr
			20					25					30		
Leu	Lys	Pro	Gly	Gln	Gln	Leu	Arg	Asp	Trp	Glu	Gln	Leu	Ile	Ser	Ala
			35				40					45			
Asp	Gly	Ile	Phe	Thr	Leu	Gly	Phe	Phe	Thr	Pro	Lys	Asp	Ser	Ser	Thr
	50					55				60					
Ser	Glu	Leu	Gly	Ser	Ala	Gly	Leu	Arg	Tyr	Leu	Gly	Ile	Trp	Pro	Gln
65					70				75						80
Ser	Ile	Pro	Ile	Asn	Leu	Val	Trp	Val	Gly	Asn	Pro	Thr	Glu	Ser	Val
				85				90					95		
Ser	Asp	Ser	Ser	Gly	Ser	Leu	Ser	Ile	Asp	Thr	Asn	Gly	Val	Leu	Lys
			100					105					110		
Ile	Thr	Gln	Ala	Asn	Ala	Ile	Pro	Ile	Leu	Val	Asn	Gln	Arg	Pro	Ala
			115					120					125		
Ala	Gln	Leu	Ser	Leu	Val	Gly	Asn	Val	Ser	Ala	Ile	Leu	Leu	Asp	Thr
			130				135				140				
Gly	Asn	Phe	Val	Val	Arg	Glu	Ile	Arg	Pro	Gly	Gly	Val	Pro	Gly	Arg
145					150				155						160
Val	Leu	Trp	Gln	Ser	Phe	Asp	His	Pro	Thr	Asn	Thr	Leu	Leu	Pro	Gly
				165				170					175		
Met	Lys	Ile	Gly	Phe	Asn	Leu	Arg	Thr	Lys	Lys	Glu	Val	Ser	Val	Thr
			180					185					190		
Ser	Trp	Ile	Thr	Asp	Gln	Val	Pro	Val	Pro	Gly	Ala	Phe	Arg	Leu	Gly
			195				200					205			
Glu	Thr	His	Gln	Glu	Leu	Thr	Ser	Tyr	Ser	Ser	Gly	Ala	Ala	Gly	Lys
			210				215				220				
Ser	Thr	Gly	Pro	Val	Glu	Ser									
225					230										

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1498914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Met	Lys	Tyr	Phe	Ser	Tyr	Ser	Ile	Lys	Lys	Ala	Asn	Ser	Ser	Val	Phe
1				5					10					15	
Ser	Ser	Trp	Phe	Leu	Asp	Thr	Leu	Gly	Gln	Ile	Thr	Val	Thr	Phe	Ser
			20					25					30		
Leu	Ser	Ser	Asn	Asn	Ser	Ser	Thr	Trp	Ile	Ser	Glu	Ser	Ser	Glu	Pro
			35				40						45		

Cys Lys Thr Asp Leu Lys Asn Ser Ser Ala Ile Cys Ile Thr Glu Lys  
50 55 60  
Pro Thr Ala Cys Arg Lys Gly Ser Glu Tyr Phe Glu Pro Arg Arg Gly  
65 70 75 80  
Tyr Met Met Glu Asn Asn Thr Gly Tyr Tyr Pro Phe Tyr Tyr Asp Asp  
85 90 95  
Ser Leu Ser Ala Gly Leu Ser Asp Cys His Gly Thr Cys Trp Arg Asn  
100 105 110  
Cys Ser Cys Ile Ala Phe Gln Ala Phe Pro Asp Gly Cys Gln Tyr Trp  
115 120 125  
Glu Lys Gly Ser Lys Phe Val Pro Tyr Asp Ser Phe Asn Ser Asn Leu  
130 135 140  
Val Thr Tyr Val Leu Asp Ser Val Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

gacataactt gcaagctgtt gagattttcc atcctcaata actttattct tccatatctc	60
tcccatttcg ctctctatct cacatcccca tataacataa tatacaatca cacatatcat	120
ttctatatag tatttaaatg ggagacagcc atgctgtgac aagctagggg tgaagaaagg	180
gccgtggacg gtggaggaag ataagaagct tataaaactc atactaacca atggccattg	240
ttgctggcgt gctttgccga agctggccgg tctccgtcgc tgtggaaaga gctgccgct	300
ccggtggact aactatctcc ggcctgactt aaaacgaggc cttctctcgc atgatgaaga	360
acaacttgct atagatcttc atgctaactc cggcaataag tggctctaaga tagcttcaag	420
attacctgga agaacagata acgaaataaa aaaccattgg aatactcata tcaagaagaa	480
acttcttaag atgggaatcg atcctatgac ccatcaaccc ctaaatacaag aaccttctaa	540
tatcgataat tccaaaacca ttccgtccaa tccagacgat gtctcagtgg aaccaaagac	600
aactaacacg aaatacgtgg agataagtgt cagcacaaca gaagaagaaa gtagtagcac	660
ggttactgat caaaacagtt cgatggataa tgaaaatcat ctaattgaca acatttatga	720
tgatgatgaa ttgtttagtt acttatggtc cgacgaaact acgaaagatg aggcctcttg	780
gagtgatagt aactttggtg ttggtggaac attatatgac cacaatatct ccggcgccga	840
tgcagatttt ccgatatggt caccggaaag aatcaatgac gagaagatgt ttttgatta	900
ttgtcaagac tttggtgttc atgattttgg gttttgactg ttcaccattg acatattggc	960
aactctatgg agatgaacac aagcattgag ttgtcatgtt tatacatacg tggcatatac	1020
atatatatat atgtacatta tatgtaaaca tatacacgca taaaaatcat aaacatgtaa	1080
ggataataaa tccatgtaaa tcagtaaggg tgcaccatgg ttttcaagta ttattaatta	1140
gggttttgta ggt	

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Gly Val Lys Lys Gly Pro  
1 5 10 15  
Trp Thr Val Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn

		20						25						30				
Gly	His	Cys	Cys	Trp	Arg	Ala	Leu	Pro	Lys	Leu	Ala	Gly	Leu	Arg	Arg			
		35					40					45						
Cys	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Thr	Asn	Tyr	Leu	Arg	Pro	Asp			
		50				55					60							
Leu	Lys	Arg	Gly	Leu	Leu	Ser	His	Asp	Glu	Glu	Gln	Leu	Val	Ile	Asp			
65					70				75					80				
Leu	His	Ala	Asn	Leu	Gly	Asn	Lys	Trp	Ser	Lys	Ile	Ala	Ser	Arg	Leu			
				85				90						95				
Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	His	Trp	Asn	Thr	His	Ile			
			100					105						110				
Lys	Lys	Lys	Leu	Leu	Lys	Met	Gly	Ile	Asp	Pro	Met	Thr	His	Gln	Pro			
		115					120					125						
Leu	Asn	Gln	Glu	Pro	Ser	Asn	Ile	Asp	Asn	Ser	Lys	Thr	Ile	Pro	Ser			
		130				135					140							
Asn	Pro	Asp	Asp	Val	Ser	Val	Glu	Pro	Lys	Thr	Thr	Asn	Thr	Lys	Tyr			
145					150					155				160				
Val	Glu	Ile	Ser	Val	Thr	Thr	Thr	Glu	Glu	Glu	Ser	Ser	Ser	Thr	Val			
				165				170						175				
Thr	Asp	Gln	Asn	Ser	Ser	Met	Asp	Asn	Glu	Asn	His	Leu	Ile	Asp	Asn			
			180					185					190					
Ile	Tyr	Asp	Asp	Asp	Glu	Leu	Phe	Ser	Tyr	Leu	Trp	Ser	Asp	Glu	Thr			
		195				200						205						
Thr	Lys	Asp	Glu	Ala	Ser	Trp	Ser	Asp	Ser	Asn	Phe	Gly	Val	Gly	Gly			
		210				215					220							
Thr	Leu	Tyr	Asp	His	Asn	Ile	Ser	Gly	Ala	Asp	Ala	Asp	Phe	Pro	Ile			
225					230				235					240				
Trp	Ser	Pro	Glu	Arg	Ile	Asn	Asp	Glu	Lys	Met	Phe	Leu	Asp	Tyr	Cys			
				245				250						255				
Gln	Asp	Phe	Gly	Val	His	Asp	Phe	Gly	Phe									
		260				265												

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1498920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met	Gly	Ile	Asp	Pro	Met	Thr	His	Gln	Pro	Leu	Asn	Gln	Glu	Pro	Ser			
1				5				10					15					
Asn	Ile	Asp	Asn	Ser	Lys	Thr	Ile	Pro	Ser	Asn	Pro	Asp	Asp	Val	Ser			
			20					25				30						
Val	Glu	Pro	Lys	Thr	Thr	Asn	Thr	Lys	Tyr	Val	Glu	Ile	Ser	Val	Thr			
		35				40					45							
Thr	Thr	Glu	Glu	Glu	Ser	Ser	Ser	Thr	Val	Thr	Asp	Gln	Asn	Ser	Ser			
		50			55					60								
Met	Asp	Asn	Glu	Asn	His	Leu	Ile	Asp	Asn	Ile	Tyr	Asp	Asp	Asp	Glu			
65					70				75					80				
Leu	Phe	Ser	Tyr	Leu	Trp	Ser	Asp	Glu	Thr	Lys	Asp	Glu	Ala	Ser				
			85					90					95					
Trp	Ser	Asp	Ser	Asn	Phe	Gly	Val	Gly	Gly	Thr	Leu	Tyr	Asp	His	Asn			
		100				105						110						
Ile	Ser	Gly	Ala	Asp	Ala	Asp	Phe	Pro	Ile	Trp	Ser	Pro	Glu	Arg	Ile			
		115				120						125						
Asn	Asp	Glu	Lys	Met	Phe	Leu	Asp	Tyr	Cys	Gln	Asp	Phe	Gly	Val	His			
		130				135					140							

Asp Phe Gly Phe  
145

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

Met	Thr	His	Gln	Pro	Leu	Asn	Gln	Glu	Pro	Ser	Asn	Ile	Asp	Asn	Ser
1				5					10					15	
Lys	Thr	Ile	Pro	Ser	Asn	Pro	Asp	Asp	Val	Ser	Val	Glu	Pro	Lys	Thr
			20					25					30		
Thr	Asn	Thr	Lys	Tyr	Val	Glu	Ile	Ser	Val	Thr	Thr	Thr	Glu	Glu	Glu
		35					40					45			
Ser	Ser	Ser	Thr	Val	Thr	Asp	Gln	Asn	Ser	Ser	Met	Asp	Asn	Glu	Asn
	50					55					60				
His	Leu	Ile	Asp	Asn	Ile	Tyr	Asp	Asp	Asp	Glu	Leu	Phe	Ser	Tyr	Leu
65					70					75				80	
Trp	Ser	Asp	Glu	Thr	Thr	Lys	Asp	Glu	Ala	Ser	Trp	Ser	Asp	Ser	Asn
			85					90					95		
Phe	Gly	Val	Gly	Gly	Thr	Leu	Tyr	Asp	His	Asn	Ile	Ser	Gly	Ala	Asp
		100						105					110		
Ala	Asp	Phe	Pro	Ile	Trp	Ser	Pro	Glu	Arg	Ile	Asn	Asp	Glu	Lys	Met
	115						120					125			
Phe	Leu	Asp	Tyr	Cys	Gln	Asp	Phe	Gly	Val	His	Asp	Phe	Gly	Phe	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

gaaacgtctt	cggacacact	ctcagtcgca	cgtcttttca	cgcgcctttt	cgatttcaca	60
ttcggatccg	atttgttcac	ccgccgaaga	tccaccggca	tcttctctaa	acggctctgt	120
cgagaaggat	cggcgctatt	attgctggag	gacgattggg	tgtttacttt	ttactagtaa	180
acggagtaat	ttcccaagcg	aaaggtttca	tttttgagct	ccacgttgaa	cgaactaagc	240
ggtttctcgg	agttctcttg	cttcctctcc	acccagcgca	atggagaaaa	cagacgaaga	300
gaggaagaag	gctcagatgc	tggacgctcg	ggccagaaac	attagccaca	atgttcgctg	360
cactgagtgt	ggaagtcagt	ccattgaaga	ctcgcaggca	gatatcgcta	ttctccttag	420
acagctgatc	cgtaatgaga	taggagctgg	aaaaactgac	aaagagatct	acagtaagct	480
ggaggatgaa	tttggggaga	cagtgcctta	tgcccaaaaa	tttgatttgc	agaccgcagc	540
cttggtggctc	acaccggtta	taattgctgg	aggtaccgct	gcaggaatag	tttaccagaa	600
gcacaggcta	aggaaaaatg	tagacatcat	ggcgttgaac	cttattagag	gtgtaccatt	660
gactccaaaa	gagagagtta	ccattcttga	tgttcttatt	ccaccttccc	ctcctcctca	720
gggagttggt	tcccgattga	ggagatggct	caaccggtag	ttcccgtgtc	tccttagctc	780
tcttgttctt	ggctcgaatc	ttgttggtgt	aacaagtaaa	caatgtgttg	aaaagagtga	840
gtacacattg	attgtcttgg	agaaacagat	agggactgct	ttgcatccat	tacaagcaaa	900
tggattcttc	tgtagaagat	cttgggatga	gatatgtatc	gagaaagcat	tattgaaagt	960
gtgatacttg	ttgtaccttt	gctgtgtgat	tgaatacaga	gagcgggtcg	atagttatat	1020

```
tacttttcggc acaaagattt atttctttcc aaatagtttt tgtgctaaat gagctttttt 1080
ccacatcttt atcttaataa gccgaagctc acaaaatgta ttgacctgcg tattgtatat 1140
acaagaagca atgagtaaac agaaagaaat agtcttgctc acaagaatga gactgtatgt 1200
tg
```

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

```
Met Glu Lys Thr Asp Glu Glu Arg Lys Lys Ala Gln Met Leu Asp Ala
1          5          10          15
Arg Ala Arg Asn Ile Ser His Asn Val Arg Cys Thr Glu Cys Gly Ser
          20          25          30
Gln Ser Ile Glu Asp Ser Gln Ala Asp Ile Ala Ile Leu Leu Arg Gln
          35          40          45
Leu Ile Arg Asn Glu Ile Gly Ala Gly Lys Thr Asp Lys Glu Ile Tyr
          50          55          60
Ser Lys Leu Glu Asp Glu Phe Gly Glu Thr Val Leu Tyr Ala Pro Lys
          65          70          75          80
Phe Asp Leu Gln Thr Ala Ala Leu Trp Leu Thr Pro Val Ile Ile Ala
          85          90          95
Gly Gly Thr Ala Ala Gly Ile Val Tyr Gln Lys His Arg Leu Arg Lys
          100          105          110
Asn Val Asp Ile Met Ala Leu Asn Leu Ile Arg Gly Val Pro Leu Thr
          115          120          125
Pro Lys Glu Arg Val Thr Ile Leu Asp Val Leu Ile Pro Pro Ser Pro
          130          135          140
Pro Pro Gln Gly Val Val Ser Arg Leu Arg Arg Trp Leu Asn Arg
          145          150          155
```

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

```
Met Leu Asp Ala Arg Ala Arg Asn Ile Ser His Asn Val Arg Cys Thr
1          5          10          15
Glu Cys Gly Ser Gln Ser Ile Glu Asp Ser Gln Ala Asp Ile Ala Ile
          20          25          30
Leu Leu Arg Gln Leu Ile Arg Asn Glu Ile Gly Ala Gly Lys Thr Asp
          35          40          45
Lys Glu Ile Tyr Ser Lys Leu Glu Asp Glu Phe Gly Glu Thr Val Leu
          50          55          60
Tyr Ala Pro Lys Phe Asp Leu Gln Thr Ala Ala Leu Trp Leu Thr Pro
          65          70          75          80
Val Ile Ile Ala Gly Gly Thr Ala Ala Gly Ile Val Tyr Gln Lys His
          85          90          95
Arg Leu Arg Lys Asn Val Asp Ile Met Ala Leu Asn Leu Ile Arg Gly
```



100 105 110  
Val Pro Leu Thr Pro Lys Glu Arg Val Thr Ile Leu Asp Val Leu Ile  
115 120 125  
Pro Pro Ser Pro Pro Pro Gln Gly Val Val Ser Arg Leu Arg Arg Trp  
130 135 140  
Leu Asn Arg  
145

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

```
aatttttcac tttctatttc tctatatcta tttttttata gatatatatt ttgtcttggt      60
tggattttgt tctcgtgggt tacttacttg agagaacctc gagacctgtc ttgtctttat      120
gcttcagaag caaatcaaag catctctcca agatttgaag ctccatctat ggctgccctt      180
cttctccttt tccttttcct cttcgcaagc tctgctctct ctcaagattc tttgatcggt      240
gtgaatattg gtactgaagt gacaaacatg ccaagtccaa cacaagtagt agcactcctc      300
aaatcacaga acatcaaccg cgtccgcctc tatgacgcag accgctcaat gcttctcgcg      360
tttgetcaca ccgggggttca agttataatc tcagtaccta acgaccagct tctcggtatc      420
agccaatcaa atgcaaccgc agccaattgg gtgactagaa atgtagctgc atattaccct      480
gcgaccaaca ttaccacaat tgctgtcggg tcagaagtcc taaccagcct aacaaacgca      540
gcttctgtcc ttgtctcagc cctcaaatac atacaagctg ctctcgtcac ggccaatctc      600
gaccgtcaga tcaaagtatc gacaccgcac tcttcaacca tcattcttga ttctttccct      660
ccttcgcaag ctttcttcaa caagacttgg gatccagtta ttgtccctct cctcaaattc      720
ctacagtcca caggatcgcc attgctgctc aacgtttacc cgtatttcga ctatgttcag      780
tccaatggag ttataccgct tgactacgcg cttttccagc ctctccaagc caacaaagaa      840
gctgtagacg ccaacacatt gttacattac acaaacgttt ttgatgcaat cgtagacgct      900
gcttattttg caatgtctta tcttaacttc accaacattc caatcgtagt cacagaatct      960
ggatggccat cttaaaggag cccttctgag cagcagcaa cggtagagaa tgcaaacact      1020
tacaatagca atttgatcca gcatgtgatc aacaagactg gaacgcaaaa acaccggga      1080
actgcagtta ctacatacat ctacgagctt tacaacgagg atacgaggcc aggaccgta      1140
tctgagaaga actgggggct gttttataca aacgggactc cggtttacac attgcggtta      1200
gcggtgagcag gggcgattct ggcaaagtat actacaaacc agacattttg tatagcgaag      1260
gaaaagggtg atagaaagat gcttcaagca gctcttgact gggcttgagg tccagggaag      1320
gtcgattgct cggcactgat gcaggagag tcattgttat aacccgacga tgtggttgca      1380
cattctactt atgcgtttta tgcttattac cagaagatgg gaaaagcttc aggaagctgt      1440
gatttcaaag gagttgctac agtcaccacc actgatccaa gtcgaggaac atgcgtgttc      1500
cctggaagtg caaaaagcaa tcagacactt ggaaacaaca cctcggcgtt ggccccctca      1560
gcgaactcta caacctctgg atgtatccca aagtactatc atcaccctca cgcattcttc      1620
ggtgacttaa cattactctc ccttctactg atcattgcct tagtattctt gtagaaactc      1680
tgaaaagaac aacaactctc aattcttggt tctctaaatt ttaacttctt tctttgcaac      1740
acttgagaca aaagagctcg gtgggtttgt tctctctgtg tctagtgtgc taccagttt      1800
tggtgatcat ctctttttta catggagttc attgagggtg gcatgtaggt tcggcttcaa      1860
gatcatggat gattgtaact aatttctgtg gttgaaagct tgattctttc ttttttatgg      1920
ctgaatattt c
```

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..557

(D) OTHER INFORMATION: / Ceres Seq. ID 1498926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

Asn	Phe	Ser	Leu	Ser	Ile	Ser	Leu	Tyr	Leu	Phe	Phe	Tyr	Arg	Tyr	Ile
1			5					10					15		
Phe	Cys	Leu	Gly	Trp	Ile	Leu	Phe	Ser	Trp	Val	Thr	Tyr	Leu	Arg	Glu
		20						25					30		
Pro	Arg	Asp	Leu	Ser	Cys	Leu	Tyr	Ala	Ser	Glu	Ala	Asn	Gln	Ser	Ile
		35					40					45			
Ser	Pro	Arg	Phe	Glu	Ala	Pro	Ser	Met	Ala	Ala	Leu	Leu	Leu	Phe	
	50					55					60				
Leu	Phe	Leu	Phe	Ala	Ser	Ser	Ala	Leu	Ser	Gln	Asp	Ser	Leu	Ile	Gly
65					70					75				80	
Val	Asn	Ile	Gly	Thr	Glu	Val	Thr	Asn	Met	Pro	Ser	Pro	Thr	Gln	Val
			85					90						95	
Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn	Ile	Asn	Arg	Val	Arg	Leu	Tyr	Asp
		100						105					110		
Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala	Phe	Ala	His	Thr	Gly	Val	Gln	Val
	115						120					125			
Ile	Ile	Ser	Val	Pro	Asn	Asp	Gln	Leu	Leu	Gly	Ile	Ser	Gln	Ser	Asn
	130					135					140				
Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr	Arg	Asn	Val	Ala	Ala	Tyr	Tyr	Pro
145					150					155					160
Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala	Val	Gly	Ser	Glu	Val	Leu	Thr	Ser
			165					170						175	
Leu	Thr	Asn	Ala	Ala	Ser	Val	Leu	Val	Ser	Ala	Leu	Lys	Tyr	Ile	Gln
		180						185					190		
Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu	Asp	Arg	Gln	Ile	Lys	Val	Ser	Thr
	195						200					205			
Pro	His	Ser	Ser	Thr	Ile	Ile	Leu	Asp	Ser	Phe	Pro	Pro	Ser	Gln	Ala
	210					215					220				
Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro	Val	Ile	Val	Pro	Leu	Leu	Lys	Phe
225					230					235					240
Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu	Leu	Leu	Asn	Val	Tyr	Pro	Tyr	Phe
			245					250						255	
Asp	Tyr	Val	Gln	Ser	Asn	Gly	Val	Ile	Pro	Leu	Asp	Tyr	Ala	Leu	Phe
		260						265					270		
Gln	Pro	Leu	Gln	Ala	Asn	Lys	Glu	Ala	Val	Asp	Ala	Asn	Thr	Leu	Leu
	275						280					285			
His	Tyr	Thr	Asn	Val	Phe	Asp	Ala	Ile	Val	Asp	Ala	Ala	Tyr	Phe	Ala
	290					295					300				
Met	Ser	Tyr	Leu	Asn	Phe	Thr	Asn	Ile	Pro	Ile	Val	Val	Thr	Glu	Ser
305					310					315					320
Gly	Trp	Pro	Ser	Lys	Gly	Gly	Pro	Ser	Glu	His	Asp	Ala	Thr	Val	Glu
			325						330					335	
Asn	Ala	Asn	Thr	Tyr	Asn	Ser	Asn	Leu	Ile	Gln	His	Val	Ile	Asn	Lys
		340						345					350		
Thr	Gly	Thr	Pro	Lys	His	Pro	Gly	Thr	Ala	Val	Thr	Thr	Tyr	Ile	Tyr
		355					360					365			
Glu	Leu	Tyr	Asn	Glu	Asp	Thr	Arg	Pro	Gly	Pro	Val	Ser	Glu	Lys	Asn
	370					375					380				
Trp	Gly	Leu	Phe	Tyr	Thr	Asn	Gly	Thr	Pro	Val	Tyr	Thr	Leu	Arg	Leu
385					390					395					400
Ala	Gly	Ala	Gly	Ala	Ile	Leu	Ala	Asn	Asp	Thr	Thr	Asn	Gln	Thr	Phe
			405					410					415		
Cys	Ile	Ala	Lys	Glu	Lys	Val	Asp	Arg	Lys	Met	Leu	Gln	Ala	Ala	Leu
		420						425					430		
Asp	Trp	Ala	Cys	Gly	Pro	Gly	Lys	Val	Asp	Cys	Ser	Ala	Leu	Met	Gln
	435						440					445			
Gly	Glu	Ser	Cys	Tyr	Glu	Pro	Asp	Asp	Val	Val	Ala	His	Ser	Thr	Tyr
	450					455					460				

Ala Phe Asn Ala Tyr Tyr Gln Lys Met Gly Lys Ala Ser Gly Ser Cys  
465 470 475 480  
Asp Phe Lys Gly Val Ala Thr Val Thr Thr Thr Asp Pro Ser Arg Gly  
485 490 495  
Thr Cys Val Phe Pro Gly Ser Ala Lys Ser Asn Gln Thr Leu Gly Asn  
500 505 510  
Asn Thr Ser Ala Leu Ala Pro Ser Ala Asn Ser Thr Thr Ser Gly Cys  
515 520 525  
Ile Pro Lys Tyr Tyr His His Pro His Ala Ser Phe Gly Asp Leu Thr  
530 535 540  
Leu Leu Ser Leu Leu Leu Ile Ile Ala Leu Val Phe Leu  
545 550 555

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1498927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

Met Ala Ala Leu Leu Leu Leu Phe Leu Phe Leu Phe Ala Ser Ser Ala  
1 5 10 15  
Leu Ser Gln Asp Ser Leu Ile Gly Val Asn Ile Gly Thr Glu Val Thr  
20 25 30  
Asn Met Pro Ser Pro Thr Gln Val Val Ala Leu Leu Lys Ser Gln Asn  
35 40 45  
Ile Asn Arg Val Arg Leu Tyr Asp Ala Asp Arg Ser Met Leu Leu Ala  
50 55 60  
Phe Ala His Thr Gly Val Gln Val Ile Ile Ser Val Pro Asn Asp Gln  
65 70 75 80  
Leu Leu Gly Ile Ser Gln Ser Asn Ala Thr Ala Ala Asn Trp Val Thr  
85 90 95  
Arg Asn Val Ala Ala Tyr Tyr Pro Ala Thr Asn Ile Thr Thr Ile Ala  
100 105 110  
Val Gly Ser Glu Val Leu Thr Ser Leu Thr Asn Ala Ala Ser Val Leu  
115 120 125  
Val Ser Ala Leu Lys Tyr Ile Gln Ala Ala Leu Val Thr Ala Asn Leu  
130 135 140  
Asp Arg Gln Ile Lys Val Ser Thr Pro His Ser Ser Thr Ile Ile Leu  
145 150 155 160  
Asp Ser Phe Pro Pro Ser Gln Ala Phe Phe Asn Lys Thr Trp Asp Pro  
165 170 175  
Val Ile Val Pro Leu Leu Lys Phe Leu Gln Ser Thr Gly Ser Pro Leu  
180 185 190  
Leu Leu Asn Val Tyr Pro Tyr Phe Asp Tyr Val Gln Ser Asn Gly Val  
195 200 205  
Ile Pro Leu Asp Tyr Ala Leu Phe Gln Pro Leu Gln Ala Asn Lys Glu  
210 215 220  
Ala Val Asp Ala Asn Thr Leu Leu His Tyr Thr Asn Val Phe Asp Ala  
225 230 235 240  
Ile Val Asp Ala Ala Tyr Phe Ala Met Ser Tyr Leu Asn Phe Thr Asn  
245 250 255  
Ile Pro Ile Val Val Thr Glu Ser Gly Trp Pro Ser Lys Gly Gly Pro  
260 265 270  
Ser Glu His Asp Ala Thr Val Glu Asn Ala Asn Thr Tyr Asn Ser Asn  
275 280 285  
Leu Ile Gln His Val Ile Asn Lys Thr Gly Thr Pro Lys His Pro Gly

290	295	300
Thr Ala Val Thr Thr Tyr Ile Tyr Glu Leu Tyr Asn Glu Asp Thr Arg		
305	310	315
Pro Gly Pro Val Ser Glu Lys Asn Trp Gly Leu Phe Tyr Thr Asn Gly		320
	325	330
Thr Pro Val Tyr Thr Leu Arg Leu Ala Gly Ala Gly Ala Ile Leu Ala		335
	340	345
Asn Asp Thr Thr Asn Gln Thr Phe Cys Ile Ala Lys Glu Lys Val Asp		350
	355	360
Arg Lys Met Leu Gln Ala Ala Leu Asp Trp Ala Cys Gly Pro Gly Lys		365
	370	375
Val Asp Cys Ser Ala Leu Met Gln Gly Glu Ser Cys Tyr Glu Pro Asp		380
385	390	395
Asp Val Val Ala His Ser Thr Tyr Ala Phe Asn Ala Tyr Tyr Gln Lys		400
	405	410
Met Gly Lys Ala Ser Gly Ser Cys Asp Phe Lys Gly Val Ala Thr Val		415
	420	425
Thr Thr Thr Asp Pro Ser Arg Gly Thr Cys Val Phe Pro Gly Ser Ala		430
	435	440
Lys Ser Asn Gln Thr Leu Gly Asn Asn Thr Ser Ala Leu Ala Pro Ser		445
	450	455
Ala Asn Ser Thr Thr Ser Gly Cys Ile Pro Lys Tyr Tyr His His Pro		460
465	470	475
His Ala Ser Phe Gly Asp Leu Thr Leu Leu Ser Leu Leu Leu Ile Ile		480
	485	490
Ala Leu Val Phe Leu		495
	500	

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1498928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

Met	Pro	Ser	Pro	Thr	Gln	Val	Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn	Ile
1				5					10					15	
Asn	Arg	Val	Arg	Leu	Tyr	Asp	Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala	Phe
		20						25					30		
Ala	His	Thr	Gly	Val	Gln	Val	Ile	Ser	Val	Pro	Asn	Asp	Gln	Leu	
		35					40					45			
Leu	Gly	Ile	Ser	Gln	Ser	Asn	Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr	Arg
		50				55					60				
Asn	Val	Ala	Ala	Tyr	Tyr	Pro	Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala	Val
65					70					75				80	
Gly	Ser	Glu	Val	Leu	Thr	Ser	Leu	Thr	Asn	Ala	Ala	Ser	Val	Leu	Val
				85					90					95	
Ser	Ala	Leu	Lys	Tyr	Ile	Gln	Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu	Asp
			100					105						110	
Arg	Gln	Ile	Lys	Val	Ser	Thr	Pro	His	Ser	Ser	Thr	Ile	Ile	Leu	Asp
		115					120						125		
Ser	Phe	Pro	Pro	Ser	Gln	Ala	Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro	Val
		130				135					140				
Ile	Val	Pro	Leu	Leu	Lys	Phe	Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu	Leu
145					150					155				160	
Leu	Asn	Val	Tyr	Pro	Tyr	Phe	Asp	Tyr	Val	Gln	Ser	Asn	Gly	Val	Ile
				165					170					175	

Pro Leu Asp Tyr Ala Leu Phe Gln Pro Leu Gln Ala Asn Lys Glu Ala  
180 185 190  
Val Asp Ala Asn Thr Leu Leu His Tyr Thr Asn Val Phe Asp Ala Ile  
195 200 205  
Val Asp Ala Ala Tyr Phe Ala Met Ser Tyr Leu Asn Phe Thr Asn Ile  
210 215 220  
Pro Ile Val Val Thr Glu Ser Gly Trp Pro Ser Lys Gly Gly Pro Ser  
225 230 235 240  
Glu His Asp Ala Thr Val Glu Asn Ala Asn Thr Tyr Asn Ser Asn Leu  
245 250 255  
Ile Gln His Val Ile Asn Lys Thr Gly Thr Pro Lys His Pro Gly Thr  
260 265 270  
Ala Val Thr Thr Tyr Ile Tyr Glu Leu Tyr Asn Glu Asp Thr Arg Pro  
275 280 285  
Gly Pro Val Ser Glu Lys Asn Trp Gly Leu Phe Tyr Thr Asn Gly Thr  
290 295 300  
Pro Val Tyr Thr Leu Arg Leu Ala Gly Ala Gly Ala Ile Leu Ala Asn  
305 310 315 320  
Asp Thr Thr Asn Gln Thr Phe Cys Ile Ala Lys Glu Lys Val Asp Arg  
325 330 335  
Lys Met Leu Gln Ala Ala Leu Asp Trp Ala Cys Gly Pro Gly Lys Val  
340 345 350  
Asp Cys Ser Ala Leu Met Gln Gly Glu Ser Cys Tyr Glu Pro Asp Asp  
355 360 365  
Val Val Ala His Ser Thr Tyr Ala Phe Asn Ala Tyr Tyr Gln Lys Met  
370 375 380  
Gly Lys Ala Ser Gly Ser Cys Asp Phe Lys Gly Val Ala Thr Val Thr  
385 390 395 400  
Thr Thr Asp Pro Ser Arg Gly Thr Cys Val Phe Pro Gly Ser Ala Lys  
405 410 415  
Ser Asn Gln Thr Leu Gly Asn Asn Thr Ser Ala Leu Ala Pro Ser Ala  
420 425 430  
Asn Ser Thr Thr Ser Gly Cys Ile Pro Lys Tyr Tyr His His Pro His  
435 440 445  
Ala Ser Phe Gly Asp Leu Thr Leu Leu Ser Leu Leu Leu Ile Ile Ala  
450 455 460  
Leu Val Phe Leu  
465

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..673
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

gcctataaag	tgatccttgt	gatgccttca	actatgagct	tagagagaag	aatcattctg	60
agggcactag	gtgcagacct	tcatcwmctg	gaccagcgca	taggccttaa	aggaatgttg	120
gagaaaactg	aagcgatttt	aagcaaaact	cctggtggtt	acattccaca	acaatttgaa	180
aatcctgcaa	accccgagat	tcattaccga	accacgggac	cggaaatatg	gagagattca	240
gccgggaaag	tagatatatt	ggtcgctggc	gtagggactg	gtggaactgc	tactggagta	300
gggaagtcc	tcaaggagca	gaacaaagac	atcaaggttt	gtgtggtgga	accagtagaa	360
agtccggtac	ttagcgagg	tcaaccaggt	ccacatttga	ttcagggaat	tggctctggt	420
atcgteccat	tcaatttga	cttaaccatt	gttgatgaaa	ttattcaagt	ggcagggtgaa	480
gaggctattg	aaacagccaa	gcttcttgcc	ctcaaagaag	gattactggt	gggaatatcc	540
tctggagccg	cagcagcggc	tgcgttaaag	gttgcaaagc	ggccagaaaa	cgcggggaaa	600
ctcattgkgg	tggtttttcc	tagtggagga	gaacgttatt	tatcgactaa	actgttcgat	660

tcgattagat atg

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

Ala	Tyr	Lys	Val	Ile	Leu	Val	Met	Pro	Ser	Thr	Met	Ser	Leu	Glu	Arg
1			5					10					15		
Arg	Ile	Ile	Leu	Arg	Ala	Leu	Gly	Ala	Asp	Leu	His	Xaa	Ser	Asp	Gln
			20					25					30		
Arg	Ile	Gly	Leu	Lys	Gly	Met	Leu	Glu	Lys	Thr	Glu	Ala	Ile	Leu	Ser
		35					40					45			
Lys	Thr	Pro	Gly	Gly	Tyr	Ile	Pro	Gln	Gln	Phe	Glu	Asn	Pro	Ala	Asn
	50					55					60				
Pro	Glu	Ile	His	Tyr	Arg	Thr	Thr	Gly	Pro	Glu	Ile	Trp	Arg	Asp	Ser
65					70					75				80	
Ala	Gly	Lys	Val	Asp	Ile	Leu	Val	Ala	Gly	Val	Gly	Thr	Gly	Gly	Thr
			85						90					95	
Ala	Thr	Gly	Val	Gly	Lys	Phe	Leu	Lys	Glu	Gln	Asn	Lys	Asp	Ile	Lys
			100					105					110		
Val	Cys	Val	Val	Glu	Pro	Val	Glu	Ser	Pro	Val	Leu	Ser	Gly	Gly	Gln
	115						120					125			
Pro	Gly	Pro	His	Leu	Ile	Gln	Gly	Ile	Gly	Ser	Gly	Ile	Val	Pro	Phe
	130					135					140				
Asn	Leu	Asp	Leu	Thr	Ile	Val	Asp	Glu	Ile	Ile	Gln	Val	Ala	Gly	Glu
145					150					155				160	
Glu	Ala	Ile	Glu	Thr	Ala	Lys	Leu	Leu	Ala	Leu	Lys	Glu	Gly	Leu	Leu
			165						170					175	
Val	Gly	Ile	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Lys	Val	Ala	
		180					185					190			
Lys	Arg	Pro	Glu	Asn	Ala	Gly	Lys	Leu	Ile	Xaa	Val	Val	Phe	Pro	Ser
	195					200						205			
Gly	Gly	Glu	Arg	Tyr	Leu	Ser	Thr	Lys	Leu	Phe	Asp	Ser	Ile	Arg	Tyr
	210					215						220			

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

Met	Pro	Ser	Thr	Met	Ser	Leu	Glu	Arg	Arg	Ile	Ile	Leu	Arg	Ala	Leu
1				5				10					15		
Gly	Ala	Asp	Leu	His	Xaa	Ser	Asp	Gln	Arg	Ile	Gly	Leu	Lys	Gly	Met
		20						25					30		
Leu	Glu	Lys	Thr	Glu	Ala	Ile	Leu	Ser	Lys	Thr	Pro	Gly	Gly	Tyr	Ile
		35					40						45		

Pro Gln Gln Phe Glu Asn Pro Ala Asn Pro Glu Ile His Tyr Arg Thr  
50 55 60  
Thr Gly Pro Glu Ile Trp Arg Asp Ser Ala Gly Lys Val Asp Ile Leu  
65 70 75 80  
Val Ala Gly Val Gly Thr Gly Gly Thr Ala Thr Gly Val Gly Lys Phe  
85 90 95  
Leu Lys Glu Gln Asn Lys Asp Ile Lys Val Cys Val Val Glu Pro Val  
100 105 110  
Glu Ser Pro Val Leu Ser Gly Gly Gln Pro Gly Pro His Leu Ile Gln  
115 120 125  
Gly Ile Gly Ser Gly Ile Val Pro Phe Asn Leu Asp Leu Thr Ile Val  
130 135 140  
Asp Glu Ile Ile Gln Val Ala Gly Glu Glu Ala Ile Glu Thr Ala Lys  
145 150 155 160  
Leu Leu Ala Leu Lys Glu Gly Leu Leu Val Gly Ile Ser Ser Gly Ala  
165 170 175  
Ala Ala Ala Ala Ala Leu Lys Val Ala Lys Arg Pro Glu Asn Ala Gly  
180 185 190  
Lys Leu Ile Xaa Val Val Phe Pro Ser Gly Gly Glu Arg Tyr Leu Ser  
195 200 205  
Thr Lys Leu Phe Asp Ser Ile Arg Tyr  
210 215

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1498932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Met Ser Leu Glu Arg Arg Ile Ile Leu Arg Ala Leu Gly Ala Asp Leu  
1 5 10 15  
His Xaa Ser Asp Gln Arg Ile Gly Leu Lys Gly Met Leu Glu Lys Thr  
20 25 30  
Glu Ala Ile Leu Ser Lys Thr Pro Gly Gly Tyr Ile Pro Gln Gln Phe  
35 40 45  
Glu Asn Pro Ala Asn Pro Glu Ile His Tyr Arg Thr Thr Gly Pro Glu  
50 55 60  
Ile Trp Arg Asp Ser Ala Gly Lys Val Asp Ile Leu Val Ala Gly Val  
65 70 75 80  
Gly Thr Gly Gly Thr Ala Thr Gly Val Gly Lys Phe Leu Lys Glu Gln  
85 90 95  
Asn Lys Asp Ile Lys Val Cys Val Val Glu Pro Val Glu Ser Pro Val  
100 105 110  
Leu Ser Gly Gly Gln Pro Gly Pro His Leu Ile Gln Gly Ile Gly Ser  
115 120 125  
Gly Ile Val Pro Phe Asn Leu Asp Leu Thr Ile Val Asp Glu Ile Ile  
130 135 140  
Gln Val Ala Gly Glu Glu Ala Ile Glu Thr Ala Lys Leu Leu Ala Leu  
145 150 155 160  
Lys Glu Gly Leu Leu Val Gly Ile Ser Ser Gly Ala Ala Ala Ala Ala  
165 170 175  
Ala Leu Lys Val Ala Lys Arg Pro Glu Asn Ala Gly Lys Leu Ile Xaa  
180 185 190  
Val Val Phe Pro Ser Gly Gly Glu Arg Tyr Leu Ser Thr Lys Leu Phe  
195 200 205  
Asp Ser Ile Arg Tyr

210

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```
ccccgggaag agagagacta ttgaatatct ttcttccttc actttggctg agagagcgac      60
gacgatggcg gaatctcgca gcaacagagc ggcgggttcag gctactaacg acgatgcatc      120
cgccagtaaa ttgtcttggt tcaaaaaggg atatatgaaa gacgactatg ttcattctctt      180
tgtgaaaaga cctgttcgaa gatctcccat cattaatcga ggttactttt cccgttgggc      240
tgccttccga aagcttatgt ctcatgttct tctaagcggg acaagttcta agaaacagat      300
actgtcactc ggagctggct ttgatactac ctattttcag ttgctggatg aggggaatgg      360
gccaatctc tatgtggaac ttgattttaa gtaggtgact agcaagaagg ctgctgttat      420
acaaaactcc agccaactca gggacaaact aggcgccaat gcatctatct ctattgacga      480
aggaagagtt ctcatgtgat attacaagtt acttccagtt gacctgcgcg atataccaaa      540
attaagagat gttatatcct ttgcagatat ggatctaagt ctgccgacgt ttattattgc      600
agaatgtggt ttgattttatc tggaccccgga ttcaagccgt gccatcgta attggtcgtc      660
aaaaacgttt tcaactgcag tatttttctt atatgagcag atccatocag atgatgcatt      720
tgggcatcaa atgattagaa atttggagag tcgggggatgt gcaactctta gcaattgatgc      780
atcaccaact ttacttgcaa aggagagatt gtttcttgat aatggatggc agagagctgt      840
tgcctgggac atgctaaaag tgtatggtag ttttgttgat actcaagaaa aacgcaggat      900
cgagcgattg gagttgtttg acgaatttga agagtggcac atgatgcagg aacattactg      960
tgtcacatat gctgtcaatg atgcaatggg aatatgttgt gatttcgggt tcacaagaga     1020
agggggcggt gaaagaatga gctcatcagc gtcatcacct tgaaaaggag gaggggtgtgt     1080
attgcattga atccccgga cttgcaactg gaatgatgat tgattgcaca aagttagaaa     1140
ggcctttctc tgggtgctga gcagaaaacg aaggaaacac gaacttgtct gcgttatctg     1200
tgcttttgat ttagtttagg ctcatggtcg agatatgtgg gccgggcctc cccttgtttt     1260
atttttgggt gtattttcta ataattgtgc aaaacaaaga aacctcacct cgggtcaagaa     1320
acgctctgaa atct
```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```
Pro Gly Lys Arg Glu Thr Ile Glu Tyr Ser Ser Ser Phe Thr Leu Ala
1           5           10           15
Glu Arg Ala Thr Thr Met Ala Glu Ser Arg Ser Asn Arg Ala Ala Val
20           25           30
Gln Ala Thr Asn Asp Asp Ala Ser Ala Ser Lys Leu Ser Cys Val Lys
35           40           45
Lys Gly Tyr Met Lys Asp Asp Tyr Val His Leu Phe Val Lys Arg Pro
50           55           60
Val Arg Arg Ser Pro Ile Ile Asn Arg Gly Tyr Phe Ser Arg Trp Ala
65           70           75           80
Ala Phe Arg Lys Leu Met Ser Gln Phe Leu Leu Ser Gly Thr Ser Ser
85           90           95
Lys Lys Gln Ile Leu Ser Leu Gly Ala Gly Phe Asp Thr Thr Tyr Phe
```



100 105 110  
Gln Leu Leu Asp Glu Gly Asn Gly Pro Asn Leu Tyr Val Glu Leu Asp  
115 120 125  
Phe Lys  
130

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

Met Asp Leu Ser Leu Pro Thr Phe Ile Ile Ala Glu Cys Val Leu Ile  
1 5 10 15  
Tyr Leu Asp Pro Asp Ser Ser Arg Ala Ile Val Asn Trp Ser Ser Lys  
20 25 30  
Thr Phe Ser Thr Ala Val Phe Phe Leu Tyr Glu Gln Ile His Pro Asp  
35 40 45  
Asp Ala Phe Gly His Gln Met Ile Arg Asn Leu Glu Ser Arg Gly Cys  
50 55 60  
Ala Leu Leu Ser Ile Asp Ala Ser Pro Thr Leu Leu Ala Lys Glu Arg  
65 70 75 80  
Leu Phe Leu Asp Asn Gly Trp Gln Arg Ala Val Ala Trp Asp Met Leu  
85 90 95  
Lys Val Tyr Gly Ser Phe Val Asp Thr Gln Glu Lys Arg Arg Ile Glu  
100 105 110  
Arg Leu Glu Leu Phe Asp Glu Phe Glu Glu Trp His Met Met Gln Glu  
115 120 125  
His Tyr Cys Val Thr Tyr Ala Val Asn Asp Ala Met Gly Ile Phe Gly  
130 135 140  
Asp Phe Gly Phe Thr Arg Glu Gly Gly Gly Glu Arg Met Ser Ser Ser  
145 150 155 160  
Ala Ser Ser Pro

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Met Ile Arg Asn Leu Glu Ser Arg Gly Cys Ala Leu Leu Ser Ile Asp  
1 5 10 15  
Ala Ser Pro Thr Leu Leu Ala Lys Glu Arg Leu Phe Leu Asp Asn Gly  
20 25 30  
Trp Gln Arg Ala Val Ala Trp Asp Met Leu Lys Val Tyr Gly Ser Phe  
35 40 45  
Val Asp Thr Gln Glu Lys Arg Arg Ile Glu Arg Leu Glu Leu Phe Asp  
50 55 60  
Glu Phe Glu Glu Trp His Met Met Gln Glu His Tyr Cys Val Thr Tyr  
65 70 75 80

Ala Val Asn Asp Ala Met Gly Ile Phe Gly Asp Phe Gly Phe Thr Arg  
85 90 95  
Glu Gly Gly Gly Glu Arg Met Ser Ser Ser Ala Ser Ser Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

aaaaatcaag aaatatggcc acaagagctt ctacatctag cagagtctct ccagctttca 60  
ctttcctcgt catcttcttc ctottatctc tcaactgctc agtagaagct gctggtcgtg 120  
gagttaacaa tgacaagaaa ggcggcggat taggagcttc tttcatattc ggagattctc 180  
tagtcgatgc cggaaataat aattatctat cgacgttgct tagggctaata atgaagccta 240  
atggtattga ttccaagact tccggaggaa ctccctaccg cgggttcacc aatggacgga 300  
ccatcggtga tatcggtggg gaagaactcg gatcagcgaa ctacgcgatc ccgttcttgg 360  
caccagacgc gaagggaata gctttattag ccggagtga ctatgcatct ggaggaggag 420  
gaatcatgaa tgccaccggg agaatctttg tgaatagatt aggtatggat gtacaagttg 480  
atttcttcaa cactacacgg aaacagtttg atgatctact tggaaaagag aaagcaaaaag 540  
attacatagc caagaaatcg atattctcaa tcactatagg agcaaatgat ttcttcaaca 600  
attatctatt cccactactc tcggtagcat tcatgattcc tcctcctggg ccaatgcatt 660  
agagagagaa aagaaagtcc ctcaaaagtc gaagacaaag aaagatggtt aatctctctc 720  
tttatttctc ttagctctgt tttttaagat ttggaacact tgtacttggt tccaaaagat 780  
gtttttttta ggataaaacc atttgagaaa tgtattagaa gctcttgatt tctctatcta 840  
tgtctctctc tcgcc

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

Lys Ser Arg Asn Met Ala Thr Arg Ala Ser Thr Ser Ser Arg Val Ser  
1 5 10 15  
Pro Ala Phe Thr Phe Leu Val Ile Phe Phe Leu Leu Ser Leu Thr Ala  
20 25 30  
Ser Val Glu Ala Ala Gly Arg Gly Val Asn Asn Asp Lys Lys Gly Gly  
35 40 45  
Gly Leu Gly Ala Ser Phe Ile Phe Gly Asp Ser Leu Val Asp Ala Gly  
50 55 60  
Asn Asn Asn Tyr Leu Ser Thr Leu Ser Arg Ala Asn Met Lys Pro Asn  
65 70 75 80  
Gly Ile Asp Phe Lys Ala Ser Gly Gly Thr Pro Thr Gly Arg Phe Thr  
85 90 95  
Asn Gly Arg Thr Ile Gly Asp Ile Val Gly Glu Glu Leu Gly Ser Ala  
100 105 110  
Asn Tyr Ala Ile Pro Phe Leu Ala Pro Asp Ala Lys Gly Lys Ala Leu  
115 120 125  
Leu Ala Gly Val Asn Tyr Ala Ser Gly Gly Gly Gly Ile Met Asn Ala  
130 135 140

Thr Gly Arg Ile Phe Val Asn Arg Leu Gly Met Asp Val Gln Val Asp  
145 150 155 160  
Phe Phe Asn Thr Thr Arg Lys Gln Phe Asp Asp Leu Leu Gly Lys Glu  
165 170 175  
Lys Ala Lys Asp Tyr Ile Ala Lys Lys Ser Ile Phe Ser Ile Thr Ile  
180 185 190  
Gly Ala Asn Asp Phe Leu Asn Asn Tyr Leu Phe Pro Leu Leu Ser Val  
195 200 205  
Ala Phe Met Ile Pro Pro Pro Gly Pro Met His  
210 215

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

Met Ala Thr Arg Ala Ser Thr Ser Ser Arg Val Ser Pro Ala Phe Thr  
1 5 10 15  
Phe Leu Val Ile Phe Phe Leu Leu Ser Leu Thr Ala Ser Val Glu Ala  
20 25 30  
Ala Gly Arg Gly Val Asn Asn Asp Lys Lys Gly Gly Gly Leu Gly Ala  
35 40 45  
Ser Phe Ile Phe Gly Asp Ser Leu Val Asp Ala Gly Asn Asn Asn Tyr  
50 55 60  
Leu Ser Thr Leu Ser Arg Ala Asn Met Lys Pro Asn Gly Ile Asp Phe  
65 70 75 80  
Lys Ala Ser Gly Gly Thr Pro Thr Gly Arg Phe Thr Asn Gly Arg Thr  
85 90 95  
Ile Gly Asp Ile Val Gly Glu Glu Leu Gly Ser Ala Asn Tyr Ala Ile  
100 105 110  
Pro Phe Leu Ala Pro Asp Ala Lys Gly Lys Ala Leu Leu Ala Gly Val  
115 120 125  
Asn Tyr Ala Ser Gly Gly Gly Gly Ile Met Asn Ala Thr Gly Arg Ile  
130 135 140  
Phe Val Asn Arg Leu Gly Met Asp Val Gln Val Asp Phe Phe Asn Thr  
145 150 155 160  
Thr Arg Lys Gln Phe Asp Asp Leu Leu Gly Lys Glu Lys Ala Lys Asp  
165 170 175  
Tyr Ile Ala Lys Lys Ser Ile Phe Ser Ile Thr Ile Gly Ala Asn Asp  
180 185 190  
Phe Leu Asn Asn Tyr Leu Phe Pro Leu Leu Ser Val Ala Phe Met Ile  
195 200 205  
Pro Pro Pro Gly Pro Met His  
210 215

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Met	Lys	Pro	Asn	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Gly	Gly	Thr	Pro	Thr
1			5						10					15	
Gly	Arg	Phe	Thr	Asn	Gly	Arg	Thr	Ile	Gly	Asp	Ile	Val	Gly	Glu	Glu
			20					25					30		
Leu	Gly	Ser	Ala	Asn	Tyr	Ala	Ile	Pro	Phe	Leu	Ala	Pro	Asp	Ala	Lys
			35				40					45			
Gly	Lys	Ala	Leu	Leu	Ala	Gly	Val	Asn	Tyr	Ala	Ser	Gly	Gly	Gly	Gly
	50					55					60				
Ile	Met	Asn	Ala	Thr	Gly	Arg	Ile	Phe	Val	Asn	Arg	Leu	Gly	Met	Asp
65					70					75				80	
Val	Gln	Val	Asp	Phe	Phe	Asn	Thr	Thr	Arg	Lys	Gln	Phe	Asp	Asp	Leu
			85						90					95	
Leu	Gly	Lys	Glu	Lys	Ala	Lys	Asp	Tyr	Ile	Ala	Lys	Lys	Ser	Ile	Phe
			100					105					110		
Ser	Ile	Thr	Ile	Gly	Ala	Asn	Asp	Phe	Leu	Asn	Asn	Tyr	Leu	Phe	Pro
		115					120					125			
Leu	Leu	Ser	Val	Ala	Phe	Met	Ile	Pro	Pro	Pro	Gly	Pro	Met	His	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

aaacttaata	aagcctcgta	ctgagagatc	aaaacaaaac	aaaacaaaac	ccaaacactt	60
accaaataca	tcaattatcg	agaatcttcc	ttcctttaat	cctcaaaaaa	aacaaaaaac	120
tttcttcacc	tcctttccct	gattcatcct	ctaggttaat	gggtgttttc	tcgaatcttc	180
gaggaccag	agccggagct	acccacgatg	aatttccggc	gaccaatggc	tctccttcgt	240
cttcttcttc	tccatcttca	tcaatcaagc	gaaaattatc	gaatttgtaa	ccactctgcg	300
ttgctctggt	agttatcgct	gagatcgggt	ttctgggtcg	gctcgataaa	gtcgctttgg	360
ttgatacggt	gactgatttc	ttcacccagt	ctccgtcact	ctcgcagtct	ccaccggcga	420
gatccgatcg	gaagaagatc	ggattattta	ctgataggag	ctgcgaggag	tggttgatga	480
gagaagattc	agttacttac	tctagagatt	ttactaaaga	tccaattttt	atctcttggt	540
gtgaaaagga	ctttcaatgg	tggtctgtgg	attgtacatt	tggagatagt	tcagggaaaa	600
caccagatgc	tgcgttttga	ttaggtcaga	aacctggaac	tcttagtata	atacgttcca	660
tggaatcagc	acagtattat	ccaaaaaatg	atcttgacac	ggcacgacgg	tgggagaggt	720
tatgatatag	tgatgaccac	tagtctatca	tcagatgttc	ctggttgata	ttttctgtgg	780
gcggagtatg	atattatgtc	tccgggtacag	ccaaaaactg	agagagctat	tgcagctgct	840
tttattttcta	attgtgggtgc	tcggaatttt	cgtctacaag	cacttgaggc	attgatgaaa	900
actaacatta	agattgattc	ttatggtggt	tgtcatcgaa	accgggatgg	gaaagttgac	960
aaggttgaag	ctcttaagcg	atacaaatcc	agtttggctt	ttgagaatac	taacgaggaa	1020
gattatgtca	cagagaagtt	ctttcaatcc	ttagttgctg	ggcccgctcc	cgtggtagtt	1080
ggtcctccaa	atatagaaga	atttgcgcct	gcttcggact	cattccttca	cattaagact	1140
atggaagatg	tagagccagt	tgcaaagaga	atgaagtatc	tcgcagctaa	ccctgctgct	1200
tataatcaga	cactaagatg	gaaatacagc	ggctccttcag	attctttcaa	ggcacttggt	1260
gatatggctg	ctgtacactc	ttcttgccgt	ctctgcattt	tcctggccac	gagggtccga	1320
gaacaagaag	aggaaagccc	taatttcaag	aaacgaccgt	gcaaatgtag	caggggagga	1380
tcagacacag	tttatcatgt	ttttgttaga	gaaagaggcc	ggtttgaaat	ggaatcagtc	1440
tttttgaggg	gtaaaagtgt	gactcaggaa	gctctagaat	ctgcagttct	cgccaagttc	1500
aagtctttta	aacatgaggg	agtgtggaag	aaggaaaggg	ctggaaactt	aaaaggagac	1560
aaagagctta	aaatacatcg	gatttaccgc	cttggcctaa	cgcaacgaca	ggctttgtac	1620
aacttcaaat	tcgaggggaaa	ttcgagtcta	agtagtcaca	ttcaaaaaca	cccttggtgt	1680
aaatttgagg	ttgtcttcgt	ctagtttcat	tcctctggat	ctgtcacagg	tatcatctca	1740
gctaagaaga	catttctctg	tgctagaatc	gcaaagtgtc	aaacaaaccg	attagatgaa	1800

```
acaaaagggtt aatagtcatg agattggtga actcattttg tttaggcagt gtatctgtaa 1860
atcgttctga cattgcagac gatgtgttct tgatagctgg atgcataaat gtttgaagat 1920
ttagagcaat ttgatagttt tgaatctctt gagagtgtgt taattaatct ttaaattttt 1980
cc
```

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

```
Met Ile Leu His Arg His Asp Gly Gly Arg Gly Tyr Asp Ile Val Met
1      5      10      15
Thr Thr Ser Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp Ala
20     25     30
Glu Tyr Asp Ile Met Ser Pro Val Gln Pro Lys Thr Glu Arg Ala Ile
35     40     45
Ala Ala Ala Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu Gln
50     55     60
Ala Leu Glu Ala Leu Met Lys Thr Asn Ile Lys Ile Asp Ser Tyr Gly
65     70     75     80
Gly Cys His Arg Asn Arg Asp Gly Lys Val Asp Lys Val Glu Ala Leu
85     90     95
Lys Arg Tyr Lys Phe Ser Leu Ala Phe Glu Asn Thr Asn Glu Glu Asp
100    105    110
Tyr Val Thr Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Ser Val Pro
115    120    125
Val Val Val Gly Pro Pro Asn Ile Glu Glu Phe Ala Pro Ala Ser Asp
130    135    140
Ser Phe Leu His Ile Lys Thr Met Glu Asp Val Glu Pro Val Ala Lys
145    150    155    160
Arg Met Lys Tyr Leu Ala Ala Asn Pro Ala Ala Tyr Asn Gln Thr Leu
165    170    175
Arg Trp Lys Tyr Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val Asp
180    185    190
Met Ala Ala Val His Ser Ser Cys Arg Leu Cys Ile Phe Leu Ala Thr
195    200    205
Arg Val Arg Glu Gln Glu Glu Ser Pro Asn Phe Lys Lys Arg Pro
210    215    220
Cys Lys Cys Ser Arg Gly Gly Ser Asp Thr Val Tyr His Val Phe Val
225    230    235    240
Arg Glu Arg Gly Arg Phe Glu Met Glu Ser Val Phe Leu Arg Gly Lys
245    250    255
Ser Val Thr Gln Glu Ala Leu Glu Ser Ala Val Leu Ala Lys Phe Lys
260    265    270
Ser Leu Lys His Glu Ala Val Trp Lys Lys Glu Arg Pro Gly Asn Leu
275    280    285
Lys Gly Asp Lys Glu Leu Lys Ile His Arg Ile Tyr Pro Leu Gly Leu
290    295    300
Thr Gln Arg Gln Ala Leu Tyr Asn Phe Lys Phe Glu Gly Asn Ser Ser
305    310    315    320
Leu Ser Ser His Ile Gln Asn Asn Pro Cys Ala Lys Phe Glu Val Val
325    330    335
Phe Val
```

(2) INFORMATION FOR SEQ ID NO:752:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 323 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..323  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

Met	Thr	Thr	Ser	Leu	Ser	Ser	Asp	Val	Pro	Val	Gly	Tyr	Phe	Ser	Trp
1				5					10					15	
Ala	Glu	Tyr	Asp	Ile	Met	Ser	Pro	Val	Gln	Pro	Lys	Thr	Glu	Arg	Ala
			20					25					30		
Ile	Ala	Ala	Ala	Phe	Ile	Ser	Asn	Cys	Gly	Ala	Arg	Asn	Phe	Arg	Leu
		35				40						45			
Gln	Ala	Leu	Glu	Ala	Leu	Met	Lys	Thr	Asn	Ile	Lys	Ile	Asp	Ser	Tyr
	50					55					60				
Gly	Gly	Cys	His	Arg	Asn	Arg	Asp	Gly	Lys	Val	Asp	Lys	Val	Glu	Ala
65					70					75				80	
Leu	Lys	Arg	Tyr	Lys	Phe	Ser	Leu	Ala	Phe	Glu	Asn	Thr	Asn	Glu	Glu
				85					90					95	
Asp	Tyr	Val	Thr	Glu	Lys	Phe	Phe	Gln	Ser	Leu	Val	Ala	Gly	Ser	Val
			100					105					110		
Pro	Val	Val	Val	Gly	Pro	Pro	Asn	Ile	Glu	Glu	Phe	Ala	Pro	Ala	Ser
		115					120						125		
Asp	Ser	Phe	Leu	His	Ile	Lys	Thr	Met	Glu	Asp	Val	Glu	Pro	Val	Ala
	130					135					140				
Lys	Arg	Met	Lys	Tyr	Leu	Ala	Ala	Asn	Pro	Ala	Ala	Tyr	Asn	Gln	Thr
145					150					155				160	
Leu	Arg	Trp	Lys	Tyr	Glu	Gly	Pro	Ser	Asp	Ser	Phe	Lys	Ala	Leu	Val
			165						170					175	
Asp	Met	Ala	Ala	Val	His	Ser	Ser	Cys	Arg	Leu	Cys	Ile	Phe	Leu	Ala
		180						185					190		
Thr	Arg	Val	Arg	Glu	Gln	Glu	Glu	Ser	Pro	Asn	Phe	Lys	Lys	Arg	
		195					200					205			
Pro	Cys	Lys	Cys	Ser	Arg	Gly	Gly	Ser	Asp	Thr	Val	Tyr	His	Val	Phe
	210					215					220				
Val	Arg	Glu	Arg	Gly	Arg	Phe	Glu	Met	Glu	Ser	Val	Phe	Leu	Arg	Gly
225				230						235				240	
Lys	Ser	Val	Thr	Gln	Glu	Ala	Leu	Glu	Ser	Ala	Val	Leu	Ala	Lys	Phe
			245						250					255	
Lys	Ser	Leu	Lys	His	Glu	Ala	Val	Trp	Lys	Lys	Glu	Arg	Pro	Gly	Asn
		260						265					270		
Leu	Lys	Gly	Asp	Lys	Glu	Leu	Lys	Ile	His	Arg	Ile	Tyr	Pro	Leu	Gly
	275					280					285				
Leu	Thr	Gln	Arg	Gln	Ala	Leu	Tyr	Asn	Phe	Lys	Phe	Glu	Gly	Asn	Ser
	290					295					300				
Ser	Leu	Ser	Ser	His	Ile	Gln	Asn	Asn	Pro	Cys	Ala	Lys	Phe	Glu	Val
305					310					315				320	
Val	Phe	Val													

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 302 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1498944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Met	Ser	Pro	Val	Gln	Pro	Lys	Thr	Glu	Arg	Ala	Ile	Ala	Ala	Ala	Phe	
1				5				10						15		
Ile	Ser	Asn	Cys	Gly	Ala	Arg	Asn	Phe	Arg	Leu	Gln	Ala	Leu	Glu	Ala	
		20						25					30			
Leu	Met	Lys	Thr	Asn	Ile	Lys	Ile	Asp	Ser	Tyr	Gly	Gly	Cys	His	Arg	
		35					40					45				
Asn	Arg	Asp	Gly	Lys	Val	Asp	Lys	Val	Glu	Ala	Leu	Lys	Arg	Tyr	Lys	
	50					55					60					
Phe	Ser	Leu	Ala	Phe	Glu	Asn	Thr	Asn	Glu	Glu	Asp	Tyr	Val	Thr	Glu	
65				70					75					80		
Lys	Phe	Phe	Gln	Ser	Leu	Val	Ala	Gly	Ser	Val	Pro	Val	Val	Val	Gly	
			85					90						95		
Pro	Pro	Asn	Ile	Glu	Glu	Phe	Ala	Pro	Ala	Ser	Asp	Ser	Phe	Leu	His	
		100						105					110			
Ile	Lys	Thr	Met	Glu	Asp	Val	Glu	Pro	Val	Ala	Lys	Arg	Met	Lys	Tyr	
	115						120					125				
Leu	Ala	Ala	Asn	Pro	Ala	Ala	Tyr	Asn	Gln	Thr	Leu	Arg	Trp	Lys	Tyr	
	130				135						140					
Glu	Gly	Pro	Ser	Asp	Ser	Phe	Lys	Ala	Leu	Val	Asp	Met	Ala	Ala	Val	
145				150					155					160		
His	Ser	Ser	Cys	Arg	Leu	Cys	Ile	Phe	Leu	Ala	Thr	Arg	Val	Arg	Glu	
			165					170						175		
Gln	Glu	Glu	Glu	Ser	Pro	Asn	Phe	Lys	Lys	Arg	Pro	Cys	Lys	Cys	Ser	
		180						185					190			
Arg	Gly	Gly	Ser	Asp	Thr	Val	Tyr	His	Val	Phe	Val	Arg	Glu	Arg	Gly	
	195						200					205				
Arg	Phe	Glu	Met	Glu	Ser	Val	Phe	Leu	Arg	Gly	Lys	Ser	Val	Thr	Gln	
	210					215					220					
Glu	Ala	Leu	Glu	Ser	Ala	Val	Leu	Ala	Lys	Phe	Lys	Ser	Leu	Lys	His	
225				230					235					240		
Glu	Ala	Val	Trp	Lys	Glu	Arg	Pro	Gly	Asn	Leu	Lys	Gly	Asp	Lys		
			245					250					255			
Glu	Leu	Lys	Ile	His	Arg	Ile	Tyr	Pro	Leu	Gly	Leu	Thr	Gln	Arg	Gln	
	260						265						270			
Ala	Leu	Tyr	Asn	Phe	Lys	Phe	Glu	Gly	Asn	Ser	Ser	Leu	Ser	Ser	His	
	275					280						285				
Ile	Gln	Asn	Asn	Pro	Cys	Ala	Lys	Phe	Glu	Val	Val	Phe	Val			
	290					295					300					

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1299 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1299

(D) OTHER INFORMATION: / Ceres Seq. ID 1498949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

cttttagaca	aaactagtgg	cagactgaaa	aatgaacgca	gcgcttgcaa	caaccaccgc	60
cacaactccc	gcactccgcc	gtgagacgcc	tcttattcat	tattgttctc	tcacaacaaa	120
atcgccgggt	taccaaata	acagagttag	attcggatct	tgctgcaaaa	cagtcagcaa	180
gaaattcttg	aaaatctcgg	cgagctctca	gagcgcttca	gcggcggtca	atatcacggc	240
ggatgcttcg	attccgaaag	agatgaaggc	gtgggtgtat	agtgactacg	gcggagttga	300
tgttttgaaa	ctggagagta	acattgctgt	gccggagatt	aaagaagatc	aggttctgat	360
taaagttgtt	gcggcgggtc	ttaatcccg	cgatgctaag	agacggcagg	ggaaatttaa	420

(2) INFORMATION FOR SEQ ID NO:755:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1498950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

Met 1	Asn	Ala	Ala	Leu	Ala	Thr	Thr	Thr	Ala	Thr	Thr	Pro	Ala	Leu	Arg
Arg	Glu	Thr	Pro	Leu	Ile	His	Tyr	Cys	Ser	Leu	Thr	Thr	Lys	Ser	Pro
Val	Tyr	Gln	Ile	Asn	Arg	Val	Arg	Phe	Gly	Ser	Cys	Val	Gln	Thr	Val
Ser	Lys	Lys	Phe	Leu	Lys	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ala	Ser	Ala
Ala 65	Val	Asn	Ile	Thr	Ala	Asp	Ala	Ser	Ile	Pro	Lys	Glu	Met	Lys	Ala
Trp	Val	Tyr	Ser	Asp	Tyr	Gly	Gly	Val	Asp	Val	Leu	Lys	Leu	Glu	Ser
Asn	Ile	Ala	Val	Pro	Glu	Ile	Lys	Glu	Asp	Gln	Val	Leu	Ile	Lys	Val
Val	Ala	Ala	Gly	Leu	Asn	Pro	Val	Asp	Ala	Lys	Arg	Arg	Gln	Gly	Lys
Phe	Lys	Ala	Thr	Asp	Ser	Pro	Leu	Pro	Thr	Val	Pro	Gly	Tyr	Asp	Val
Ala 145	Gly	Val	Val	Val	Lys	Val	Gly	Ser	Ala	Val	Lys	Asp	Phe	Lys	Glu
Gly	Asp	Glu	Val	Tyr	Ala	Asn	Val	Ser	Glu	Lys	Ala	Leu	Glu	Gly	Pro
Lys	Gln	Phe	Gly	Ser	Leu	Ala	Glu	Tyr	Thr	Ala	Val	Glu	Glu	Lys	Leu
Leu	Ala	Leu	Lys	Pro	Lys	Asn	Ile	Asp	Phe	Ala	Gln	Ala	Ala	Gly	Leu
Pro	Leu	Ala	Ile	Glu	Thr	Ala	Asp	Glu	Gly	Leu	Val	Arg	Thr	Glu	Phe
Ser 225	Ala	Gly	Lys	Ser	Ile	Leu	Val	Leu	Asn	Gly	Ala	Gly	Gly	Val	Gly
Ser	Leu	Met	Ile	Gln	Leu	Ala	Lys	His	Val	Tyr	Gly	Ala	Ser	Lys	Val
Ala	Ala	Thr	Ala	Ser	Thr	Gly	Lys	Leu	Glu	Leu	Val	Arg	Ser	Leu	Gly



Ala Asp Leu Ala Ile Asp Tyr Thr Lys Glu Asn Ile Glu Asp Leu Pro  
275 280 285  
Asp Lys Tyr Asp Val Val Phe Asp Ala Ile Gly Met Cys Asp Lys Ala  
290 295 300  
Val Lys Val Ile Lys Glu Gly Gly Lys Val Val Ala Leu Thr Gly Ala  
305 310 315 320  
Val Thr Pro Pro Gly Phe Arg Phe Val Val Thr Ser Asn Gly Asp Val  
325 330 335  
Leu Lys Lys Leu Asn Pro Tyr Ile Glu Ser Gly Lys Val Lys Pro Val  
340 345 350  
Val Asp Pro Lys Gly Pro Phe Pro Phe Ser Arg Val Ala Asp Ala Phe  
355 360 365  
Ser Tyr Leu Glu Thr Asn His Ala Thr Gly Lys Val Val Val Tyr Pro  
370 375 380  
Ile Pro  
385

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1498951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Met Lys Ala Trp Val Tyr Ser Asp Tyr Gly Gly Val Asp Val Leu Lys  
1 5 10 15  
Leu Glu Ser Asn Ile Ala Val Pro Glu Ile Lys Glu Asp Gln Val Leu  
20 25 30  
Ile Lys Val Val Ala Ala Gly Leu Asn Pro Val Asp Ala Lys Arg Arg  
35 40 45  
Gln Gly Lys Phe Lys Ala Thr Asp Ser Pro Leu Pro Thr Val Pro Gly  
50 55 60  
Tyr Asp Val Ala Gly Val Val Val Lys Val Gly Ser Ala Val Lys Asp  
65 70 75 80  
Phe Lys Glu Gly Asp Glu Val Tyr Ala Asn Val Ser Glu Lys Ala Leu  
85 90 95  
Glu Gly Pro Lys Gln Phe Gly Ser Leu Ala Glu Tyr Thr Ala Val Glu  
100 105 110  
Glu Lys Leu Leu Ala Leu Lys Pro Lys Asn Ile Asp Phe Ala Gln Ala  
115 120 125  
Ala Gly Leu Pro Leu Ala Ile Glu Thr Ala Asp Glu Gly Leu Val Arg  
130 135 140  
Thr Glu Phe Ser Ala Gly Lys Ser Ile Leu Val Leu Asn Gly Ala Gly  
145 150 155 160  
Gly Val Gly Ser Leu Met Ile Gln Leu Ala Lys His Val Tyr Gly Ala  
165 170 175  
Ser Lys Val Ala Ala Thr Ala Ser Thr Gly Lys Leu Glu Leu Val Arg  
180 185 190  
Ser Leu Gly Ala Asp Leu Ala Ile Asp Tyr Thr Lys Glu Asn Ile Glu  
195 200 205  
Asp Leu Pro Asp Lys Tyr Asp Val Val Phe Asp Ala Ile Gly Met Cys  
210 215 220  
Asp Lys Ala Val Lys Val Ile Lys Glu Gly Gly Lys Val Val Ala Leu  
225 230 235 240  
Thr Gly Ala Val Thr Pro Pro Gly Phe Arg Phe Val Val Thr Ser Asn  
245 250 255  
Gly Asp Val Leu Lys Lys Leu Asn Pro Tyr Ile Glu Ser Gly Lys Val

```

                260                265                270
Lys Pro Val Val Asp Pro Lys Gly Pro Phe Pro Phe Ser Arg Val Ala
                275                280                285
Asp Ala Phe Ser Tyr Leu Glu Thr Asn His Ala Thr Gly Lys Val Val
                290                295                300
Val Tyr Pro Ile Pro
305
```

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1347

(D) OTHER INFORMATION: / Ceres Seq. ID 1498952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

```

acgaataaga aaagaagaga aacatcaaac atctttgggtt tgcttccctc gtacccgttc      60
ttcatacaag tatgatcatc tgctgtctct atatagacat acatacaaaa aaaacttgta      120
taagatttga aactaaaata ttaaatttat cctctatttt gcaggcacgc ctttaattat      180
ggattgtcat agaaagtcgt tcttgttgaa gtttttgtgc gtggcatttc tgttaaacta      240
cagcaatgtt ggctttgtag acgcagcaac aaacattggc ttgaactacg gcctccttgg      300
agacaacctc ccgcctccat ctgaagttat caacctctac aagtccttaa gtgttaccaa      360
tattcggatc ttcgacacga ctacggatgt ccttaacgcc tttcgaggga atcgcgatat      420
tggagttatg gtaggcgtga agaaccaaga cttagaggct ctttcggtca gcgaagacgc      480
tgттаacacc tggttcgtga caaacattga gccttactta gctgatgtca acatcacgtt      540
cattgctgtc gggaacgaag tcatcccagg ggaaatcggc tcttatgtgc taccgcgtcat      600
gaaatctctc accaacattg tcaagtcgag gagtctcccg atcttgatca gcaccacggt      660
ggctatgacc aaccttggcc agtcgtatcc accttcggcc ggagatttca tacctcaagc      720
gcgtgaacaa cttaccccgg tgctgaagtt tttgtctcaa acaaatacgc ctatcctcgt      780
caacatctac ccctacttcg catatgctgc tgatcctatc aacattcagc ttgattatgc      840
catcttcaac accaacaagg ttgtgggtcca agttatacaa acatgttcga tgtgatattt      900
gatgctttcg tatgggcaat ggagaaagag ggcgtgaagg atttaccaat ggtggtaaca      960
gagaccggat ggccatctgc tggtaacgga aacttaacaa ctccagatat cgcattctata      1020
tacaatacca attttgttaa acatgtggaa agcggtaaaag ggacgcaaaa gagaccaaaag      1080
agtggcatta gtggatttct atttgcgacg ttcaatgaga atcaaaaagcc agcgggaacc      1140
gaacaaaatt ttgggttata taatccaaca gatatgaagc ccattctaaa gatgttttga      1200
tttttagatt cttgatttta tagacaatcc caaatcatta gtaaattaat gatgctctaa      1260
tagttgtaat agagcgggat aaaatcaaga tctacaacaa cattcatttt atatgttgta      1320
tgatcttctt aaataaaaaa acttaag
```

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1498953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

```

Met Asp Cys His Arg Lys Ser Phe Leu Leu Lys Phe Leu Cys Val Ala
1                5                10                15
Phe Leu Leu Asn Tyr Ser Asn Val Gly Phe Val Asp Ala Ala Thr Asn
                20                25                30
Ile Gly Leu Asn Tyr Gly Leu Leu Gly Asp Asn Leu Pro Pro Ser
                35                40                45
Glu Val Ile Asn Leu Tyr Lys Ser Leu Ser Val Thr Asn Ile Arg Ile
```

50					55					60					
Phe	Asp	Thr	Thr	Thr	Asp	Val	Leu	Asn	Ala	Phe	Arg	Gly	Asn	Arg	Asp
65					70					75					80
Ile	Gly	Val	Met	Val	Gly	Val	Lys	Asn	Gln	Asp	Leu	Glu	Ala	Leu	Ser
				85					90					95	
Val	Ser	Glu	Asp	Ala	Val	Asn	Thr	Trp	Phe	Val	Thr	Asn	Ile	Glu	Pro
			100					105					110		
Tyr	Leu	Ala	Asp	Val	Asn	Ile	Thr	Phe	Ile	Ala	Val	Gly	Asn	Glu	Val
		115					120					125			
Ile	Pro	Gly	Glu	Ile	Gly	Ser	Tyr	Val	Leu	Pro	Val	Met	Lys	Ser	Leu
130						135					140				
Thr	Asn	Ile	Val	Lys	Ser	Arg	Ser	Leu	Pro	Ile	Leu	Ile	Ser	Thr	Thr
145					150					155					160
Val	Ala	Met	Thr	Asn	Leu	Gly	Gln	Ser	Tyr	Pro	Pro	Ser	Ala	Gly	Asp
				165					170					175	
Phe	Ile	Pro	Gln	Ala	Arg	Glu	Gln	Leu	Thr	Pro	Val	Leu	Lys	Phe	Leu
			180					185					190		
Ser	Gln	Thr	Asn	Thr	Pro	Ile	Leu	Val	Asn	Ile	Tyr	Pro	Tyr	Phe	Ala
		195					200					205			
Tyr	Ala	Ala	Asp	Pro	Ile	Asn	Ile	Gln	Leu	Asp	Tyr	Ala	Ile	Phe	Asn
210						215					220				
Thr	Asn	Lys	Val	Val	Val	Gln	Val	Ile	Gln	Thr	Cys	Ser	Met		
225					230					235					

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1498954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

Met	Val	Gly	Val	Lys	Asn	Gln	Asp	Leu	Glu	Ala	Leu	Ser	Val	Ser	Glu
1			5					10						15	
Asp	Ala	Val	Asn	Thr	Trp	Phe	Val	Thr	Asn	Ile	Glu	Pro	Tyr	Leu	Ala
		20					25					30			
Asp	Val	Asn	Ile	Thr	Phe	Ile	Ala	Val	Gly	Asn	Glu	Val	Ile	Pro	Gly
		35				40					45				
Glu	Ile	Gly	Ser	Tyr	Val	Leu	Pro	Val	Met	Lys	Ser	Leu	Thr	Asn	Ile
		50				55				60					
Val	Lys	Ser	Arg	Ser	Leu	Pro	Ile	Leu	Ile	Ser	Thr	Thr	Val	Ala	Met
65					70					75					80
Thr	Asn	Leu	Gly	Gln	Ser	Tyr	Pro	Pro	Ser	Ala	Gly	Asp	Phe	Ile	Pro
			85					90					95		
Gln	Ala	Arg	Glu	Gln	Leu	Thr	Pro	Val	Leu	Lys	Phe	Leu	Ser	Gln	Thr
		100					105					110			
Asn	Thr	Pro	Ile	Leu	Val	Asn	Ile	Tyr	Pro	Tyr	Phe	Ala	Tyr	Ala	Ala
		115					120				125				
Asp	Pro	Ile	Asn	Ile	Gln	Leu	Asp	Tyr	Ala	Ile	Phe	Asn	Thr	Asn	Lys
	130					135					140				
Val	Val	Val	Gln	Val	Ile	Gln	Thr	Cys	Ser	Met					
145				150						155					

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1453 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1453

(D) OTHER INFORMATION: / Ceres Seq. ID 1498958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

```
aaaagaaaat tgtcaatttc gaaaaatgtt gagcacaagc tctgatcttc atggccgtct 60
tctccgatta tcagaaccaa tagcagagat tcttagacgt acacagtaca caccgcaaga 120
gagcagcaaa gtatccacca aagatatact cttgtccttg ttaccaaaca cttcgtcttc 180
tcgtctcgcc aatgaagaat cgvtcaaaag tctcgcgctt gcttgtgccc ttctcgcttc 240
ttcacgttca tccactcacg aacttctctc atgggattycc agaaaacctc tctgtcatgg 300
gggaatctac attttgggag atttcaaggg attgtttcag tgatttttct agcaacagta 360
atgctgagaa gcttgtggaa ttggtagagg atagtggaaa gatcgaaatg ttgccgatag 420
ttttgccgga gttaaaagat ggaatcgaaa agagttcact tggtaaaggc agtgatgcag 480
aggatgtttc agctgcaatg gctagaacac ctgttggtta tgctatactt gctgctcacc 540
agctcaggtg gtttgttact cagggttaaaa aaccgaattt ggtgaaattt tgtaacttgg 600
tggttccctg tgctttgaca gcacttgatc attggtctcc tgaagtcaaa gggcagggta 660
tgataacctt tgttcatctt gctaaaaatg tgagttccgg tgatcttggg ttgtatggag 720
atgtggttct tgatgcgtgt tgccagaata tagcttccga tgatgagatt tggatacatg 780
tggtagagtt atctgtgctt cttgttacta aaatccaccc aaataatcct cgaagcccgt 840
ggtagagaaa gatcatgaat gagatgctcg ggcatttgga acgccaacca agaaataagg 900
agcgacgtat cacttggcta agatttgttg agccactctt gaactctcta gggcttttct 960
tacttgctca ttttcgacgt atcttccctc ttttctttca gtggatgcat tcagacgacg 1020
ccgaaacagt tctgttggtt cttgagagac tggagacagt tgtgagggtt acgtggatta 1080
gacactcacc tgtgttccca agattggttg atgagcttgt ttccttgtag aaagagtcac 1140
cgatgcgtaa ggatcgcgat gatattagac ctcttatcct ccgtatcttg atgctactcc 1200
gccagtgcaa aggtctacgg tttgagtcag cgtggagtca ataccaggag gatccaaatc 1260
tgagtactgt tagtcaacat atattgacta gttcaagttg atctcaagag cgtatggttg 1320
actaaaacag ccattttttt tctaattttc gatattagtt tgggtctaggc ctagtgatgc 1380
aagtaattac tggcgaatcc tcgaattttt gtaagcattt ggctcttgac tcttcttaag 1440
ctaattctgat ttg
```

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1498959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

```
Met Lys Asn Xaa Ser Lys Val Ser Arg Leu Leu Val Pro Phe Ser Leu
1          5          10          15
Leu His Val His Pro Leu Thr Asn Phe Ser His Gly Xaa Pro Glu Asn
20          25          30
Leu Ser Val Met Gly Glu Ser Thr Phe Trp Glu Ile Ser Arg Asp Cys
35          40          45
Phe Ser Asp Phe Ser Ser Asn Ser Asn Ala Glu Lys Leu Val Glu Leu
50          55          60
Val Glu Asp Ser Glu Lys Ile Glu Met Leu Pro Ile Val Leu Pro Glu
65          70          75          80
Leu Lys Asp Gly Ile Glu Lys Ser Ser Leu Gly Lys Gly Ser Asp Ala
85          90          95
Glu Asp Val Ser Ala Ala Met Ala Arg Thr Pro Val Gly Tyr Ala Ile
100          105          110
Leu Ala Ala His Gln Leu Arg Trp Phe Val Thr Gln Val Lys Lys Pro
115          120          125
Asn Leu Val Lys Phe Cys Asn Leu Val Val Pro Cys Ala Leu Thr Ala
130          135          140
```

Leu	Asp	His	Trp	Ser	Pro	Glu	Val	Lys	Gly	Gln	Gly	Met	Ile	Thr	Phe
145					150					155					160
Val	His	Leu	Ala	Lys	Asn	Val	Ser	Ser	Gly	Asp	Leu	Gly	Leu	Tyr	Gly
			165						170						175
Asp	Val	Val	Leu	Asp	Ala	Cys	Cys	Gln	Asn	Ile	Ala	Ser	Asp	Asp	Glu
			180					185					190		
Ile	Trp	Ile	His	Val	Val	Glu	Leu	Ser	Val	Leu	Leu	Val	Thr	Lys	Ile
	195					200						205			
His	Pro	Asn	Asn	Pro	Arg	Ser	Pro	Trp	Tyr	Glu	Lys	Ile	Met	Asn	Glu
	210				215						220				
Met	Leu	Gly	His	Leu	Glu	Arg	Gln	Pro	Arg	Asn	Lys	Glu	Arg	Arg	Ile
225					230					235					240
Thr	Trp	Leu	Arg	Phe	Val	Glu	Pro	Leu	Leu	Asn	Ser	Leu	Gly	Leu	Phe
			245					250						255	
Leu	Leu	Ala	His	Phe	Arg	Arg	Ile	Phe	Pro	Leu	Phe	Phe	Gln	Trp	Met
			260					265					270		
His	Ser	Asp	Asp	Ala	Glu	Thr	Val	Leu	Leu	Val	Leu	Glu	Arg	Leu	Glu
	275						280					285			
Thr	Val	Val	Arg	Leu	Thr	Trp	Ile	Arg	His	Ser	Pro	Val	Phe	Pro	Arg
	290					295					300				
Leu	Val	Asp	Glu	Leu	Val	Ser	Leu	Tyr	Lys	Glu	Ser	Ser	Met	Arg	Lys
305					310					315					320
Asp	Arg	Asp	Asp	Ile	Arg	Pro	Leu	Ile	Leu	Arg	Ile	Leu	Met	Leu	Leu
			325					330					335		
Arg	Gln	Cys	Lys	Gly	Leu	Arg	Phe	Glu	Ser	Ala	Trp	Ser	Gln	Tyr	Gln
		340						345					350		
Glu	Asp	Pro	Asn	Leu	Ser	Thr	Val	Ser	Gln	His	Ile	Trp	Thr	Ser	Ser
	355						360					365			
Ser															

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

Met	Gly	Glu	Ser	Thr	Phe	Trp	Glu	Ile	Ser	Arg	Asp	Cys	Phe	Ser	Asp
1			5				10							15	
Phe	Ser	Ser	Asn	Ser	Asn	Ala	Glu	Lys	Leu	Val	Glu	Leu	Val	Glu	Asp
			20				25						30		
Ser	Glu	Lys	Ile	Glu	Met	Leu	Pro	Ile	Val	Leu	Pro	Glu	Leu	Lys	Asp
		35				40						45			
Gly	Ile	Glu	Lys	Ser	Ser	Leu	Gly	Lys	Gly	Ser	Asp	Ala	Glu	Asp	Val
	50					55					60				
Ser	Ala	Ala	Met	Ala	Arg	Thr	Pro	Val	Gly	Tyr	Ala	Ile	Leu	Ala	Ala
65					70				75					80	
His	Gln	Leu	Arg	Trp	Phe	Val	Thr	Gln	Val	Lys	Lys	Pro	Asn	Leu	Val
			85					90					95		
Lys	Phe	Cys	Asn	Leu	Val	Val	Pro	Cys	Ala	Leu	Thr	Ala	Leu	Asp	His
		100					105					110			
Trp	Ser	Pro	Glu	Val	Lys	Gly	Gln	Gly	Met	Ile	Thr	Phe	Val	His	Leu
	115					120					125				
Ala	Lys	Asn	Val	Ser	Ser	Gly	Asp	Leu	Gly	Leu	Tyr	Gly	Asp	Val	Val
	130					135					140				
Leu	Asp	Ala	Cys	Cys	Gln	Asn	Ile	Ala	Ser	Asp	Asp	Glu	Ile	Trp	Ile

145		150		155		160									
His	Val	Val	Glu	Leu	Ser	Val	Leu	Leu	Val	Thr	Lys	Ile	His	Pro	Asn
			165						170					175	
Asn	Pro	Arg	Ser	Pro	Trp	Tyr	Glu	Lys	Ile	Met	Asn	Glu	Met	Leu	Gly
			180					185					190		
His	Leu	Glu	Arg	Gln	Pro	Arg	Asn	Lys	Glu	Arg	Arg	Ile	Thr	Trp	Leu
		195					200					205			
Arg	Phe	Val	Glu	Pro	Leu	Leu	Asn	Ser	Leu	Gly	Leu	Phe	Leu	Leu	Ala
	210					215					220				
His	Phe	Arg	Arg	Ile	Phe	Pro	Leu	Phe	Phe	Gln	Trp	Met	His	Ser	Asp
225				230						235				240	
Asp	Ala	Glu	Thr	Val	Leu	Leu	Val	Leu	Glu	Arg	Leu	Glu	Thr	Val	Val
			245						250				255		
Arg	Leu	Thr	Trp	Ile	Arg	His	Ser	Pro	Val	Phe	Pro	Arg	Leu	Val	Asp
		260						265					270		
Glu	Leu	Val	Ser	Leu	Tyr	Lys	Glu	Ser	Ser	Met	Arg	Lys	Asp	Arg	Asp
	275						280					285			
Asp	Ile	Arg	Pro	Leu	Ile	Leu	Arg	Ile	Leu	Met	Leu	Leu	Arg	Gln	Cys
	290				295					300					
Lys	Gly	Leu	Arg	Phe	Glu	Ser	Ala	Trp	Ser	Gln	Tyr	Gln	Glu	Asp	Pro
305				310						315				320	
Asn	Leu	Ser	Thr	Val	Ser	Gln	His	Ile	Trp	Thr	Ser	Ser	Ser		
			325						330						

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

Met	Leu	Pro	Ile	Val	Leu	Pro	Glu	Leu	Lys	Asp	Gly	Ile	Glu	Lys	Ser
1			5					10					15		
Ser	Leu	Gly	Lys	Gly	Ser	Asp	Ala	Glu	Asp	Val	Ser	Ala	Ala	Met	Ala
		20					25					30			
Arg	Thr	Pro	Val	Gly	Tyr	Ala	Ile	Leu	Ala	Ala	His	Gln	Leu	Arg	Trp
	35					40					45				
Phe	Val	Thr	Gln	Val	Lys	Lys	Pro	Asn	Leu	Val	Lys	Phe	Cys	Asn	Leu
	50				55					60					
Val	Val	Pro	Cys	Ala	Leu	Thr	Ala	Leu	Asp	His	Trp	Ser	Pro	Glu	Val
65			70					75					80		
Lys	Gly	Gln	Gly	Met	Ile	Thr	Phe	Val	His	Leu	Ala	Lys	Asn	Val	Ser
			85				90						95		
Ser	Gly	Asp	Leu	Gly	Leu	Tyr	Gly	Asp	Val	Val	Leu	Asp	Ala	Cys	Cys
	100						105					110			
Gln	Asn	Ile	Ala	Ser	Asp	Asp	Glu	Ile	Trp	Ile	His	Val	Val	Glu	Leu
	115					120					125				
Ser	Val	Leu	Leu	Val	Thr	Lys	Ile	His	Pro	Asn	Asn	Pro	Arg	Ser	Pro
	130				135					140					
Trp	Tyr	Glu	Lys	Ile	Met	Asn	Glu	Met	Leu	Gly	His	Leu	Glu	Arg	Gln
145			150					155					160		
Pro	Arg	Asn	Lys	Glu	Arg	Arg	Ile	Thr	Trp	Leu	Arg	Phe	Val	Glu	Pro
			165					170					175		
Leu	Leu	Asn	Ser	Leu	Gly	Leu	Phe	Leu	Leu	Ala	His	Phe	Arg	Arg	Ile
		180				185						190			
Phe	Pro	Leu	Phe	Phe	Gln	Trp	Met	His	Ser	Asp	Asp	Ala	Glu	Thr	Val
	195					200						205			

Leu Leu Val Leu Glu Arg Leu Glu Thr Val Val Arg Leu Thr Trp Ile  
210 215 220  
Arg His Ser Pro Val Phe Pro Arg Leu Val Asp Glu Leu Val Ser Leu  
225 230 235 240  
Tyr Lys Glu Ser Ser Met Arg Lys Asp Arg Asp Asp Ile Arg Pro Leu  
245 250 255  
Ile Leu Arg Ile Leu Met Leu Leu Arg Gln Cys Lys Gly Leu Arg Phe  
260 265 270  
Glu Ser Ala Trp Ser Gln Tyr Gln Glu Asp Pro Asn Leu Ser Thr Val  
275 280 285  
Ser Gln His Ile Trp Thr Ser Ser Ser  
290 295

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..637
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

rgaatttcac	cgcatgtatc	gtgcattggc	tgaacggtat	gatcaagcta	gtggtgagct	60
acagaagaac	catacatctg	agatccagtc	acagagctct	cttgagttat	catctcctac	120
caaagagaag	ttgagtcgcc	gtcaatctgg	ccataaagaa	gaggaagatt	catcatcttt	180
gacagattcc	ggttctgatt	ctgatcattc	ctctgccaat	gatgaagacg	gtgacgaggc	240
attgatccgt	agaatggctg	aacttgagct	tgagcttcaa	gagacgaaac	agaagctcct	300
tctccagcag	gaaagtgttg	atggtgacaa	caatgttgat	ctccttcaca	aaattactac	360
atatgagga	gagcttaaag	aagctaata	gaagatgcga	atgcacgaag	acgagattgc	420
taatctgaag	aatcagcttc	agagctgcat	gtcctttgac	gcagaggatc	aacttggtag	480
tgcagaaaag	agtcttgatt	tggataaaga	ggacactgaa	gcagatgcag	aagctacaaa	540
agtgtagccc	ttggaggaag	agctgagtat	cgcgaaagag	aagcttcagc	actttgagaa	600
agagacttat	tctctgaaaa	atgagctcga	gattagtt			

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

Glu Xaa His Arg Met Tyr Arg Ala Leu Ala Glu Arg Tyr Asp Gln Ala	
1 5 10 15	
Ser Gly Glu Leu Gln Lys Asn His Thr Ser Glu Ile Gln Ser Gln Ser	
20 25 30	
Ser Leu Glu Leu Ser Ser Pro Thr Lys Glu Lys Leu Ser Arg Arg Gln	
35 40 45	
Ser Gly His Lys Glu Glu Glu Asp Ser Ser Ser Leu Thr Asp Ser Gly	
50 55 60	
Ser Asp Ser Asp His Ser Ser Ala Asn Asp Glu Asp Gly Asp Glu Ala	
65 70 75 80	
Leu Ile Arg Arg Met Ala Glu Leu Glu Leu Glu Leu Gln Glu Thr Lys	
85 90 95	
Gln Lys Leu Leu Leu Gln Gln Glu Ser Val Asp Gly Asp Asn Asn Val	
100 105 110	

Asp Leu Leu His Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala  
115 120 125  
Asn Glu Lys Met Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn  
130 135 140  
Gln Leu Gln Ser Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr  
145 150 155 160  
Ala Glu Lys Ser Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala  
165 170 175  
Glu Ala Thr Lys Val Leu Ala Leu Glu Glu Leu Ser Ile Ala Lys  
180 185 190  
Glu Lys Leu Gln His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu  
195 200 205  
Leu Glu Ile Ser  
210

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

Met Tyr Arg Ala Leu Ala Glu Arg Tyr Asp Gln Ala Ser Gly Glu Leu  
1 5 10 15  
Gln Lys Asn His Thr Ser Glu Ile Gln Ser Gln Ser Ser Leu Glu Leu  
20 25 30  
Ser Ser Pro Thr Lys Glu Lys Leu Ser Arg Arg Gln Ser Gly His Lys  
35 40 45  
Glu Glu Glu Asp Ser Ser Ser Leu Thr Asp Ser Gly Ser Asp Ser Asp  
50 55 60  
His Ser Ser Ala Asn Asp Glu Asp Gly Asp Glu Ala Leu Ile Arg Arg  
65 70 75 80  
Met Ala Glu Leu Glu Leu Glu Leu Gln Glu Thr Lys Gln Lys Leu Leu  
85 90 95  
Leu Gln Gln Glu Ser Val Asp Gly Asp Asn Asn Val Asp Leu Leu His  
100 105 110  
Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala Asn Glu Lys Met  
115 120 125  
Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn Gln Leu Gln Ser  
130 135 140  
Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr Ala Glu Lys Ser  
145 150 155 160  
Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala Glu Ala Thr Lys  
165 170 175  
Val Leu Ala Leu Glu Glu Glu Leu Ser Ile Ala Lys Glu Lys Leu Gln  
180 185 190  
His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu Leu Glu Ile Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

Met	Ala	Glu	Leu	Glu	Leu	Glu	Leu	Gln	Glu	Thr	Lys	Gln	Lys	Leu	Leu
1			5						10					15	
Leu	Gln	Gln	Glu	Ser	Val	Asp	Gly	Asp	Asn	Asn	Val	Asp	Leu	Leu	His
		20					25					30			
Lys	Ile	Thr	Thr	Tyr	Glu	Gly	Glu	Leu	Lys	Glu	Ala	Asn	Glu	Lys	Met
	35					40					45				
Arg	Met	His	Glu	Asp	Glu	Ile	Ala	Asn	Leu	Lys	Asn	Gln	Leu	Gln	Ser
	50					55					60				
Cys	Met	Ser	Phe	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Thr	Ala	Glu	Lys	Ser
65					70					75				80	
Leu	Asp	Leu	Asp	Lys	Glu	Asp	Thr	Glu	Ala	Asp	Ala	Glu	Ala	Thr	Lys
				85					90					95	
Val	Leu	Ala	Leu	Glu	Glu	Glu	Leu	Ser	Ile	Ala	Lys	Glu	Lys	Leu	Gln
			100					105					110		
His	Phe	Glu	Lys	Glu	Thr	Tyr	Ser	Leu	Lys	Asn	Glu	Leu	Glu	Ile	Ser
		115					120						125		

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

aaaacaaact	ctcgcttctc	gcacgcttga	ttctccaaaa	ccagttttca	ctctctattg	60
ccgattctcg	tttcgtttga	tatcttagga	atctataaac	aaaggcatgg	gttcagtatt	120
ctgttgattt	tctcaatcaa	tttctcagct	atcttcagtc	ttaaggctct	gggtccatggg	180
ttgctcgaga	aaatgtggaa	aaagtgatgg	tctgagtact	taatcgtaaa	atgcaaatac	240
aaagcttttg	tgggtttatt	aaagttggta	acttttgata	gaattttgag	gactcttact	300
tgtttgctta	catgcctgcg	tagtgtttgt	ttaaagtgcct	gtgagaaata	cttttttagtg	360
aaaagctctt	tttttttttt	tttgtttagt	gttcgtttta	gtagatatgt	aatgtgaaac	420
taatttctga	atctctgttt	tgagtactgt	agagttatga	aattgggtatt	ttgctaattgc	480
atgtctacat	tgtgtccaga	ttcttataaa	aacagaaact	ttgatcttat	cttatggatg	540
aattacttta	ggttactgat	gatgatttgt	ataacctaga	tgttcgtttc	agagaaaaac	600
ctggaaatta	ctgtctactt	ccttttcctt	tctctgtgat	ctttcagttt	tgattttttc	660
cagagtcttt	ctcatatctt	tcctttgaga	agaatgtgat	gtagtaaaag	tattttctatt	720
ctctggatca	atgatgatag	ctatgtgaca	ttgctttgat	ttggttttga	aggttgaaca	780
atgtttctca	aagtccaatt	accatggaac	gtgatgattc	cagctgaaaa	catggatgcc	840
aaagggctga	tgttgaagag	agctatacta	gtagagttac	tagaggcggt	cgcttccaag	900
aaagcaacca	aggagcttgg	ctactacgtg	gcagtcacaa	ctttggacaa	gattggagaa	960
ggcaaatca	gggagcacac	cgggtgaagtt	ttgttcccgg	taatgttcag	cggaatgact	1020
ttcaagatct	tcaaaggaga	gataattcac	gggtgtgtgc	acaagggtgt	gaagcacggt	1080
gtcttcatga	ggtgtggtcc	aatcgagaat	gtttacctct	cctacacgaa	gatgccggat	1140
tacaagtata	tccctggaga	gaacccgatc	ttcatgaatg	agaagacgtc	taggatttcag	1200
gttgagacta	cagtgaagggt	tgtttgtgatt	gggataaagt	ggatggaagt	agagagggag	1260
tttcaggcgt	tggctagctt	ggaagggtgac	tatcttggac	cattatctga	agagtgatct	1320
gcttgatttc	ttcatgtgat	ggcgtttttg	ggcaatctct	tatgtctata	taactcggct	1380
ttagttcatg	tttggtagta	actagtaact	actctctagc	tgtgcaataa	atgaaaacat	1440
tgatctttga	atgtaaatgaa	atcctccacc	ttcaaggagga	aagattggtc	taatttaggt	1500
tttttgatt	ggc					

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

```
Met Phe Leu Lys Val Gln Leu Pro Trp Asn Val Met Ile Pro Ala Glu
1      5      10      15
Asn Met Asp Ala Lys Gly Leu Met Leu Lys Arg Ala Ile Leu Val Glu
      20      25      30
Leu Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr Lys Glu Leu Gly Tyr
      35      40      45
Tyr Val Ala Val Thr Thr Leu Asp Lys Ile Gly Glu Gly Lys Ile Arg
      50      55      60
Glu His Thr Gly Glu Val Leu Phe Pro Val Met Phe Ser Gly Met Thr
      65      70      75      80
Phe Lys Ile Phe Lys Gly Glu Ile Ile His Gly Val Val His Lys Val
      85      90      95
Leu Lys His Gly Val Phe Met Arg Cys Gly Pro Ile Glu Asn Val Tyr
      100     105     110
Leu Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr Ile Pro Gly Glu Asn
      115     120     125
Pro Ile Phe Met Asn Glu Lys Thr Ser Arg Ile Gln Val Glu Thr Thr
      130     135     140
Val Arg Val Val Val Ile Gly Ile Lys Trp Met Glu Val Glu Arg Glu
      145     150     155     160
Phe Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr Leu Gly Pro Leu Ser
      165     170     175
Glu Glu
```

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

```
Met Ile Pro Ala Glu Asn Met Asp Ala Lys Gly Leu Met Leu Lys Arg
1      5      10      15
Ala Ile Leu Val Glu Leu Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr
      20      25      30
Lys Glu Leu Gly Tyr Tyr Val Ala Val Thr Thr Leu Asp Lys Ile Gly
      35      40      45
Glu Gly Lys Ile Arg Glu His Thr Gly Glu Val Leu Phe Pro Val Met
      50      55      60
Phe Ser Gly Met Thr Phe Lys Ile Phe Lys Gly Glu Ile Ile His Gly
      65      70      75      80
Val Val His Lys Val Leu Lys His Gly Val Phe Met Arg Cys Gly Pro
      85      90      95
Ile Glu Asn Val Tyr Leu Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr
```

	100		105		110										
Ile	Pro	Gly	Glu	Asn	Pro	Ile	Phe	Met	Asn	Glu	Lys	Thr	Ser	Arg	Ile
	115						120						125		
Gln	Val	Glu	Thr	Thr	Val	Arg	Val	Val	Val	Ile	Gly	Ile	Lys	Trp	Met
	130						135					140			
Glu	Val	Glu	Arg	Glu	Phe	Gln	Ala	Leu	Ala	Ser	Leu	Glu	Gly	Asp	Tyr
145					150					155					160
Leu	Gly	Pro	Leu	Ser	Glu	Glu									
					165										

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1498969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Met	Asp	Ala	Lys	Gly	Leu	Met	Leu	Lys	Arg	Ala	Ile	Leu	Val	Glu	Leu
1			5					10						15	
Leu	Glu	Ala	Phe	Ala	Ser	Lys	Lys	Ala	Thr	Lys	Glu	Leu	Gly	Tyr	Tyr
		20						25					30		
Val	Ala	Val	Thr	Thr	Leu	Asp	Lys	Ile	Gly	Glu	Gly	Lys	Ile	Arg	Glu
		35					40					45			
His	Thr	Gly	Glu	Val	Leu	Phe	Pro	Val	Met	Phe	Ser	Gly	Met	Thr	Phe
	50					55					60				
Lys	Ile	Phe	Lys	Gly	Glu	Ile	Ile	His	Gly	Val	Val	His	Lys	Val	Leu
65				70					75					80	
Lys	His	Gly	Val	Phe	Met	Arg	Cys	Gly	Pro	Ile	Glu	Asn	Val	Tyr	Leu
			85					90					95		
Ser	Tyr	Thr	Lys	Met	Pro	Asp	Tyr	Lys	Tyr	Ile	Pro	Gly	Glu	Asn	Pro
			100					105					110		
Ile	Phe	Met	Asn	Glu	Lys	Thr	Ser	Arg	Ile	Gln	Val	Glu	Thr	Thr	Val
		115				120						125			
Arg	Val	Val	Val	Ile	Gly	Ile	Lys	Trp	Met	Glu	Val	Glu	Arg	Glu	Phe
	130					135					140				
Gln	Ala	Leu	Ala	Ser	Leu	Glu	Gly	Asp	Tyr	Leu	Gly	Pro	Leu	Ser	Glu
145					150					155					160
Glu															

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..695

(D) OTHER INFORMATION: / Ceres Seq. ID 1498970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

caactsgagt	ggtatggcat	ggaatccgta	tttagggcgw	acgaaattga	ttcaaccaag	60
aaaaaaactc	cacagatatg	acaagtttgc	tcttggtatc	gacaacaacc	gtaaccacaa	120
aatttttgagg	tttctttatg	aggggagtc	aagaaacgtc	attattgatg	tttacgattt	180
tagctctgat	tcatggagg	ttcttgatat	tgatatagat	tggtcatgaac	tgtttagtca	240
cwwtagcsys	tswwtgmccg	gaaatactta	cttttttggt	cgawaggac	cacktttgcc	300
tatgctgttt	aaacctcywt	ctcgtcggtt	tgaatatattg	actctatctt	gtgttagaaa	360

tgagaaactc gctgtgttat acagccacct caacagattt ggcacaatag agatttgtat 420  
ttcgactaag attgatccca gtgcagtatc atggaccact tttttgagaa ttgatatgac 480  
actaatcaat ggtttaccgg ataacttttt tgttctactt tatgctwcga gctttttctt 540  
ckaygakgag aaraakgtcg ytgwkctttt cggkacaaac agatatagag gacgtgagac 600  
ctgtcagtac taccagagag cttgcatcgt tggagatagt ggatacttca aagctgtcaa 660  
catcgaacta gttttcaatt cacagctgca atctt

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

Asn	Xaa	Ser	Val	Met	Ala	Trp	Asn	Pro	Tyr	Leu	Gly	Xaa	Thr	Lys	Leu
1			5					10						15	
Ile	Gln	Pro	Arg	Lys	Lys	Leu	His	Arg	Tyr	Asp	Lys	Phe	Ala	Leu	Gly
			20					25					30		
Tyr	Asp	Asn	Asn	Arg	Asn	His	Lys	Ile	Leu	Arg	Phe	Leu	Tyr	Glu	Gly
			35				40					45			
Ser	Pro	Arg	Asn	Val	Ile	Ile	Asp	Val	Tyr	Asp	Phe	Ser	Ser	Asp	Ser
			50				55				60				
Trp	Arg	Val	Leu	Asp	Ile	Asp	Ile	Asp	Trp	His	Glu	Leu	Phe	Ser	His
65					70					75					80
Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Gly	Asn	Thr	Tyr	Phe	Phe	Gly	Arg	Xaa	Gly
			85					90						95	
Pro	Xaa	Leu	Pro	Met	Leu	Phe	Lys	Pro	Xaa	Ser	Arg	Arg	Phe	Glu	Tyr
			100					105					110		
Leu	Thr	Leu	Ser	Cys	Val	Arg	Asn	Glu	Lys	Leu	Ala	Val	Leu	Tyr	Ser
			115					120				125			
His	Leu	Asn	Arg	Phe	Gly	Thr	Ile	Glu	Ile	Cys	Ile	Ser	Thr	Lys	Ile
			130				135				140				
Asp	Pro	Ser	Ala	Val	Ser	Trp	Thr	Thr	Phe	Leu	Arg	Ile	Asp	Met	Thr
145					150					155					160
Leu	Ile	Asn	Gly	Leu	Pro	Asp	Asn	Phe	Phe	Val	His	Ser	Tyr	Ala	Xaa
			165					170						175	
Ser	Phe	Phe	Phe	Xaa	Xaa	Glu	Xaa	Xaa	Val	Xaa	Xaa	Leu	Phe	Xaa	Thr
			180					185					190		
Asn	Arg	Tyr	Arg	Gly	Arg	Glu	Thr	Cys	Gln	Tyr	Tyr	Gln	Arg	Ala	Cys
			195				200					205			
Ile	Val	Gly	Asp	Ser	Gly	Tyr	Phe	Lys	Ala	Val	Asn	Ile	Glu	Leu	Val
	210					215					220				
Phe	Asn	Ser	Gln	Leu	Gln	Ser									
225					230										

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1498972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Met Ala Trp Asn Pro Tyr Leu Gly Xaa Thr Lys Leu Ile Gln Pro Arg

1				5					10					15	
Lys	Lys	Leu	His	Arg	Tyr	Asp	Lys	Phe	Ala	Leu	Gly	Tyr	Asp	Asn	Asn
			20					25					30		
Arg	Asn	His	Lys	Ile	Leu	Arg	Phe	Leu	Tyr	Glu	Gly	Ser	Pro	Arg	Asn
		35					40					45			
Val	Ile	Ile	Asp	Val	Tyr	Asp	Phe	Ser	Ser	Asp	Ser	Trp	Arg	Val	Leu
	50					55					60				
Asp	Ile	Asp	Ile	Asp	Trp	His	Glu	Leu	Phe	Ser	His	Xaa	Ser	Xaa	Xaa
65					70				75						80
Xaa	Xaa	Gly	Asn	Thr	Tyr	Phe	Phe	Gly	Arg	Xaa	Gly	Pro	Xaa	Leu	Pro
			85					90						95	
Met	Leu	Phe	Lys	Pro	Xaa	Ser	Arg	Arg	Phe	Glu	Tyr	Leu	Thr	Leu	Ser
			100					105					110		
Cys	Val	Arg	Asn	Glu	Lys	Leu	Ala	Val	Leu	Tyr	Ser	His	Leu	Asn	Arg
		115					120					125			
Phe	Gly	Thr	Ile	Glu	Ile	Cys	Ile	Ser	Thr	Lys	Ile	Asp	Pro	Ser	Ala
	130					135					140				
Val	Ser	Trp	Thr	Thr	Phe	Leu	Arg	Ile	Asp	Met	Thr	Leu	Ile	Asn	Gly
145					150				155						160
Leu	Pro	Asp	Asn	Phe	Phe	Val	His	Ser	Tyr	Ala	Xaa	Ser	Phe	Phe	Phe
			165					170						175	
Xaa	Xaa	Glu	Xaa	Xaa	Val	Xaa	Xaa	Leu	Phe	Xaa	Thr	Asn	Arg	Tyr	Arg
		180					185					190			
Gly	Arg	Glu	Thr	Cys	Gln	Tyr	Tyr	Gln	Arg	Ala	Cys	Ile	Val	Gly	Asp
	195					200					205				
Ser	Gly	Tyr	Phe	Lys	Ala	Val	Asn	Ile	Glu	Leu	Val	Phe	Asn	Ser	Gln
	210					215					220				
Leu	Gln	Ser													
225															

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1498973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

Met	Leu	Phe	Lys	Pro	Xaa	Ser	Arg	Arg	Phe	Glu	Tyr	Leu	Thr	Leu	Ser
1			5						10					15	
Cys	Val	Arg	Asn	Glu	Lys	Leu	Ala	Val	Leu	Tyr	Ser	His	Leu	Asn	Arg
		20					25					30			
Phe	Gly	Thr	Ile	Glu	Ile	Cys	Ile	Ser	Thr	Lys	Ile	Asp	Pro	Ser	Ala
	35					40					45				
Val	Ser	Trp	Thr	Thr	Phe	Leu	Arg	Ile	Asp	Met	Thr	Leu	Ile	Asn	Gly
	50					55				60					
Leu	Pro	Asp	Asn	Phe	Phe	Val	His	Ser	Tyr	Ala	Xaa	Ser	Phe	Phe	Phe
65					70				75						80
Xaa	Xaa	Glu	Xaa	Xaa	Val	Xaa	Xaa	Leu	Phe	Xaa	Thr	Asn	Arg	Tyr	Arg
		85					90						95		
Gly	Arg	Glu	Thr	Cys	Gln	Tyr	Tyr	Gln	Arg	Ala	Cys	Ile	Val	Gly	Asp
	100						105					110			
Ser	Gly	Tyr	Phe	Lys	Ala	Val	Asn	Ile	Glu	Leu	Val	Phe	Asn	Ser	Gln
	115					120					125				
Leu	Gln	Ser													
130															

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1266
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498974
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

```
gaaaatggaa taatgcttgt gagcagagag agagagcgag cgaggaggct agagaatcga      60
gaatcgatct tcgccgaacc accttgtctt ctcttagctc atcgaatctc tccgtcgccg      120
tcgattcttc ccgccgaaga ggagggtcatg gacgtttctg ctagaaagtc acaaaaagct      180
gggcgcgaaa agttgaggag ggaaaaactg aatgagcatt ttgttgaact gggaaatgta      240
ctcgatccag agagacccaa gaatgacaaa gccacgattc tgactgatac tgttcagttg      300
ttgaaagagc tcacatctga agtcaacaaa ctgaaatctg agtacaccgc attgacagat      360
gagtcccgcg agttgacaca ggagaaaaaac gacctgagag aagaaaagac atcgctgaaa      420
tcagatatag agaattctca ttttcaatac cagcagagat taaggtcaat gtctccatgg      480
ggagctgcga tggatcacac agtcatgatg gctccaccac cctcctttcc ataccctatg      540
cctattgcta tgcctcccgg gtcaatccca atgcatccat caatgccatc ttacacatac      600
tttgggaacc agaaccctag catgatccca gctccatgtc ctacatacat gccctacatg      660
cctcctaata cagtcggtga gcaacaatcc gtgcacattc cacagaaccc cggtaaccgt      720
tctcgggaac ctagagcaaa ggtttcaaga gagagcagat ctgagaaagc agaggactcc      780
aacgaagttg caacacaact cgaattaaaa acccctggat ctacttctga taaggatata      840
ttgcaaaggc cagagaagac aaagagatgt aagagaaaca acaacaacaa ctcaatagaa      900
gaaagctctc attctagcaa gtgttcatct tctccgagcg tacgagacca cagttcttcc      960
agtagcgtag ctggtggcca aaaacctgat gatgcaaaat gattcgaaag aatctgatgt     1020
tgatcatctc aagtatccaa gtatcgtttc gatgagtact gtatatagtg cgagatacaa     1080
atgcacttag ctgtttaaag cagtgttttg atgcaccgtg gcattcgttt tcctcggata     1140
gtcatttctc agatgatttt catccttaat aggtctgtct tagttctaaa actcggatga     1200
tttgtaattd ccagtggtcca aatctactaa ttttattaat cctataaatt aaacaaactt     1260
atatcc
```

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 333 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..333
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498975
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

```
Glu Asn Gly Ile Met Leu Val Ser Arg Glu Arg Ala Arg Arg
1          5          10          15
Leu Glu Asn Arg Glu Ser Ile Phe Ala Glu Pro Pro Cys Leu Leu Leu
20          25          30
Ala His Arg Ile Ser Pro Ser Pro Ser Ile Leu Pro Ala Glu Glu Glu
35          40          45
Val Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys
50          55          60
Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val
65          70          75          80
Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp
85          90          95
Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys
100         105         110
Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu
115         120         125
Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu
```

130	135	140
Asn Leu Asn Leu Gln Tyr	Gln Gln Arg Leu Arg	Ser Met Ser Pro Trp
145	150	155
Gly Ala Ala Met Asp His	Thr Val Met Met Ala	Pro Pro Pro Ser Phe
	165	170
Pro Tyr Pro Met Pro Ile	Ala Met Pro Pro Gly	Ser Ile Pro Met His
	180	185
Pro Ser Met Pro Ser Tyr	Thr Tyr Phe Gly Asn	Gln Asn Pro Ser Met
	195	200
Ile Pro Ala Pro Cys Pro	Thr Tyr Met Pro Tyr	Met Pro Pro Asn Thr
	210	220
Val Val Glu Gln Gln Ser	Val His Ile Pro Gln	Asn Pro Gly Asn Arg
225	230	235
Ser Arg Glu Pro Arg Ala	Lys Val Ser Arg Glu	Ser Arg Ser Glu Lys
	245	250
Ala Glu Asp Ser Asn Glu	Val Ala Thr Gln Leu	Glu Leu Lys Thr Pro
	260	265
Gly Ser Thr Ser Asp Lys	Asp Thr Leu Gln Arg	Pro Glu Lys Thr Lys
	275	280
Arg Cys Lys Arg Asn Asn	Asn Asn Ser Ile Glu	Glu Ser Ser Ser His
	290	295
Ser Ser Lys Cys Ser Ser	Ser Pro Ser Val Arg	Asp His Ser Ser Ser
305	310	315
Ser Ser Val Ala Gly Gly	Gln Lys Pro Asp Asp	Ala Lys
	325	330

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met Leu Val Ser Arg Glu Arg Glu Arg Ala Arg Arg Leu Glu Asn Arg	
1	5 10 15
Glu Ser Ile Phe Ala Glu Pro Pro Cys Leu Leu Leu Ala His Arg Ile	
	20 25 30
Ser Pro Ser Pro Ser Ile Leu Pro Ala Glu Glu Glu Val Met Asp Val	
	35 40 45
Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys Leu Arg Arg Glu	
	50 55 60
Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu Asp Pro Glu	
65	70 75 80
Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr Val Gln Leu	
	85 90 95
Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser Glu Tyr Thr	
	100 105 110
Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys Asn Asp Leu	
	115 120 125
Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn Leu Asn Leu	
	130 135 140
Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly Ala Ala Met	
145	150 155 160
Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro Tyr Pro Met	
	165 170 175
Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro Ser Met Pro	
	180 185 190

Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile Pro Ala Pro  
195 200 205  
Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val Val Glu Gln  
210 215 220  
Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser Arg Glu Pro  
225 230 235 240  
Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala Glu Asp Ser  
245 250 255  
Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly Ser Thr Ser  
260 265 270  
Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg Cys Lys Arg  
275 280 285  
Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser Ser Lys Cys  
290 295 300  
Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser Ser Val Ala  
305 310 315 320  
Gly Gly Gln Lys Pro Asp Asp Ala Lys  
325

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1498977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys Leu  
1 5 10 15  
Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu  
20 25 30  
Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr  
35 40 45  
Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser  
50 55 60  
Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys  
65 70 75 80  
Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn  
85 90 95  
Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly  
100 105 110  
Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro  
115 120 125  
Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro  
130 135 140  
Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile  
145 150 155 160  
Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val  
165 170 175  
Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser  
180 185 190  
Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala  
195 200 205  
Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly  
210 215 220  
Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg  
225 230 235 240  
Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser



245 250 255  
Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser  
260 265 270  
Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys  
275 280

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

gtcaaagcaa ccaaacacat aaaagagaga ttaatacaa aagaaagaga aaaaagaaa	60
atatggcagg actcatcaac aagatcggag acgcactcca cattggagga ggcaacaagg	120
aaggtgagca caagaaggaa gaggaacaca agaaacacgt tgacgagcac aagartggtg	180
agcacaaga aggtattggt gacaagatca aagacaagat ccacggtggt gaaggtaaaa	240
gccacgacgg agaaggcaaa agccacgacg gtgagaagaa aaagaagaag gacaagaagg	300
agaagaaaca tcatgatgat ggtcaccaca gcagcagcag tgacagcgac agcgagttaa	360
ggtgaggaag tgaggaggat cgcttgaata aaacagatct ggttctggct attattaatt	420
aatgttgctg tatgttctta tcatcttaga gagaggtaa agacaggaga accgtgcac	480
tatctttgat cttgtcaaca ataccttctt tgtgtcacc actcttatga actcttttct	540
ctttaatgtc ggtctcattc tctctgttc tatcagtgtg attcaattct gcgccactgc	600
atttgatat tatgtcaag ccaccgcgc tcaggagata tttggccaca ctttgcagtc	660
ccttcgcggt attaagtacc tctacaagta caatgtgttc cagatcgggt ttgttgtcct	720
cgctggattg acctttttat attacattgc ctttggatgg agaagaaaaa agccgagcgg	780
cagattccag ctctctacct aatgtaaatc tcttcttttg attttatcgt ttatgtttcc	840
tcgtctctgg gatcgatcgc gtgccactga ggattgctgt gtccacaatt ataccgagat	900
tggtctcatg atctgtgcaa gtggtcttat atcataagaa caagcacctg cccaaaaagc	960
ttctctttct tctgtctctc tttgctgctg aggtttgttt tcattttact tgaatgtaaa	1020
attattcttc tttttctctt atcttttctc ctgtatctat tgctttatatt ttgtttgatt	1080
aattacaaga aagatctctt tgtcgccgtc ttctcatggc ctattgaatg atttcgaata	1140
ctttcttgta accattactt ggttgagagt ttgactgtc agaacaaatt caggttttgg	1200
agttatttgt gtgtatagt gtatgacaag agacttcat	

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

Val Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn Thr Lys Glu Arg	
1 5 10 15	
Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg Ser Glu Thr His	
20 25 30	
Ser Thr Leu Glu Glu Ala Thr Arg Lys Val Ser Thr Arg Arg Lys Arg	
35 40 45	
Asn Thr Arg Asn Thr Leu Thr Ser Thr Arg Xaa Val Ser Thr Lys Lys	
50 55 60	
Val Leu Leu Thr Arg Ser Lys Thr Arg Ser Thr Val Val Lys Val Lys	
65 70 75 80	
Ala Thr Thr Glu Lys Ala Lys Ala Thr Thr Val Arg Arg Lys Arg Arg	

85 90 95  
Arg Thr Arg Arg Arg Arg Asn Ile Met Met Met Val Thr Thr Ala Ala  
100 105 110  
Ala Val Thr Ala Thr Ala Ser  
115

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Ile Gly Gly  
1 5 10 15  
Gly Asn Lys Glu Gly Glu His Lys Lys Glu Glu Glu His Lys Lys His  
20 25 30  
Val Asp Glu His Lys Xaa Gly Glu His Lys Glu Gly Ile Val Asp Lys  
35 40 45  
Ile Lys Asp Lys Ile His Gly Gly Glu Gly Lys Ser His Asp Gly Glu  
50 55 60  
Gly Lys Ser His Asp Gly Glu Lys Lys Lys Lys Lys Asp Lys Lys Glu  
65 70 75 80  
Lys Lys His His Asp Asp Gly His His Ser Ser Ser Ser Asp Ser Asp  
85 90 95  
Ser Glu Leu Arg  
100

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met Asn Ser Phe Leu Phe Asn Val Gly Leu Ile Leu Leu Cys Ser Ile  
1 5 10 15  
Ser Val Ile Gln Phe Cys Ala Thr Ala Phe Gly Tyr Tyr Ala Gln Ala  
20 25 30  
Thr Ala Ala Gln Glu Ile Phe Gly His Thr Leu Gln Ser Leu Arg Gly  
35 40 45  
Ile Lys Tyr Leu Tyr Lys Tyr Asn Val Phe Gln Ile Gly Phe Val Val  
50 55 60  
Leu Ala Gly Leu Thr Phe Leu Tyr Tyr Ile Ala Phe Gly Trp Arg Arg  
65 70 75 80  
Lys Lys Pro Ser Gly Arg Phe Gln Leu Ser Thr  
85 90

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

```
agagctctag aatctctcaa caatggcgga atcgattttc agaaagctca gagatggtgg      60
cgaagaaggc gaactcgcac cagctctcac tatagaagaa actgtagctt cccctttcgg      120
actcgatgtc tccggtatc ttctcacaaa tctatcttct tcaatttttag ctggaaaatc      180
ctcgtcgcag ggtcttgtgt tgatcacatt ctgcgggagc cttcgttcta tttgcaattg      240
ttgaagcaaa aaggaatcgt tgtctcttca tcttctaaat ggattcgtat tttggattgt      300
tacactgata cattgggatg gattgatcaa tcttcaacta gttttagtga aggttcaagt      360
ttgattaagt tacataagtg tgtgagtgc ttgaaaaagc ttttttcttc aatcattgaa      420
gcaggaagag agttggttgg aactgggaag acacgtttct gcgttgccat tgattcggta      480
aatgagttgc taagacattc agcgatgcca ttagtttctg gtcttttaac agatcttcga      540
agccatgcgc aaatttccag tgtcttttgg tcattgaaca ctgaccttca ccaagagaag      600
gtcaciaaat cgcttgaata tatatccaca atgaaagcga acttagaacc tttgtgtcca      660
tcttcagatg ggcaaaaggaa tgcttttagaa aacctctttt cggttcatca ggatttcggg      720
aaaggacggg ttcattgtccg gtttaagctt agaaaaggac gtgtgagagt aatgtctgaa      780
gaatatcatg ttgatcaatc ggggataaac ttttcaccca tttcctctgt ggatactgtt      840
attgcagcca ctaaaagcct ttgacctaa gttcaattca atctccagtt gtctgagaaa      900
gaacgggtcg agaaagaaaa agttgtgctt ccttttgagc accaagatga tggaaaatcg      960
aacgagatct atgatgggag gagatctctt gtggatggca agattgagac aacaccattg     1020
tcgtcaatgg agttgcagac cgatgtgggt tcgtcgggta aggggtggta gattatatat     1080
ttcagagatt cagacgatga gcacctgat tctgatgaag atcctgatga tgatttggac     1140
atttaagggt cttaatttac acttgaaga ccagagaata gctccagttt tggttttggc     1200
aatagttggg atcttagtat ccaactttgt aactaaata gaagatttga ttggttatta     1260
gatgtgtatt acagttataa ttgttacagt aatgatctca tcttctatta ttcttgagtt     1320
gtttgttgt
```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1498983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

```
Arg Ala Leu Glu Ser Leu Asn Asn Gly Gly Ile Asp Phe Gln Lys Ala
1          5          10          15
Gln Arg Trp Trp Arg Arg Arg Arg Thr Arg Thr Ser Ser His Tyr Arg
20          25          30
Arg Asn Cys Ser Phe Pro Phe Arg Thr Arg Cys Leu Arg Leu Ser Ser
35          40          45
His Lys Ser Ile Phe Phe Asn Phe Ser Trp Lys Ile Leu Val Ala Gly
50          55          60
Ser Cys Val Asp His Ile Leu Ala Glu Pro Ser Phe Tyr Leu Gln Leu
65          70          75          80
Leu Lys Gln Lys Gly Ile Val Val Ser Ser Ser Ser Lys Trp Ile Arg
85          90          95
Ile Leu Asp Cys Tyr Thr Asp Pro Leu Gly Trp Ile Asp Gln Ser Ser
100         105         110
Thr Ser Phe Ser Glu Gly Ser Ser Leu Ile Lys Leu His Lys Cys Val
115         120         125
Ser Asp Leu Lys Lys Leu Phe Ser Ser Ile Ile Glu Ala Gly Arg Glu
130         135         140
Leu Val Gly Thr Gly Lys Thr Arg Phe Cys Val Ala Ile Asp Ser Val
145         150         155         160
```

Asn	Glu	Leu	Leu	Arg	His	Ser	Ala	Met	Pro	Leu	Val	Ser	Gly	Leu	Leu
				165					170					175	
Thr	Asp	Leu	Arg	Ser	His	Ala	Gln	Ile	Ser	Ser	Val	Phe	Trp	Ser	Leu
		180						185					190		
Asn	Thr	Asp	Leu	His	Gln	Glu	Lys	Val	Thr	Asn	Ala	Leu	Glu	Tyr	Ile
		195					200					205			
Ser	Thr	Met	Lys	Ala	Asn	Leu	Glu	Pro	Leu	Cys	Pro	Ser	Ser	Asp	Gly
		210				215					220				
Gln	Arg	Asn	Ala	Leu	Glu	Asn	Leu	Phe	Ser	Val	His	Gln	Asp	Phe	Gly
		225				230				235				240	
Lys	Gly	Arg	Phe	His	Val	Arg	Phe	Lys	Leu	Arg	Lys	Gly	Arg	Val	Arg
			245					250						255	
Val	Met	Ser	Glu	Glu	Tyr	His	Val	Asp	Gln	Ser	Gly	Ile	Asn	Phe	Ser
			260					265					270		
Pro	Ile	Ser	Ser	Val	Asp	Thr	Val	Ile	Ala	Ala	Thr	Lys	Ser	Leu	Leu
			275				280					285			
Pro	Lys	Val	Gln	Phe	Asn	Leu	Gln	Leu	Ser	Glu	Lys	Glu	Arg	Val	Glu
			290			295					300				
Lys	Glu	Lys	Val	Val	Leu	Pro	Phe	Glu	His	Gln	Asp	Asp	Gly	Lys	Ser
					310					315				320	
Asn	Glu	Ile	Tyr	Asp	Gly	Arg	Arg	Ser	Leu	Val	Asp	Gly	Lys	Ile	Glu
				325					330					335	
Thr	Thr	Pro	Leu	Ser	Ser	Met	Glu	Leu	Gln	Thr	Asp	Val	Val	Ser	Ser
			340					345					350		
Gly	Lys	Gly	Gly	Glu	Ile	Ile	Tyr	Phe	Arg	Asp	Ser	Asp	Asp	Glu	His
			355				360					365			
Pro	Asp	Ser	Asp	Glu	Asp	Pro	Asp	Asp	Asp	Leu	Asp	Ile			
			370			375					380				

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Met	Pro	Leu	Val	Ser	Gly	Leu	Leu	Thr	Asp	Leu	Arg	Ser	His	Ala	Gln
1				5				10						15	
Ile	Ser	Ser	Val	Phe	Trp	Ser	Leu	Asn	Thr	Asp	Leu	His	Gln	Glu	Lys
			20					25					30		
Val	Thr	Asn	Ala	Leu	Glu	Tyr	Ile	Ser	Thr	Met	Lys	Ala	Asn	Leu	Glu
			35				40					45			
Pro	Leu	Cys	Pro	Ser	Ser	Asp	Gly	Gln	Arg	Asn	Ala	Leu	Glu	Asn	Leu
			50			55					60				
Phe	Ser	Val	His	Gln	Asp	Phe	Gly	Lys	Gly	Arg	Phe	His	Val	Arg	Phe
					70				75					80	
Lys	Leu	Arg	Lys	Gly	Arg	Val	Arg	Val	Met	Ser	Glu	Glu	Tyr	His	Val
				85				90					95		
Asp	Gln	Ser	Gly	Ile	Asn	Phe	Ser	Pro	Ile	Ser	Ser	Val	Asp	Thr	Val
			100					105					110		
Ile	Ala	Ala	Thr	Lys	Ser	Leu	Leu	Pro	Lys	Val	Gln	Phe	Asn	Leu	Gln
			115				120					125			
Leu	Ser	Glu	Lys	Glu	Arg	Val	Glu	Lys	Glu	Lys	Val	Val	Leu	Pro	Phe
			130			135					140				
Glu	His	Gln	Asp	Asp	Gly	Lys	Ser	Asn	Glu	Ile	Tyr	Asp	Gly	Arg	Arg
					150				155					160	
Ser	Leu	Val	Asp	Gly	Lys	Ile	Glu	Thr	Thr	Pro	Leu	Ser	Ser	Met	Glu

(2) INFORMATION FOR SEQ ID NO:787:

(A) LENGTH: 1944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1944

(D) OTHER INFORMATION: / Ceres Seq. ID 1498985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

(X1) SEQUENCE ALIGNMENT: SEQ ID NO: 1						
tttttttccc	cattttctta	ctctcttgcc	ctttcttttc	tcactctccg	gcgactgtta	60
cgagttttta	acacttccgt	ctctcttcca	gttggtgttg	ttgtttatga	caagatcttg	120
ttctatccat	taaaaccaa	gaaatggagg	aaggtcataa	agaaccattg	gtgctaagag	180
ttgaaggatc	acattgttct	ttatcagaga	tggatgattt	tgatctaact	cgggctttag	240
agaagccgag	gcagctaaag	atcgaacgga	agagatcggt	tgacgaaagg	tcgatgagcg	300
agttatcgac	tggctatgta	agacaagata	gcatttttaga	aatggctcat	tctccgaagt	360
agggtcaatgg	tggacactcc	tctctctggt	aggaactcct	tcgagcctca	tccgatgggt	420
gctgaggcct	gggaagcttt	gagaaggtca	atgggtgtct	tctgtgttca	acccggtggg	480
accattgcag	cttatgacca	tgcctccgag	gaggtcctga	actatgatca	ggtgtttgta	540
cgtgactttg	taccaagtg	attggcggtt	ctgatgaatg	gagagcccga	tatagtga	600
aacttctttg	tcaagacact	tcagcttcaa	ggttgggaga	aacgggttga	ccggttcaag	660
cttggggaag	gcgttatgcc	agcgagtttc	aaggtgcttc	atgatccagt	tcgtaaaacc	720
gacacaatta	ttgcggattt	tggagaaagc	gctataggaa	gagtagcacc	ggtggattca	780
ggattctggg	ggatcatact	tctccgtgct	tacacgaaat	ctacggggaga	tttgacttta	840
tctgagacac	cagagtgtca	gaggggaatg	aggcttatac	tctctctttg	cttatccgaa	900
ggtttttgata	ctttccctac	gcttctttgt	gctgacgggt	gttctatggt	tgataggaga	960
atggggtgttt	atggtatatt	aatatagatt	caagctctgt	ttttcatggc	attgagatgc	1020
gccttgttga	tgcttaaacc	agacgaggaa	ggctcgagatt	tcatagaaag	gattgtgaag	1080
agacttcacg	cgctgagttt	ccatatgcgc	agttactttt	ggcttgactt	tcaacaactc	1140
aacgatattct	ataggtacaa	gacagaggag	tactcacaca	ccgcgggtga	caagttcaac	1200
gtgatgccgg	actcgatacc	agactgggtt	ttcgacttta	tgccctctccg	tggaggatat	1260
tttgctggga	atgtaagccc	ggcccgtatg	gatttccagg	ggttttccct	aggaaattgt	1320
gtctccatcc	tttttctctt	ggcaactccg	gatacgtcaa	ttgctattat	ggacctcctc	1380
gagacacgct	ggtaggagct	agtagcgag	atgccgtcca	agatatgtta	cccttgcatc	1440
gaaagccacg	agtggcggat	tgttaccggt	tgtgataccta	aaaacacgag	gtggagttac	1500
cacaacgggtg	gatcttggcc	agtattgctg	tggacgctga	cggaggcatg	catcaagact	1560
ggacggcctc	aaatagcgag	acgtgcgatt	gatctaattg	aatcacggct	acaccgagat	1620
tgctggccgg	aatactatga	tggttaagcaa	ggaaggtacg	ttggaaaaca	agcaagggaag	1680
taccagactt	ggtcaatcgc	gggttacttg	gttgcgaaaa	tgatgcttga	agatccttca	1740
catattggaa	tgatctctct	tgaagaagac	aaacagatga	aacctgttat	caagagactct	1800
gctttcatga	cttgctgaat	tttgtttcct	gttttgtatt	ataatgtcat	ttgattaagc	1860
attcaaaaga	cccttaataca	gcgagagagt	agttctgttt	gtattttctct	ttgatccaac	1920
tatgqtttat	tttcaacttga	ggct				

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1498986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Met	Val	Asp	Thr	Pro	Leu	Ser	Val	Arg	Asn	Ser	Phe	Glu	Pro	His	Pro
1				5					10					15	
Met	Val	Ala	Glu	Ala	Trp	Glu	Ala	Leu	Arg	Arg	Ser	Met	Val	Phe	Phe
		20						25					30		
Arg	Gly	Gln	Pro	Val	Gly	Thr	Ile	Ala	Ala	Tyr	Asp	His	Ala	Ser	Glu
	35					40						45			
Glu	Val	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Val	Arg	Asp	Phe	Val	Pro	Ser
	50					55					60				
Ala	Leu	Ala	Phe	Leu	Met	Asn	Gly	Glu	Pro	Asp	Ile	Val	Lys	Asn	Phe
65				70						75				80	
Leu	Leu	Lys	Thr	Leu	Gln	Leu	Gln	Gly	Trp	Glu	Lys	Arg	Val	Asp	Arg
			85						90					95	
Phe	Lys	Leu	Gly	Glu	Gly	Val	Met	Pro	Ala	Ser	Phe	Lys	Val	Leu	His
			100					105					110		
Asp	Pro	Val	Arg	Lys	Thr	Asp	Thr	Ile	Ile	Ala	Asp	Phe	Gly	Glu	Ser
	115						120						125		
Ala	Ile	Gly	Arg	Val	Ala	Pro	Val	Asp	Ser	Gly	Phe	Trp	Trp	Ile	Ile
	130					135					140				
Leu	Leu	Arg	Ala	Tyr	Thr	Lys	Ser	Thr	Gly	Asp	Leu	Thr	Leu	Ser	Glu
145					150					155				160	
Thr	Pro	Glu	Cys	Gln	Arg	Gly	Met	Arg	Leu	Ile	Leu	Ser	Leu	Cys	Leu
			165					170						175	
Ser	Glu	Gly	Phe	Asp	Thr	Phe	Pro	Thr	Leu	Leu	Cys	Ala	Asp	Gly	Cys
			180					185					190		
Ser	Met	Val	Asp	Arg	Arg	Met	Gly	Val	Tyr	Gly	Tyr	Pro	Ile	Glu	Ile
	195						200					205			
Gln	Ala	Leu	Phe	Phe	Met	Ala	Leu	Arg	Cys	Ala	Leu	Ser	Met	Leu	Lys
	210				215						220				
Pro	Asp	Glu	Glu	Gly	Arg	Asp	Phe	Ile	Glu	Arg	Ile	Val	Lys	Arg	Leu
225					230					235				240	
His	Ala	Leu	Ser	Phe	His	Met	Arg	Ser	Tyr	Phe	Trp	Leu	Asp	Phe	Gln
			245						250					255	
Gln	Leu	Asn	Asp	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Thr
		260						265					270		
Ala	Val	Asn	Lys	Phe	Asn	Val	Met	Pro	Asp	Ser	Ile	Pro	Asp	Trp	Val
		275					280					285			
Phe	Asp	Phe	Met	Pro	Leu	Arg	Gly	Gly	Tyr	Phe	Val	Gly	Asn	Val	Ser
	290					295					300				
Pro	Ala	Arg	Met	Asp	Phe	Arg	Trp	Phe	Ser	Leu	Gly	Asn	Cys	Val	Ser
305					310					315				320	
Ile	Leu	Ser	Ser	Leu	Ala	Thr	Pro	Asp	Gln	Ser	Met	Ala	Ile	Met	Asp
			325						330					335	
Leu	Leu	Glu	His	Arg	Trp	Glu	Glu	Leu	Val	Gly	Glu	Met	Pro	Leu	Lys
		340						345					350		
Ile	Cys	Tyr	Pro	Cys	Ile	Glu	Ser	His	Glu	Trp	Arg	Ile	Val	Thr	Gly
	355						360					365			
Cys	Asp	Pro	Lys	Asn	Thr	Arg	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp
	370					375					380				
Pro	Val	Leu	Leu	Trp	Thr	Leu	Thr	Glu	Ala	Cys	Ile	Lys	Thr	Gly	Arg
385					390					395				400	
Pro	Gln	Ile	Ala	Arg	Arg	Ala	Ile	Asp	Leu	Ile	Glu	Ser	Arg	Leu	His
			405						410					415	
Arg	Asp	Cys	Trp	Pro	Glu	Tyr	Tyr	Asp	Gly	Lys	Gln	Gly	Arg	Tyr	Val
		420						425					430		
Gly	Lys	Gln	Ala	Arg	Lys	Tyr	Gln	Thr	Trp	Ser	Ile	Ala	Gly	Tyr	Leu
		435					440					445			
Val	Ala	Lys	Met	Met	Leu	Glu	Asp	Pro	Ser	His	Ile	Gly	Met	Ile	Ser
	450						455					460			

Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile Lys Arg Ser Ala Ser  
465 470 475 480  
Trp Thr Cys

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..467
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

Met	Val	Ala	Glu	Ala	Trp	Glu	Ala	Leu	Arg	Arg	Ser	Met	Val	Phe	Phe
1			5					10						15	
Arg	Gly	Gln	Pro	Val	Gly	Thr	Ile	Ala	Ala	Tyr	Asp	His	Ala	Ser	Glu
			20					25					30		
Glu	Val	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Val	Arg	Asp	Phe	Val	Pro	Ser
		35				40						45			
Ala	Leu	Ala	Phe	Leu	Met	Asn	Gly	Glu	Pro	Asp	Ile	Val	Lys	Asn	Phe
	50					55					60				
Leu	Leu	Lys	Thr	Leu	Gln	Leu	Gln	Gly	Trp	Glu	Lys	Arg	Val	Asp	Arg
65					70					75				80	
Phe	Lys	Leu	Gly	Glu	Gly	Val	Met	Pro	Ala	Ser	Phe	Lys	Val	Leu	His
			85						90					95	
Asp	Pro	Val	Arg	Lys	Thr	Asp	Thr	Ile	Ile	Ala	Asp	Phe	Gly	Glu	Ser
			100					105					110		
Ala	Ile	Gly	Arg	Val	Ala	Pro	Val	Asp	Ser	Gly	Phe	Trp	Trp	Ile	Ile
		115					120					125			
Leu	Leu	Arg	Ala	Tyr	Thr	Lys	Ser	Thr	Gly	Asp	Leu	Thr	Leu	Ser	Glu
	130					135					140				
Thr	Pro	Glu	Cys	Gln	Arg	Gly	Met	Arg	Leu	Ile	Leu	Ser	Leu	Cys	Leu
145				150						155				160	
Ser	Glu	Gly	Phe	Asp	Thr	Phe	Pro	Thr	Leu	Leu	Cys	Ala	Asp	Gly	Cys
			165						170					175	
Ser	Met	Val	Asp	Arg	Arg	Met	Gly	Val	Tyr	Gly	Tyr	Pro	Ile	Glu	Ile
			180					185					190		
Gln	Ala	Leu	Phe	Phe	Met	Ala	Leu	Arg	Cys	Ala	Leu	Ser	Met	Leu	Lys
		195				200						205			
Pro	Asp	Glu	Glu	Gly	Arg	Asp	Phe	Ile	Glu	Arg	Ile	Val	Lys	Arg	Leu
	210					215						220			
His	Ala	Leu	Ser	Phe	His	Met	Arg	Ser	Tyr	Phe	Trp	Leu	Asp	Phe	Gln
225					230					235				240	
Gln	Leu	Asn	Asp	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Thr
			245						250					255	
Ala	Val	Asn	Lys	Phe	Asn	Val	Met	Pro	Asp	Ser	Ile	Pro	Asp	Trp	Val
		260						265					270		
Phe	Asp	Phe	Met	Pro	Leu	Arg	Gly	Tyr	Phe	Val	Gly	Asn	Val	Ser	
	275						280					285			
Pro	Ala	Arg	Met	Asp	Phe	Arg	Trp	Phe	Ser	Leu	Gly	Asn	Cys	Val	Ser
	290					295					300				
Ile	Leu	Ser	Ser	Leu	Ala	Thr	Pro	Asp	Gln	Ser	Met	Ala	Ile	Met	Asp
305					310					315				320	
Leu	Leu	Glu	His	Arg	Trp	Glu	Glu	Leu	Val	Gly	Glu	Met	Pro	Leu	Lys
			325						330					335	
Ile	Cys	Tyr	Pro	Cys	Ile	Glu	Ser	His	Glu	Trp	Arg	Ile	Val	Thr	Gly
			340					345					350		
Cys	Asp	Pro	Lys	Asn	Thr	Arg	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp

355 360 365  
Pro Val Leu Leu Trp Thr Leu Thr Glu Ala Cys Ile Lys Thr Gly Arg  
370 375 380  
Pro Gln Ile Ala Arg Arg Ala Ile Asp Leu Ile Glu Ser Arg Leu His  
385 390 395 400  
Arg Asp Cys Trp Pro Glu Tyr Tyr Asp Gly Lys Gln Gly Arg Tyr Val  
405 410 415  
Gly Lys Gln Ala Arg Lys Tyr Gln Thr Trp Ser Ile Ala Gly Tyr Leu  
420 425 430  
Val Ala Lys Met Met Leu Glu Asp Pro Ser His Ile Gly Met Ile Ser  
435 440 445  
Leu Glu Asp Lys Gln Met Lys Pro Val Ile Lys Arg Ser Ala Ser  
450 455 460  
Trp Thr Cys  
465

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..455

(D) OTHER INFORMATION: / Ceres Seq. ID 1498988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Met Val Phe Phe Arg Gly Gln Pro Val Gly Thr Ile Ala Ala Tyr Asp  
1 5 10 15  
His Ala Ser Glu Glu Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp  
20 25 30  
Phe Val Pro Ser Ala Leu Ala Phe Leu Met Asn Gly Glu Pro Asp Ile  
35 40 45  
Val Lys Asn Phe Leu Leu Lys Thr Leu Gln Leu Gln Gly Trp Glu Lys  
50 55 60  
Arg Val Asp Arg Phe Lys Leu Gly Glu Gly Val Met Pro Ala Ser Phe  
65 70 75 80  
Lys Val Leu His Asp Pro Val Arg Lys Thr Asp Thr Ile Ile Ala Asp  
85 90 95  
Phe Gly Glu Ser Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Phe  
100 105 110  
Trp Trp Ile Ile Leu Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu  
115 120 125  
Thr Leu Ser Glu Thr Pro Glu Cys Gln Arg Gly Met Arg Leu Ile Leu  
130 135 140  
Ser Leu Cys Leu Ser Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys  
145 150 155 160  
Ala Asp Gly Cys Ser Met Val Asp Arg Arg Met Gly Val Tyr Gly Tyr  
165 170 175  
Pro Ile Glu Ile Gln Ala Leu Phe Phe Met Ala Leu Arg Cys Ala Leu  
180 185 190  
Ser Met Leu Lys Pro Asp Glu Glu Gly Arg Asp Phe Ile Glu Arg Ile  
195 200 205  
Val Lys Arg Leu His Ala Leu Ser Phe His Met Arg Ser Tyr Phe Trp  
210 215 220  
Leu Asp Phe Gln Gln Leu Asn Asp Ile Tyr Arg Tyr Lys Thr Glu Glu  
225 230 235 240  
Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Met Pro Asp Ser Ile  
245 250 255  
Pro Asp Trp Val Phe Asp Phe Met Pro Leu Arg Gly Gly Tyr Phe Val  
260 265 270



Gly Asn Val Ser Pro Ala Arg Met Asp Phe Arg Trp Phe Ser Leu Gly  
275 280 285  
Asn Cys Val Ser Ile Leu Ser Ser Leu Ala Thr Pro Asp Gln Ser Met  
290 295 300  
Ala Ile Met Asp Leu Leu Glu His Arg Trp Glu Glu Leu Val Gly Glu  
305 310 315 320  
Met Pro Leu Lys Ile Cys Tyr Pro Cys Ile Glu Ser His Glu Trp Arg  
325 330 335  
Ile Val Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp Ser Tyr His Asn  
340 345 350  
Gly Gly Ser Trp Pro Val Leu Leu Trp Thr Leu Thr Glu Ala Cys Ile  
355 360 365  
Lys Thr Gly Arg Pro Gln Ile Ala Arg Arg Ala Ile Asp Leu Ile Glu  
370 375 380  
Ser Arg Leu His Arg Asp Cys Trp Pro Glu Tyr Tyr Asp Gly Lys Gln  
385 390 395 400  
Gly Arg Tyr Val Gly Lys Gln Ala Arg Lys Tyr Gln Thr Trp Ser Ile  
405 410 415  
Ala Gly Tyr Leu Val Ala Lys Met Met Leu Glu Asp Pro Ser His Ile  
420 425 430  
Gly Met Ile Ser Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile Lys  
435 440 445  
Arg Ser Ala Ser Trp Thr Cys  
450 455

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

ctgggtgaaa	catagaaaaag	tttctcttgc	tcaagttaat	gataaaagg	tgagagcaat	60
aaacgctgat	aagccttgtc	tggtccttgg	aattttgaat	tttctttttc	tatcttactt	120
atagtattgg	tagttgaggg	tgctcgatgat	aagttgttgt	aggatttggt	gctctggctc	180
tggtggtagg	tctatgaaat	caacccatat	cgtgaatgga	ctgcaacatg	gtatcttcgt	240
cccagtgagg	ttgggagcat	ttgatcatgt	ccaatccgtc	aaggactgaa	gatgacagca	300
aacagctacc	tactgagtgg	gaaattgaaa	aagggtgaagg	aattgaaatc	atagttccac	360
atttctcagg	ccttgagaga	gtcagtagtg	gctctgccac	cagcttcttg	cacactgctg	420
tatcgaaaag	ctcacagtcg	acctctatca	actcatcatc	tcccgaagcc	aaacgatgca	480
agcttgcatc	agaaagtccc	cctggagatt	cttgcagcaa	catagacttt	gtccagggtga	540
aggctcccac	agctctcgag	gtatccgttg	cctcagctga	atcagatcct	tgtttaaaac	600
taggaaaagc	gacataactc	gaagaatact	ggggtagaaa	caataatgaa	atttcagcgg	660
tttctatgaa	gttggttaact	ccatctgttg	tcgctgggaa	atccaaattg	tgtgggtcaga	720
gcatgccagt	cccgcgttgc	caaattgatg	gctgtgaact	ggatctctca	tctgctaagg	780
gttatcatcg	taagcacaaa	gtctgcgaaa	agcattcaaa	gtgcccgaag	gttagcgtga	840
gtggcctgga	acgtcgggtc	tgccaacagt	gtagcagggt	ccatgctgtc	tctgaatttg	900
atgagaagaa	acgaagctgc	cgaaaacgtc	tttctcatca	taatgcgagg	cgtcgtaaag	960
cacaaggagt	attttcaatg	aatcccagaa	gggtgtatga	tcgaagacag	catacaaata	1020
tgttggtgaa	tgggggtgtc	cttaacgcga	gatctgaaa	aaatgtatga	atggggtaat	1080
aaactttatg	atacaaaagc	tagacaaaag	gaaaaaagct	ttactctgag	cttccagaga	1140
ggtaatggct	ctgaggacca	gctgggttgc	agtagcagcc	gtatgttctc	tacatctcaa	1200
acctcagggt	ggttcccagc	aggaaagtcc	aagtttcaac	ttcatggcga	agatgtggga	1260
gaatactcag	gagtcctcca	tgaatctcaa	gatatccacc	gtgctctctc	tcttctgtca	1320
acctcttcgg	atcccctggc	ccaaccacat	gtgcagccat	tttctctact	ctgttcatat	1380
gatgttgtag	caaaatagat	gagtaagtaa	tgtgtaattt	gtaaacctgt	tactcagttg	1440
gtggataactt	ttcc					

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Met	Asp	Cys	Asn	Met	Val	Ser	Ser	Ser	Gln	Trp	Asp	Trp	Glu	His	Leu
1				5					10					15	
Ile	Met	Ser	Asn	Pro	Ser	Arg	Thr	Glu	Asp	Asp	Ser	Lys	Gln	Leu	Pro
			20					25					30		
Thr	Glu	Trp	Glu	Ile	Glu	Lys	Gly	Glu	Gly	Ile	Glu	Ser	Ile	Val	Pro
			35				40					45			
His	Phe	Ser	Gly	Leu	Glu	Arg	Val	Ser	Ser	Gly	Ser	Ala	Thr	Ser	Phe
	50					55				60					
Trp	His	Thr	Ala	Val	Ser	Lys	Ser	Ser	Gln	Ser	Thr	Ser	Ile	Asn	Ser
65				70					75					80	
Ser	Ser	Pro	Glu	Ala	Lys	Arg	Cys	Lys	Leu	Ala	Ser	Glu	Ser	Ser	Pro
			85					90					95		
Gly	Asp	Ser	Cys	Ser	Asn	Ile	Asp	Phe	Val	Gln	Val	Lys	Ala	Pro	Thr
			100					105					110		
Ala	Leu	Glu	Val	Ser	Val	Ala	Ser	Ala	Glu	Ser	Asp	Leu	Cys	Leu	Lys
			115				120					125			
Leu	Gly	Lys	Arg	Thr	Tyr	Ser	Glu	Glu	Tyr	Trp	Gly	Arg	Asn	Asn	Asn
			130			135					140				
Glu	Ile	Ser	Ala	Val	Ser	Met	Lys	Leu	Leu	Thr	Pro	Ser	Val	Val	Ala
145					150					155				160	
Gly	Lys	Ser	Lys	Leu	Cys	Gly	Gln	Ser	Met	Pro	Val	Pro	Arg	Cys	Gln
			165					170					175		
Ile	Asp	Gly	Cys	Glu	Leu	Asp	Leu	Ser	Ser	Ala	Lys	Gly	Tyr	His	Arg
			180					185					190		
Lys	His	Lys	Val	Cys	Glu	Lys	His	Ser	Lys	Cys	Pro	Lys	Val	Ser	Val
			195				200					205			
Ser	Gly	Leu	Glu	Arg	Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Ala
			210			215				220					
Val	Ser	Glu	Phe	Asp	Glu	Lys	Lys	Arg	Ser	Cys	Arg	Lys	Arg	Leu	Ser
225					230					235				240	
His	His	Asn	Ala	Arg	Arg	Arg	Lys	Pro	Gln	Gly	Val	Phe	Ser	Met	Asn
			245						250					255	
Pro	Glu	Arg	Val	Tyr	Asp	Arg	Arg	Gln	His	Thr	Asn	Met	Leu	Trp	Asn
			260					265					270		
Gly	Val	Ser	Leu	Asn	Ala	Arg	Ser	Glu	Arg	Asn	Val				
			275				280								

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu Ile Met Ser Asn

1				5					10					15		
Pro	Ser	Arg	Thr	Glu	Asp	Asp	Ser	Lys	Gln	Leu	Pro	Thr	Glu	Trp	Glu	
			20					25					30			
Ile	Glu	Lys	Gly	Glu	Gly	Ile	Glu	Ser	Ile	Val	Pro	His	Phe	Ser	Gly	
		35					40					45				
Leu	Glu	Arg	Val	Ser	Ser	Gly	Ser	Ala	Thr	Ser	Phe	Trp	His	Thr	Ala	
	50					55					60					
Val	Ser	Lys	Ser	Ser	Gln	Ser	Thr	Ser	Ile	Asn	Ser	Ser	Ser	Pro	Glu	
65					70					75					80	
Ala	Lys	Arg	Cys	Lys	Leu	Ala	Ser	Glu	Ser	Ser	Pro	Gly	Asp	Ser	Cys	
				85					90					95		
Ser	Asn	Ile	Asp	Phe	Val	Gln	Val	Lys	Ala	Pro	Thr	Ala	Leu	Glu	Val	
			100					105					110			
Ser	Val	Ala	Ser	Ala	Glu	Ser	Asp	Leu	Cys	Leu	Lys	Leu	Gly	Lys	Arg	
		115					120						125			
Thr	Tyr	Ser	Glu	Glu	Tyr	Trp	Gly	Arg	Asn	Asn	Asn	Glu	Ile	Ser	Ala	
	130					135						140				
Val	Ser	Met	Lys	Leu	Leu	Thr	Pro	Ser	Val	Val	Ala	Gly	Lys	Ser	Lys	
145					150					155					160	
Leu	Cys	Gly	Gln	Ser	Met	Pro	Val	Pro	Arg	Cys	Gln	Ile	Asp	Gly	Cys	
				165					170					175		
Glu	Leu	Asp	Leu	Ser	Ser	Ala	Lys	Gly	Tyr	His	Arg	Lys	His	Lys	Val	
			180					185					190			
Cys	Glu	Lys	His	Ser	Lys	Cys	Pro	Lys	Val	Ser	Val	Ser	Gly	Leu	Glu	
		195					200					205				
Arg	Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Ala	Val	Ser	Glu	Phe	
	210					215					220					
Asp	Glu	Lys	Lys	Arg	Ser	Cys	Arg	Lys	Arg	Leu	Ser	His	His	Asn	Ala	
225					230					235					240	
Arg	Arg	Arg	Lys	Pro	Gln	Gly	Val	Phe	Ser	Met	Asn	Pro	Glu	Arg	Val	
				245				250						255		
Tyr	Asp	Arg	Arg	Gln	His	Thr	Asn	Met	Leu	Trp	Asn	Gly	Val	Ser	Leu	
			260					265					270			
Asn	Ala	Arg	Ser	Glu	Arg	Asn	Val									
		275				280										

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

Met	Ser	Asn	Pro	Ser	Arg	Thr	Glu	Asp	Asp	Ser	Lys	Gln	Leu	Pro	Thr	
1				5					10					15		
Glu	Trp	Glu	Ile	Glu	Lys	Gly	Glu	Gly	Ile	Glu	Ser	Ile	Val	Pro	His	
		20					25					30				
Phe	Ser	Gly	Leu	Glu	Arg	Val	Ser	Gly	Ser	Ala	Thr	Ser	Phe	Trp		
		35				40					45					
His	Thr	Ala	Val	Ser	Lys	Ser	Gln	Ser	Thr	Ser	Ile	Asn	Ser	Ser		
	50					55				60						
Ser	Pro	Glu	Ala	Lys	Arg	Cys	Lys	Leu	Ala	Ser	Glu	Ser	Ser	Pro	Gly	
65					70					75				80		
Asp	Ser	Cys	Ser	Asn	Ile	Asp	Phe	Val	Gln	Val	Lys	Ala	Pro	Thr	Ala	
			85					90					95			
Leu	Glu	Val	Ser	Val	Ala	Ser	Ala	Glu	Ser	Asp	Leu	Cys	Leu	Lys	Leu	
			100					105					110			

Gly Lys Arg Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu  
115 120 125  
Ile Ser Ala Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly  
130 135 140  
Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile  
145 150 155 160  
Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys  
165 170 175  
His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser  
180 185 190  
Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val  
195 200 205  
Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His  
210 215 220  
His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro  
225 230 235 240  
Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly  
245 250 255  
Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val  
260 265

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

aagcgacgac	tgactcttct	tcctcctcct	cctccacctc	ttgttttaggt	tcttagcact	60
gaaatttgat	cagaaggtgt	tgacggtgta	gagcttcacg	aaacataaac	tttcatttct	120
tctagcttct	tgatttgctc	ttaaagggtgc	atggttgaagt	gattgaaagc	gattttacatg	180
tgacttgacg	ctcggtcaga	cattatacat	tacactcaac	acgagattgg	aaaggatgct	240
tgagaatcca	aagttcgatt	tgacgctgt	tggcaatcac	aacaacgaca	acaattacta	300
tgccctcacc	caagactttt	atcaaaagct	cggggaagaa	ggtacaaaca	tgtctgttga	360
cagtatgcag	acaagtaatg	ctggagggtc	tgtgtcaatg	tctgtcgata	acagtagcgt	420
tggttcgagt	gatgctctta	ttggccatcc	tggtttgaag	cctatgcgcc	atccctactc	480
tctctcggat	ggccaaagcg	tatttcggcc	aggaaaagtt	actcatgcac	ttaacgatga	540
tgcccttagca	caagcgttga	tggatagtaa	gtatccaacc	gagggactgg	tgaactatga	600
agagtggaca	atagatctga	ggaaactaca	tatgggtcct	gcttttgctc	aaggggcttt	660
tggaaagtta	tacagagga	cttacaacgg	agaagatgta	gccattaagc	tactcgagag	720
gtcagatagc	aaccctgaaa	aggcacaagc	cctcgaacag	cagtttcagc	aggaagtttc	780
tatgcttgca	tttttgaaagc	atcctaacat	cgttagggtt	attggtgcgt	gcattaaacc	840
gatggtgtgg	tgcatcgtga	ctgaatatgc	aaaaggaggg	tctgtcagac	agtttctgac	900
taagagacaa	aaccgagctg	tgcccttgaa	gttagctgtt	atgcaggcgt	tggatgttgc	960
caggggtatg	gcttacgtcc	atgagcgcaa	ctttatacac	cgggatctaa	agtcagataa	1020
cctcctcata	tcagctgac	ggtccatcaa	gattgctgat	tttgggtgtg	caagaattga	1080
agttcaaacc	gaagggatga	caccagagac	tggaaacttac	agatggatgg	caccagagat	1140
gatccagcac	agaccctaca	ctcaaaaagt	ggacgtgtat	agttttggaa	tcgtgtgtg	1200
ggagttgatt	acaggtctgt	taccgttcca	gaacatgacg	gcggttcagg	ctgcatttgc	1260
agtgggtgaac	agaggagtcc	gtccaacagt	cccagcagat	tgtcttcctg	tgcttgagaa	1320
gatcatgaca	cgttgctggg	atgocggacc	tgaagtccgt	ccttgttttg	cagagattgt	1380
caatcttctg	gaggcggcgg	aaactgagat	aatgacgaat	gtgagaaaag	cccgtttcag	1440
atgttgcatg	acgcaaccaa	tgacagtoga	ctaactctgt	gtgaagaaag	agagaggaga	1500
agaagaggaa	tgaacaaaga	agagaacata	aaagaaaaaa	acagagagag	agagagagaa	1560
agcaagaagg	gcttttagata	tatgtaagtt	tgtgtgtgta	tctatctatc	tatatatata	1620
tatccgattg	c					

(2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 412 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..412  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499002  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

Met	Leu	Glu	Asn	Pro	Lys	Phe	Asp	Leu	His	Ala	Val	Gly	Asn	His	Asn
1				5					10					15	
Asn	Asp	Asn	Asn	Tyr	Tyr	Ala	Phe	Thr	Gln	Asp	Phe	Tyr	Gln	Lys	Leu
			20					25					30		
Gly	Glu	Glu	Gly	Thr	Asn	Met	Ser	Val	Asp	Ser	Met	Gln	Thr	Ser	Asn
		35					40					45			
Ala	Gly	Gly	Ser	Val	Ser	Met	Ser	Val	Asp	Asn	Ser	Ser	Val	Gly	Ser
	50					55					60				
Ser	Asp	Ala	Leu	Ile	Gly	His	Pro	Gly	Leu	Lys	Pro	Met	Arg	His	Pro
65					70					75				80	
Tyr	Ser	Leu	Ser	Asp	Gly	Gln	Ser	Val	Phe	Arg	Pro	Gly	Lys	Val	Thr
			85						90					95	
His	Ala	Leu	Asn	Asp	Asp	Ala	Leu	Ala	Gln	Ala	Leu	Met	Asp	Ser	Lys
			100					105					110		
Tyr	Pro	Thr	Glu	Gly	Leu	Val	Asn	Tyr	Glu	Glu	Trp	Thr	Ile	Asp	Leu
		115					120					125			
Arg	Lys	Leu	His	Met	Gly	Pro	Ala	Phe	Ala	Gln	Gly	Ala	Phe	Gly	Lys
	130					135					140				
Leu	Tyr	Arg	Gly	Thr	Tyr	Asn	Gly	Glu	Asp	Val	Ala	Ile	Lys	Leu	Leu
145					150					155				160	
Glu	Arg	Ser	Asp	Ser	Asn	Pro	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Gln	Gln
			165						170					175	
Phe	Gln	Gln	Glu	Val	Ser	Met	Leu	Ala	Phe	Leu	Lys	His	Pro	Asn	Ile
			180					185					190		
Val	Arg	Phe	Ile	Gly	Ala	Cys	Ile	Lys	Pro	Met	Val	Trp	Cys	Ile	Val
		195					200					205			
Thr	Glu	Tyr	Ala	Lys	Gly	Gly	Ser	Val	Arg	Gln	Phe	Leu	Thr	Lys	Arg
	210					215					220				
Gln	Asn	Arg	Ala	Val	Pro	Leu	Lys	Leu	Ala	Val	Met	Gln	Ala	Leu	Asp
225					230					235				240	
Val	Ala	Arg	Gly	Met	Ala	Tyr	Val	His	Glu	Arg	Asn	Phe	Ile	His	Arg
			245						250					255	
Asp	Leu	Lys	Ser	Asp	Asn	Leu	Leu	Ile	Ser	Ala	Asp	Arg	Ser	Ile	Lys
		260					265						270		
Ile	Ala	Asp	Phe	Gly	Val	Ala	Arg	Ile	Glu	Val	Gln	Thr	Glu	Gly	Met
	275						280					285			
Thr	Pro	Glu	Thr	Gly	Thr	Tyr	Arg	Trp	Met	Ala	Pro	Glu	Met	Ile	Gln
	290					295					300				
His	Arg	Pro	Tyr	Thr	Gln	Lys	Val	Asp	Val	Tyr	Ser	Phe	Gly	Ile	Val
305					310					315				320	
Leu	Trp	Glu	Leu	Ile	Thr	Gly	Leu	Leu	Pro	Phe	Gln	Asn	Met	Thr	Ala
			325						330					335	
Val	Gln	Ala	Ala	Phe	Ala	Val	Val	Asn	Arg	Gly	Val	Arg	Pro	Thr	Val
		340						345					350		
Pro	Ala	Asp	Cys	Leu	Pro	Val	Leu	Gly	Glu	Ile	Met	Thr	Arg	Cys	Trp
	355						360					365			
Asp	Ala	Asp	Pro	Glu	Val	Arg	Pro	Cys	Phe	Ala	Glu	Ile	Val	Asn	Leu
	370					375					380				
Leu	Glu	Ala	Ala	Glu	Thr	Glu	Ile	Met	Thr	Asn	Val	Arg	Lys	Ala	Arg
385					390					395				400	

(2) INFORMATION FOR SEQ ID NO:797:

(A) LENGTH: 374 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

[illegible]

370

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1499004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Met	Gln	Thr	Ser	Asn	Ala	Gly	Gly	Ser	Val	Ser	Met	Ser	Val	Asp	Asn	
1				5				10						15		
Ser	Ser	Val	Gly	Ser	Ser	Asp	Ala	Leu	Ile	Gly	His	Pro	Gly	Leu	Lys	
		20						25					30			
Pro	Met	Arg	His	Pro	Tyr	Ser	Leu	Ser	Asp	Gly	Gln	Ser	Val	Phe	Arg	
		35					40					45				
Pro	Gly	Lys	Val	Thr	His	Ala	Leu	Asn	Asp	Asp	Ala	Leu	Ala	Gln	Ala	
	50					55					60					
Leu	Met	Asp	Ser	Lys	Tyr	Pro	Thr	Glu	Gly	Leu	Val	Asn	Tyr	Glu	Glu	
65					70					75				80		
Trp	Thr	Ile	Asp	Leu	Arg	Lys	Leu	His	Met	Gly	Pro	Ala	Phe	Ala	Gln	
			85						90					95		
Gly	Ala	Phe	Gly	Lys	Leu	Tyr	Arg	Gly	Thr	Tyr	Asn	Gly	Glu	Asp	Val	
			100					105					110			
Ala	Ile	Lys	Leu	Leu	Glu	Arg	Ser	Asp	Ser	Asn	Pro	Glu	Lys	Ala	Gln	
		115					120					125				
Ala	Leu	Glu	Gln	Gln	Phe	Gln	Gln	Glu	Val	Ser	Met	Leu	Ala	Phe	Leu	
	130					135					140					
Lys	His	Pro	Asn	Ile	Val	Arg	Phe	Ile	Gly	Ala	Cys	Ile	Lys	Pro	Met	
145				150						155				160		
Val	Trp	Cys	Ile	Val	Thr	Glu	Tyr	Ala	Lys	Gly	Gly	Ser	Val	Arg	Gln	
			165						170					175		
Phe	Leu	Thr	Lys	Arg	Gln	Asn	Arg	Ala	Val	Pro	Leu	Lys	Leu	Ala	Val	
		180						185					190			
Met	Gln	Ala	Leu	Asp	Val	Ala	Arg	Gly	Met	Ala	Tyr	Val	His	Glu	Arg	
		195					200					205				
Asn	Phe	Ile	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Leu	Leu	Ile	Ser	Ala	
		210				215					220					
Asp	Arg	Ser	Ile	Lys	Ile	Ala	Asp	Phe	Gly	Val	Ala	Arg	Ile	Glu	Val	
225				230						235				240		
Gln	Thr	Glu	Gly	Met	Thr	Pro	Glu	Thr	Gly	Thr	Tyr	Arg	Trp	Met	Ala	
			245						250					255		
Pro	Glu	Met	Ile	Gln	His	Arg	Pro	Tyr	Thr	Gln	Lys	Val	Asp	Val	Tyr	
		260						265					270			
Ser	Phe	Gly	Ile	Val	Leu	Trp	Glu	Leu	Ile	Thr	Gly	Leu	Leu	Pro	Phe	
		275					280					285				
Gln	Asn	Met	Thr	Ala	Val	Gln	Ala	Ala	Phe	Ala	Val	Val	Asn	Arg	Gly	
	290					295					300					
Val	Arg	Pro	Thr	Val	Pro	Ala	Asp	Cys	Leu	Pro	Val	Leu	Gly	Glu	Ile	
305				310					315					320		
Met	Thr	Arg	Cys	Trp	Asp	Ala	Asp	Pro	Glu	Val	Arg	Pro	Cys	Phe	Ala	
			325						330					335		
Glu	Ile	Val	Asn	Leu	Leu	Glu	Ala	Ala	Glu	Thr	Glu	Ile	Met	Thr	Asn	
		340					345					350				
Val	Arg	Lys	Ala	Arg	Phe	Arg	Cys	Cys	Met	Thr	Gln	Pro	Met	Thr	Val	
		355					360					365				

Asp

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

agattaagtc	ttcttcgtca	tcttcgagtg	tgagtggatc	cagagagaga	attagatatt	60
tccgacacga	ggcaaattcc	tagtggctca	tggcgctcatc	atctgatcac	acggcgaaga	120
taatcgacgg	caaggcgatt	gctcatacca	tcagatcaga	gatcgccgag	gaagttcgcg	180
gtctatctga	gaaacacggc	aaggtcccag	gactagctgt	agttattgtt	gggagccgaa	240
aggattcaca	gacctatgtg	aatacgaaga	ggaaagcgtg	cgctgaggtt	gggattaagt	300
catttgacgt	gggcctacca	gaggaagttt	ctgaagctga	tcttattagc	aaagttcatg	360
aactaaattc	aaatccggat	gtccatggca	tattagttca	actcccattg	ccgaaacata	420
ttaatgagga	gaatatattg	ggtgcaatca	gcattgataa	agatgtcgat	ggcttccatc	480
ctttgaatat	tggtaagcta	gccatgaaag	gcagagaacc	cctcttcctt	ccttgcaccc	540
caaagggatg	tttggaaactc	ctagctagaa	gcggcgtaaa	gataaagggg	caacgagcag	600
ttgttgtagg	tcggaagtaac	attgttggtt	tgcccgtttc	acttcttttg	ctcaaggctg	660
atgctactgt	cacaactgta	cattctcaca	ccaaggatcc	tgaggctatc	atacgggaag	720
ctgacattgt	tattgctgca	tgcggacaag	cccacatgat	taagggcaac	tggataaagc	780
caggggctgc	agtaattgat	gttggaaacta	atgcagtcag	cgacccgagc	aagaaatcag	840
gataccgggt	ggttggagat	gttgatttcg	cagaagcttc	aaaagttgca	ggtttcataa	900
ctccgggtccc	tgggtggtgta	ggcccaatga	cagtggaact	gcttctcagg	aacaccgtag	960
acggtgccaa	gcgtgtcttt	ggcgagtaaa	acaatctact	gtatgtaata	aagaaaccaa	1020
gagtttctcc	attctgtaat	tgtgtacttg	gcttgacgat	atttttccac	tcaaataaat	1080
tgaaattggc	gttccctttg	gattacctta	cattgtttctg	caactagcta	gaacgattat	1140
ttccgcaatt	cagttaaata	caagggtgtc	atcatgtgac	cc		

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..299
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

Met	Ala	Ser	Ser	Ser	Asp	His	Thr	Ala	Lys	Ile	Ile	Asp	Gly	Lys	Ala
1				5					10					15	
Ile	Ala	His	Thr	Ile	Arg	Ser	Glu	Ile	Ala	Glu	Glu	Val	Arg	Gly	Leu
			20					25					30		
Ser	Glu	Lys	His	Gly	Lys	Val	Pro	Gly	Leu	Ala	Val	Val	Ile	Val	Gly
		35					40					45			
Ser	Arg	Lys	Asp	Ser	Gln	Thr	Tyr	Val	Asn	Thr	Lys	Arg	Lys	Ala	Cys
		50				55					60				
Ala	Glu	Val	Gly	Ile	Lys	Ser	Phe	Asp	Val	Gly	Leu	Pro	Glu	Glu	Val
65				70					75					80	
Ser	Glu	Ala	Asp	Leu	Ile	Ser	Lys	Val	His	Glu	Leu	Asn	Ser	Asn	Pro
			85					90						95	
Asp	Val	His	Gly	Ile	Leu	Val	Gln	Leu	Pro	Leu	Pro	Lys	His	Ile	Asn
		100						105					110		
Glu	Glu	Asn	Ile	Leu	Gly	Ala	Ile	Ser	Ile	Asp	Lys	Asp	Val	Asp	Gly
		115					120					125			
Phe	His	Pro	Leu	Asn	Ile	Gly	Lys	Leu	Ala	Met	Lys	Gly	Arg	Glu	Pro



(2) INFORMATION FOR SEO ID NO:801:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1499011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1542

(D) OTHER INFORMATION: / Ceres Seq. ID 1499012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```
cttgcgtttt cgtcccaaa tctttgtcgt ggttttctgc tgtcttcttc tccgtcgaac      60
ttctccgacc acttcgtata gagagagaga gtgacgaaga gtttacgga tccaatccaa      120
taatgagtac tgcgtcggct tttagttaa tccaaggatg ctgggtcaag ggcgaagga      180
aaattcgtgt agcggataag cgagccaaga ggcttacttt gggatcccat gtggcttcgc      240
catcttcaat gagcttcaga gtttcagcta gtagttctgt taaacctgaa aaggatatta      300
ggattggtct tcttggtgca agtggctaca ctggtgctga gatcgtagg cttcttgcaa      360
atcatccgca tttccaggtc actttgatga ctgctgatag aaaagctggc cagtcaatgg      420
aaagcgtttt cccacacctg agagctcaaa aactacctac tttggtctcs gtaaaggatg      480
cagatttttc tactgtggat gctgtattct gctgtttacc tcacggaaca actcaggaaa      540
tcatcaagga actgcctact gcattgaaaa tcggtgatct ttcagcggac ttccggttgc      600
gtaatatgtc agaatatgaa gaatggtatg gtcagcctca caaggcagta gagttacaga      660
aagaagttgt gtatggtcta acagagatac taaggaggga cataaaaaag gcacgaactg      720
tggtcaaccc aggtctgtac ccgactacga ttcaacttcc tcttgttcct ttactaaagg      780
caaatctcat caaacatgaa aacatcatta tcgatgcaaa atctggtggt agtggagcag      840
gacgtgggtg taaggaggca aatctttact ctgagatagc tgaaggcatt tcttcttatg      900
gtgtcaccog tcatcgccat gttcctgaaa ttgaacaggg attatctgat gttgcacagt      960
caaaagtaac agtcagtttt acgccacatc tcatgccaat gatccgtgga atgcaatcga     1020
ctatatatgt ggaaatggct cccgggggta gaaccgaaga ttacaccag caattgaaga     1080
cgtcttatga ggatgaagaa tttgtcaaaag tggttgatga aggagttgtt cctcggacac     1140
acaacgtagg aggatccaac tattgtcata tgagtgtctt tcctgatcga attcctggaa     1200
gagctatcat aatctcagtg attgataatc ttgtgaaagg agcttcggga caagcgttgc     1260
agaatcttaa cataatggtg ggatatcccg aaacaacggg gctcctacac cagccgcttt     1320
tcccttaaaa atcccacctt taaatcgatg accaatctga agctggtgag acggcaatgt     1380
taagcataaa gatggttggt tatatgattc atatttatag acaataaagc ctcttctttt     1440
accattacaa ataaatgggt ttgtgttttg tttattaagg ttttgatgaa cctttattct     1500
tgttatctct attttctgaa ttgcaatttt cgtttgagtc gc
```

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1499013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

```
Cys Val Phe Val Pro Gln Ser Leu Ser Trp Phe Ser Ala Val Phe Phe
1          5          10          15
Ser Val Glu Leu Leu Arg Pro Leu Arg Ile Glu Arg Glu Ser Asp Glu
20          25          30
Glu Phe Thr Glu Ser Asn Pro Ile Met Ser Thr Ala Ser Ala Phe Ser
35          40          45
Ser Ile Gln Gly Cys Trp Phe Lys Gly Glu Arg Lys Ile Arg Val Ala
50          55          60
Asp Lys Arg Ala Lys Arg Leu Thr Leu Gly Ser His Val Ala Ser Pro
65          70          75          80
Ser Ser Met Ser Phe Arg Val Ser Ala Ser Ser Ser Val Lys Pro Glu
85          90          95
Lys Asp Ile Arg Ile Gly Leu Leu Gly Ala Ser Gly Tyr Thr Gly Ala
100         105         110
Glu Ile Val Arg Leu Leu Ala Asn Pro His Phe Gln Val Thr Leu
115         120         125
Met Thr Ala Asp Arg Lys Ala Gly Gln Ser Met Glu Ser Val Phe Pro
```

130	135	140
His Leu Arg Ala Gln Lys	Leu Pro Thr Leu Val	Xaa Val Lys Asp Ala
145	150	155
Asp Phe Ser Thr Val Asp	Ala Val Phe Cys Cys	Leu Pro His Gly Thr
165	170	175
Thr Gln Glu Ile Ile Lys	Glu Leu Pro Thr Ala	Leu Lys Ile Val Asp
180	185	190
Leu Ser Ala Asp Phe Arg	Leu Arg Asn Ile Ala	Glu Tyr Glu Glu Trp
195	200	205
Tyr Gly Gln Pro His Lys	Ala Val Glu Leu Gln	Lys Glu Val Val Tyr
210	215	220
Gly Leu Thr Glu Ile Leu	Arg Glu Asp Ile Lys	Lys Ala Arg Leu Val
225	230	235
Ala Asn Pro Gly Cys Tyr	Pro Thr Thr Ile Gln	Leu Pro Leu Val Pro
245	250	255
Leu Leu Lys Ala Asn Leu	Ile Lys His Glu Asn	Ile Ile Ile Asp Ala
260	265	270
Lys Ser Gly Val Ser Gly	Ala Gly Arg Gly Ala	Lys Glu Ala Asn Leu
275	280	285
Tyr Ser Glu Ile Ala Glu	Gly Ile Ser Ser Tyr	Gly Val Thr Arg His
290	295	300
Arg His Val Pro Glu Ile	Glu Gln Gly Leu Ser	Asp Val Ala Gln Ser
305	310	315
Lys Val Thr Val Ser Phe	Thr Pro His Leu Met	Pro Met Ile Arg Gly
325	330	335
Met Gln Ser Thr Ile Tyr	Val Glu Met Ala Pro	Gly Val Arg Thr Glu
340	345	350
Asp Leu His Gln Gln Leu	Lys Thr Ser Tyr Glu	Asp Glu Glu Phe Val
355	360	365
Lys Val Leu Asp Glu Gly	Val Val Pro Arg Thr	His Asn Val Arg Gly
370	375	380
Ser Asn Tyr Cys His Met	Ser Val Phe Pro Asp	Arg Ile Pro Gly Arg
385	390	395
Ala Ile Ile Ile Ser Val	Ile Asp Asn Leu Val	Lys Gly Ala Ser Gly
405	410	415
Gln Ala Leu Gln Asn Leu	Asn Ile Met Leu Gly	Tyr Pro Glu Thr Thr
420	425	430
Gly Leu Leu His Gln Pro	Leu Phe Pro	
435	440	

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1499014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

Met Ser Thr Ala Ser Ala	Phe Ser Ser Ile Gln	Gly Cys Trp Phe Lys
1	5	10
Gly Glu Arg Lys Ile Arg	Val Ala Asp Lys Arg	Ala Lys Arg Leu Thr
20	25	30
Leu Gly Ser His Val Ala	Ser Pro Ser Ser Met	Ser Phe Arg Val Ser
35	40	45
Ala Ser Ser Ser Val Lys	Pro Glu Lys Asp Ile	Arg Ile Gly Leu Leu
50	55	60
Gly Ala Ser Gly Tyr Thr	Gly Ala Glu Ile Val	Arg Leu Leu Ala Asn
65	70	75
		80

His	Pro	His	Phe	Gln	Val	Thr	Leu	Met	Thr	Ala	Asp	Arg	Lys	Ala	Gly	
				85					90					95		
Gln	Ser	Met	Glu	Ser	Val	Phe	Pro	His	Leu	Arg	Ala	Gln	Lys	Leu	Pro	
			100					105					110			
Thr	Leu	Val	Xaa	Val	Lys	Asp	Ala	Asp	Phe	Ser	Thr	Val	Asp	Ala	Val	
		115					120					125				
Phe	Cys	Cys	Leu	Pro	His	Gly	Thr	Thr	Gln	Glu	Ile	Ile	Lys	Glu	Leu	
	130					135					140					
Pro	Thr	Ala	Leu	Lys	Ile	Val	Asp	Leu	Ser	Ala	Asp	Phe	Arg	Leu	Arg	
145				150						155					160	
Asn	Ile	Ala	Glu	Tyr	Glu	Glu	Trp	Tyr	Gly	Gln	Pro	His	Lys	Ala	Val	
			165					170							175	
Glu	Leu	Gln	Lys	Glu	Val	Val	Tyr	Gly	Leu	Thr	Glu	Ile	Leu	Arg	Glu	
		180						185					190			
Asp	Ile	Lys	Lys	Ala	Arg	Leu	Val	Ala	Asn	Pro	Gly	Cys	Tyr	Pro	Thr	
	195						200					205				
Thr	Ile	Gln	Leu	Pro	Leu	Val	Pro	Leu	Leu	Lys	Ala	Asn	Leu	Ile	Lys	
	210					215						220				
His	Glu	Asn	Ile	Ile	Ile	Asp	Ala	Lys	Ser	Gly	Val	Ser	Gly	Ala	Gly	
225					230					235					240	
Arg	Gly	Ala	Lys	Glu	Ala	Asn	Leu	Tyr	Ser	Glu	Ile	Ala	Glu	Gly	Ile	
			245					250						255		
Ser	Ser	Tyr	Gly	Val	Thr	Arg	His	Arg	His	Val	Pro	Glu	Ile	Glu	Gln	
		260						265						270		
Gly	Leu	Ser	Asp	Val	Ala	Gln	Ser	Lys	Val	Thr	Val	Ser	Phe	Thr	Pro	
	275						280					285				
His	Leu	Met	Pro	Met	Ile	Arg	Gly	Met	Gln	Ser	Thr	Ile	Tyr	Val	Glu	
	290					295					300					
Met	Ala	Pro	Gly	Val	Arg	Thr	Glu	Asp	Leu	His	Gln	Gln	Leu	Lys	Thr	
305				310						315					320	
Ser	Tyr	Glu	Asp	Glu	Glu	Phe	Val	Lys	Val	Leu	Asp	Glu	Gly	Val	Val	
			325					330						335		
Pro	Arg	Thr	His	Asn	Val	Arg	Gly	Ser	Asn	Tyr	Cys	His	Met	Ser	Val	
		340						345						350		
Phe	Pro	Asp	Arg	Ile	Pro	Gly	Arg	Ala	Ile	Ile	Ile	Ser	Val	Ile	Asp	
	355					360						365				
Asn	Leu	Val	Lys	Gly	Ala	Ser	Gly	Gln	Ala	Leu	Gln	Asn	Leu	Asn	Ile	
	370					375					380					
Met	Leu	Gly	Tyr	Pro	Glu	Thr	Thr	Gly	Leu	Leu	His	Gln	Pro	Leu	Phe	
385					390					395					400	
Pro																

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

Met	Ser	Phe	Arg	Val	Ser	Ala	Ser	Ser	Ser	Val	Lys	Pro	Glu	Lys	Asp	
1				5					10					15		
Ile	Arg	Ile	Gly	Leu	Leu	Gly	Ala	Ser	Gly	Tyr	Thr	Gly	Ala	Glu	Ile	
		20					25						30			
Val	Arg	Leu	Leu	Ala	Asn	His	Pro	His	Phe	Gln	Val	Thr	Leu	Met	Thr	
	35					40					45					
Ala	Asp	Arg	Lys	Ala	Gly	Gln	Ser	Met	Glu	Ser	Val	Phe	Pro	His	Leu	

50	55	60
Arg Ala Gln Lys Leu	Pro Thr Leu Val Xaa Val	Lys Asp Ala Asp Phe
65	70	75
Ser Thr Val Asp Ala	Val Phe Cys Cys Leu	Pro His Gly Thr Thr Gln
85	90	95
Glu Ile Ile Lys Glu	Leu Pro Thr Ala Leu	Lys Ile Val Asp Leu Ser
100	105	110
Ala Asp Phe Arg Leu	Arg Asn Ile Ala Glu	Tyr Glu Glu Trp Tyr Gly
115	120	125
Gln Pro His Lys Ala	Val Glu Leu Gln Lys	Glu Val Val Tyr Gly Leu
130	135	140
Thr Glu Ile Leu Arg	Glu Asp Ile Lys Lys	Ala Arg Leu Val Ala Asn
145	150	155
Pro Gly Cys Tyr Pro	Thr Thr Ile Gln Leu	Pro Leu Val Pro Leu Leu
165	170	175
Lys Ala Asn Leu Ile	Lys His Glu Asn Ile	Ile Ile Asp Ala Lys Ser
180	185	190
Gly Val Ser Gly Ala	Gly Arg Gly Ala Lys	Glu Ala Asn Leu Tyr Ser
195	200	205
Glu Ile Ala Glu Gly	Ile Ser Ser Tyr Gly	Val Thr Arg His Arg His
210	215	220
Val Pro Glu Ile Glu	Gln Gly Leu Ser Asp	Val Ala Gln Ser Lys Val
225	230	235
Thr Val Ser Phe Thr	Pro His Leu Met Pro	Met Ile Arg Gly Met Gln
245	250	255
Ser Thr Ile Tyr Val	Glu Met Ala Pro Gly	Val Arg Thr Glu Asp Leu
260	265	270
His Gln Gln Leu Lys	Thr Ser Tyr Glu Asp	Glu Glu Phe Val Lys Val
275	280	285
Leu Asp Glu Gly Val	Val Pro Arg Thr His	Asn Val Arg Gly Ser Asn
290	295	300
Tyr Cys His Met Ser	Val Phe Pro Asp Arg	Ile Pro Gly Arg Ala Ile
305	310	315
Ile Ile Ser Val Ile	Asp Asn Leu Val Lys	Gly Ala Ser Gly Gln Ala
325	330	335
Leu Gln Asn Leu Asn	Ile Met Leu Gly Tyr	Pro Glu Thr Thr Gly Leu
340	345	350
Leu His Gln Pro Leu	Phe Pro	
355		

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

gcggttacact acaactctct atctctctct cttcttttct gctcattttt	gggtaattct	60
tctggtttta tgttcttggt cctattactg actcacaatc agccaacgca	aatctttctt	120
tgaccatttt taatagattc tcttagtcac ttgttggtt tcaaatgcaa	agttgacctc	180
atcttcttct tcttcgaggt tttatacaag ttactccata aaccttcgag	cttcagcaa	240
ctttggcttc tctgttggtg attattgctt attatatcct caacacgaaa	tcaaaatgcc	300
aagaccaaga gtttcagagt tgtctcagag gcaagctcca aggtgaggt	catcgtcac	360
tacttctgat tccaatcatt ccaaccgtct gatcactacg gatcaaagtt	ttaagcccgg	420
tgttgaccgt aaatctcctc gaagcgttgg acctaacagt gatccgcttg	gtcagaagaa	480
acttggggga cgaatatcgg atctagagtc gcagtttaga caagcgcaag	aggaactgag	540
attgctcaag gagcagttgg ctaatgctga agctgtgaag aaacaagctc	aagatgagct	600

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tcataagaag tccaagaaac caaacccgct ggctcgagtg gaggaatctg caactgaggc 660
tgagaggatt gatagagacg aaatcccttg tgatgtgcag aaagagactg atgtgtttga 720
ggttcccgtt gaaaagattg cagtagaaga agaagaactg agaagcggca atgacgaagc 780
tgagaaattg gttgcaaagg aagatgagat aaagatgctg aaagctagac tctatgacat 840
ggagaaagag catgaatcac taggcaaaga aaacgagagc ttgaagaatc agttgagcga 900
ttcagcttca gagatttcta atgtgaaagc taatgaagat gagatggttt caaaggtgag 960
taggattggg gaagagttag aagaaagcag agcaaagacg gctcacctga aggagaagct 1020
tgagtccatg gaagaagcaa aagatgcttt agaggctgag atgaagaagc tcagggttca 1080
aaccgagcag tggaggaagg cagcggatgc tgcagcagca gttctttctg gagagtttga 1140
gatgaatggg cgggatcgat ctgggtcaac tgagaagtat tatgcaggtg ggttctttga 1200
cccgtcagct gggttcatgg atccaccggg aatggctgat gattatgatg atggactggg 1260
aagtggcaag aggaagagtt ctgggatgaa gatgtttggg gagttgtgga ggaagaaagg 1320
gcaaaagtga gttacagatt gtgtggagtg tcattcaaga aatggtgtgc tcaccgttcc 1380
tctcttttat tttgctgtat ttacctgsaa gtttttgtaa gtgggtccgc ttcacagaa 1440
gctaactatc aatccaaatc aattgcaaaa acaatttcat g
```

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```
Met Pro Arg Pro Arg Val Ser Glu Leu Ser Gln Arg Gln Ala Pro Arg
1          5          10          15
Leu Arg Ser Ser Ser Ser Thr Ser Asp Ser Asn His Ser Asn Arg Leu
20          25          30
Ile Thr Thr Asp Gln Ser Phe Lys Pro Gly Val Asp Arg Lys Ser Pro
35          40          45
Arg Ser Gly Gly Pro Asn Ser Asp Pro Leu Gly Gln Lys Lys Leu Gly
50          55          60
Gly Arg Ile Ser Asp Leu Glu Ser Gln Leu Gly Gln Ala Gln Glu Glu
65          70          75          80
Leu Arg Leu Leu Lys Glu Gln Leu Ala Asn Ala Glu Ala Val Lys Lys
85          90          95
Gln Ala Gln Asp Glu Leu His Lys Lys Ser Lys Lys Pro Asn Pro Leu
100          105          110
Ala Arg Val Glu Glu Ser Ala Thr Glu Ala Glu Arg Ile Asp Arg Asp
115          120          125
Glu Ile Pro Gly Asp Val Gln Lys Glu Thr Asp Val Phe Glu Val Pro
130          135          140
Val Glu Lys Ile Ala Val Glu Glu Glu Glu Leu Arg Ser Gly Asn Asp
145          150          155          160
Glu Ala Glu Lys Leu Val Ala Lys Glu Asp Glu Ile Lys Met Leu Lys
165          170          175
Ala Arg Leu Tyr Asp Met Glu Lys Glu His Glu Ser Leu Gly Lys Glu
180          185          190
Asn Glu Ser Leu Lys Asn Gln Leu Ser Asp Ser Ala Ser Glu Ile Ser
195          200          205
Asn Val Lys Ala Asn Glu Asp Glu Met Val Ser Lys Val Ser Arg Ile
210          215          220
Gly Glu Glu Leu Glu Glu Ser Arg Ala Lys Thr Ala His Leu Lys Glu
225          230          235          240
Lys Leu Glu Ser Met Glu Glu Ala Lys Asp Ala Leu Glu Ala Glu Met
245          250          255
Lys Lys Leu Arg Val Gln Thr Glu Gln Trp Arg Lys Ala Ala Asp Ala
260          265          270
```

Ala Ala Ala Val Leu Ser Gly Glu Phe Glu Met Asn Gly Arg Asp Arg  
275 280 285  
Ser Gly Ser Thr Glu Lys Tyr Tyr Ala Gly Gly Phe Phe Asp Pro Ser  
290 295 300  
Ala Gly Phe Met Asp Pro Pro Gly Met Ala Asp Asp Tyr Asp Asp Gly  
305 310 315 320  
Leu Gly Ser Gly Lys Arg Lys Ser Ser Gly Met Lys Met Phe Gly Glu  
325 330 335  
Leu Trp Arg Lys Lys Gly Gln Lys  
340

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..559
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

ggcttctttc	aaccactctt	ggctctcttc	tccactcacc	gaaactccca	ctttcttttt	60
tcctccatct	ccacacccaa	aatccttgaa	actctcactt	ttccgaactc	ggagcaactc	120
gtcctcaccg	gaccgctcgt	cagaggttga	gctcgatgtg	gatccggtga	agctcgcatt	180
gaagaaagcc	gaagcttata	agaaatcgaa	atcagagcaa	aaagaaccag	agaaaaacgc	240
cggcgacgag	gaattgccgc	tctctgttaa	ggctgctatg	caaaaagcca	atgcttataa	300
gaaaaggaaa	ggacttgcaa	ctgatgcagt	cgcaaaagct	aaaccagta	atacagagca	360
aagttttgtt	agattaacaa	ataaggttgt	tgaagataat	gatgttaaga	agaaagaatt	420
gaaagtctcc	agcattgatt	tcattggggt	tggctttgct	gataagaaga	gcacaagggg	480
gcttccagcg	ggacttggtc	ctgttggtga	ctatcttcct	gaaggagact	tacctgaggt	540
ggagtttatt	gttggtgat					

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

Ala Ser Phe Asn His Ser Trp Leu Ser Ser Pro Leu Thr Glu Thr Pro	
1 5 10 15	
Thr Phe Phe Phe Pro Pro Ser Pro His Pro Lys Ser Leu Lys Leu Ser	
20 25 30	
Leu Phe Arg Thr Arg Ser Asn Ser Ser Pro Asp Arg Ser Ser Glu	
35 40 45	
Val Glu Leu Asp Val Asp Pro Val Lys Leu Ala Leu Lys Lys Ala Glu	
50 55 60	
Ala Tyr Lys Lys Ser Lys Ser Glu Gln Lys Glu Pro Glu Lys Asn Ala	
65 70 75 80	
Gly Asp Glu Glu Leu Pro Leu Ser Val Lys Ala Ala Met Gln Lys Ala	
85 90 95	
Asn Ala Tyr Lys Lys Arg Lys Gly Leu Gly Thr Asp Ala Val Ala Lys	
100 105 110	
Ala Lys Pro Ser Asn Thr Glu Gln Ser Phe Val Arg Leu Thr Asn Lys	
115 120 125	
Val Val Glu Asp Asn Asp Val Lys Lys Lys Glu Leu Lys Val Ser Ser	

130 135 140  
Ile Asp Phe Met Gly Leu Gly Phe Ala Asp Lys Lys Ser Thr Arg Gly  
145 150 155 160  
Leu Pro Ala Gly Leu Val Pro Val Val Asp Tyr Leu Pro Glu Gly Asp  
165 170 175  
Leu Pro Glu Val Glu Phe Ile Val Gly Asp  
180 185

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1499023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

Met Gln Lys Ala Asn Ala Tyr Lys Lys Arg Lys Gly Leu Gly Thr Asp  
1 5 10 15  
Ala Val Ala Lys Ala Lys Pro Ser Asn Thr Glu Gln Ser Phe Val Arg  
20 25 30  
Leu Thr Asn Lys Val Val Glu Asp Asn Asp Val Lys Lys Lys Glu Leu  
35 40 45  
Lys Val Ser Ser Ile Asp Phe Met Gly Leu Gly Phe Ala Asp Lys Lys  
50 55 60  
Ser Thr Arg Gly Leu Pro Ala Gly Leu Val Pro Val Val Asp Tyr Leu  
65 70 75 80  
Pro Glu Gly Asp Leu Pro Glu Val Glu Phe Ile Val Gly Asp  
85 90

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1527

(D) OTHER INFORMATION: / Ceres Seq. ID 1499024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

aacgcattat tgacacgtgt cttttcattt ctcttcttcc ggcgttttct ctccgccggtt 60  
tcgccaccgt acgtgacaat gtctgtttct ctctccgccg cctctcactt actctgttcc 120  
tcaccagag tctctcttcc ccccgccgtc acctcttctg cctcgtcccc tgtcgttgct 180  
ctttcttctt ctacatcgcc acattctctt ggaagcgtcg catcttcttc tctgtttcct 240  
cactcctcck tcgtgcttca gaaaaaacat ccgatcaatg ggacgagcac gaggatgatt 300  
tcacaaaaat gtgccgcttc tgatgcagct caattgataa gcgctaaaga agatatcaaa 360  
gttcttctcc ggactaagtt ttgccatccc atcttggtta gattgggggtg gcacgatgct 420  
ggtacttata acaagaatat tgaggagtgg ccactgagag gtggagctaa tggaagtctt 480  
aggtttgagg ctgagcttaa gcattgtgca aatgctggtc tgcttaatgc tttaaagctc 540  
attcagcctc tcaaagacaa gtatcctaac atctcttatg cggacttatt ccagttagct 600  
agtgccacag caatagagga ggctggtggt cctgatatcc cgatgaaata tgggagagtt 660  
gatgtttag cactgaaca gtgtccagaa gaaggaagac tccctgatgc tggacctcct 720  
tcaccagctg atcatttag agatgttttc tacagaatgg gacttgatga caaggaaata 780  
gttgccctgt ctggtgcaca taccttaggg agagccagac cagaccgtag tggttgggga 840  
aaacctgaga caaagtacac gaaaactgga cctggagaag caggaggaca gtcattggga 900  
gtgaaatggc tcaagttcga caactcttat ttcaaggata tcaaagaaaa gagggacgac 960  
gatcttctgg tgttaccac tgatgcggcg ctatttgaag atccttcatt caagaactat 1020  
gcagagaagt atgctgaaga tgtggctgca tttttcaagg actacgctga agcccatgcc 1080



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aagcttagca atctcgggtgc aaaatttgat cctcccgagg gcatagtcac tgaaaacggt 1140
ccagagaagt tcgtagctgc aaagtattct acgggaaaga aggagctttc ggattcgatg 1200
aaaaagaaga taagagcaga gtatgaagca attggaggaa gccagataa gccattaccc 1260
acaaattact tcctcaacat cataattgcc attggcgttt tggctctctt gtccactctc 1320
tttggtggtg ataacaactc cgattttctct ggtttctaata tgacaaatta tatattttga 1380
tttctcttac ctacatacat aattacgtgg tgatcatata ttccttgcaa acaaaaacat 1440
cattgtaaag tttgcttgaa taaaatcacc ttataaataa cattggtttat ttgggtttta 1500
gaattttgag attagtgtga gtttctt
```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..452

(D) OTHER INFORMATION: / Ceres Seq. ID 1499025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

```
Asn Ala Leu Leu Thr Arg Val Phe Ser Phe Leu Phe Phe Arg Arg Phe
1      5      10      15
Leu Ser Ala Val Ser Pro Pro Tyr Val Thr Met Ser Val Ser Leu Ser
20     25     30
Ala Ala Ser His Leu Leu Cys Ser Ser Thr Arg Val Ser Leu Ser Pro
35     40     45
Ala Val Thr Ser Ser Ser Ser Ser Pro Val Val Ala Leu Ser Ser Ser
50     55     60
Thr Ser Pro His Ser Leu Gly Ser Val Ala Ser Ser Ser Leu Phe Pro
65     70     75     80
His Ser Ser Xaa Val Leu Gln Lys Lys His Pro Ile Asn Gly Thr Ser
85     90     95
Thr Arg Met Ile Ser Pro Lys Cys Ala Ala Ser Asp Ala Ala Gln Leu
100    105    110
Ile Ser Ala Lys Glu Asp Ile Lys Val Leu Leu Arg Thr Lys Phe Cys
115    120    125
His Pro Ile Leu Val Arg Leu Gly Trp His Asp Ala Gly Thr Tyr Asn
130    135    140
Lys Asn Ile Glu Glu Trp Pro Leu Arg Gly Gly Ala Asn Gly Ser Leu
145    150    155    160
Arg Phe Glu Ala Glu Leu Lys His Ala Ala Asn Ala Gly Leu Leu Asn
165    170    175
Ala Leu Lys Leu Ile Gln Pro Leu Lys Asp Lys Tyr Pro Asn Ile Ser
180    185    190
Tyr Ala Asp Leu Phe Gln Leu Ala Ser Ala Thr Ala Ile Glu Glu Ala
195    200    205
Gly Gly Pro Asp Ile Pro Met Lys Tyr Gly Arg Val Asp Val Val Ala
210    215    220
Pro Glu Gln Cys Pro Glu Glu Gly Arg Leu Pro Asp Ala Gly Pro Pro
225    230    235    240
Ser Pro Ala Asp His Leu Arg Asp Val Phe Tyr Arg Met Gly Leu Asp
245    250    255
Asp Lys Glu Ile Val Ala Leu Ser Gly Ala His Thr Leu Gly Arg Ala
260    265    270
Arg Pro Asp Arg Ser Gly Trp Gly Lys Pro Glu Thr Lys Tyr Thr Lys
275    280    285
Thr Gly Pro Gly Glu Ala Gly Gly Gln Ser Trp Thr Val Lys Trp Leu
290    295    300
Lys Phe Asp Asn Ser Tyr Phe Lys Asp Ile Lys Glu Lys Arg Asp Asp
305    310    315    320
Asp Leu Leu Val Leu Pro Thr Asp Ala Ala Leu Phe Glu Asp Pro Ser
```

325 330 335  
Phe Lys Asn Tyr Ala Glu Lys Tyr Ala Glu Asp Val Ala Ala Phe Phe  
340 345 350  
Lys Asp Tyr Ala Glu Ala His Ala Lys Leu Ser Asn Leu Gly Ala Lys  
355 360 365  
Phe Asp Pro Pro Glu Gly Ile Val Ile Glu Asn Val Pro Glu Lys Phe  
370 375 380  
Val Ala Ala Lys Tyr Ser Thr Gly Lys Lys Glu Leu Ser Asp Ser Met  
385 390 395 400  
Lys Lys Lys Ile Arg Ala Glu Tyr Glu Ala Ile Gly Gly Ser Pro Asp  
405 410 415  
Lys Pro Leu Pro Thr Asn Tyr Phe Leu Asn Ile Ile Ile Ala Ile Gly  
420 425 430  
Val Leu Val Leu Leu Ser Thr Leu Phe Gly Gly Asn Asn Asn Ser Asp  
435 440 445  
Phe Ser Gly Phe  
450

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1499026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

Met Ser Val Ser Leu Ser Ala Ala Ser His Leu Leu Cys Ser Ser Thr  
1 5 10 15  
Arg Val Ser Leu Ser Pro Ala Val Thr Ser Ser Ser Ser Ser Pro Val  
20 25 30  
Val Ala Leu Ser Ser Ser Thr Ser Pro His Ser Leu Gly Ser Val Ala  
35 40 45  
Ser Ser Ser Leu Phe Pro His Ser Ser Xaa Val Leu Gln Lys Lys His  
50 55 60  
Pro Ile Asn Gly Thr Ser Thr Arg Met Ile Ser Pro Lys Cys Ala Ala  
65 70 75 80  
Ser Asp Ala Ala Gln Leu Ile Ser Ala Lys Glu Asp Ile Lys Val Leu  
85 90 95  
Leu Arg Thr Lys Phe Cys His Pro Ile Leu Val Arg Leu Gly Trp His  
100 105 110  
Asp Ala Gly Thr Tyr Asn Lys Asn Ile Glu Glu Trp Pro Leu Arg Gly  
115 120 125  
Gly Ala Asn Gly Ser Leu Arg Phe Glu Ala Glu Leu Lys His Ala Ala  
130 135 140  
Asn Ala Gly Leu Leu Asn Ala Leu Lys Leu Ile Gln Pro Leu Lys Asp  
145 150 155 160  
Lys Tyr Pro Asn Ile Ser Tyr Ala Asp Leu Phe Gln Leu Ala Ser Ala  
165 170 175  
Thr Ala Ile Glu Glu Ala Gly Gly Pro Asp Ile Pro Met Lys Tyr Gly  
180 185 190  
Arg Val Asp Val Val Ala Pro Glu Gln Cys Pro Glu Glu Gly Arg Leu  
195 200 205  
Pro Asp Ala Gly Pro Pro Ser Pro Ala Asp His Leu Arg Asp Val Phe  
210 215 220  
Tyr Arg Met Gly Leu Asp Asp Lys Glu Ile Val Ala Leu Ser Gly Ala  
225 230 235 240  
His Thr Leu Gly Arg Ala Arg Pro Asp Arg Ser Gly Trp Gly Lys Pro  
245 250 255

Glu Thr Lys Tyr Thr Lys Thr Gly Pro Gly Glu Ala Gly Gly Gln Ser  
260 265 270  
Trp Thr Val Lys Trp Leu Lys Phe Asp Asn Ser Tyr Phe Lys Asp Ile  
275 280 285  
Lys Glu Lys Arg Asp Asp Asp Leu Leu Val Leu Pro Thr Asp Ala Ala  
290 295 300  
Leu Phe Glu Asp Pro Ser Phe Lys Asn Tyr Ala Glu Lys Tyr Ala Glu  
305 310 315 320  
Asp Val Ala Ala Phe Phe Lys Asp Tyr Ala Glu Ala His Ala Lys Leu  
325 330 335  
Ser Asn Leu Gly Ala Lys Phe Asp Pro Glu Gly Ile Val Ile Glu  
340 345 350  
Asn Val Pro Glu Lys Phe Val Ala Ala Lys Tyr Ser Thr Gly Lys Lys  
355 360 365  
Glu Leu Ser Asp Ser Met Lys Lys Lys Ile Arg Ala Glu Tyr Glu Ala  
370 375 380  
Ile Gly Gly Ser Pro Asp Lys Pro Leu Pro Thr Asn Tyr Phe Leu Asn  
385 390 395 400  
Ile Ile Ile Ala Ile Gly Val Leu Val Leu Leu Ser Thr Leu Phe Gly  
405 410 415  
Gly Asn Asn Asn Ser Asp Phe Ser Gly Phe  
420 425

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

Met Ile Ser Pro Lys Cys Ala Ala Ser Asp Ala Ala Gln Leu Ile Ser  
1 5 10 15  
Ala Lys Glu Asp Ile Lys Val Leu Leu Arg Thr Lys Phe Cys His Pro  
20 25 30  
Ile Leu Val Arg Leu Gly Trp His Asp Ala Gly Thr Tyr Asn Lys Asn  
35 40 45  
Ile Glu Glu Trp Pro Leu Arg Gly Gly Ala Asn Gly Ser Leu Arg Phe  
50 55 60  
Glu Ala Glu Leu Lys His Ala Ala Asn Ala Gly Leu Leu Asn Ala Leu  
65 70 75 80  
Lys Leu Ile Gln Pro Leu Lys Asp Lys Tyr Pro Asn Ile Ser Tyr Ala  
85 90 95  
Asp Leu Phe Gln Leu Ala Ser Ala Thr Ala Ile Glu Glu Ala Gly Gly  
100 105 110  
Pro Asp Ile Pro Met Lys Tyr Gly Arg Val Asp Val Val Ala Pro Glu  
115 120 125  
Gln Cys Pro Glu Glu Gly Arg Leu Pro Asp Ala Gly Pro Pro Ser Pro  
130 135 140  
Ala Asp His Leu Arg Asp Val Phe Tyr Arg Met Gly Leu Asp Asp Lys  
145 150 155 160  
Glu Ile Val Ala Leu Ser Gly Ala His Thr Leu Gly Arg Ala Arg Pro  
165 170 175  
Asp Arg Ser Gly Trp Gly Lys Pro Glu Thr Lys Tyr Thr Lys Thr Gly  
180 185 190  
Pro Gly Glu Ala Gly Gly Gln Ser Trp Thr Val Lys Trp Leu Lys Phe  
195 200 205  
Asp Asn Ser Tyr Phe Lys Asp Ile Lys Glu Lys Arg Asp Asp Asp Leu

210	215	220
Leu Val Leu Pro Thr Asp	Ala Ala Leu Phe Glu	Asp Pro Ser Phe Lys
225	230	235
Asn Tyr Ala Glu Lys Tyr	Ala Glu Asp Val Ala	Ala Phe Phe Lys Asp
	245	250
Tyr Ala Glu Ala His Ala	Lys Leu Ser Asn Leu	Gly Ala Lys Phe Asp
	260	265
Pro Pro Glu Gly Ile Val	Ile Glu Asn Val Pro	Glu Lys Phe Val Ala
	275	280
Ala Lys Tyr Ser Thr Gly	Lys Lys Glu Leu Ser	Asp Ser Met Lys Lys
290	295	300
Lys Ile Arg Ala Glu Tyr	Glu Ala Ile Gly Gly	Ser Pro Asp Lys Pro
305	310	315
Leu Pro Thr Asn Tyr Phe	Leu Asn Ile Ile Ile	Ala Ile Gly Val Leu
	325	330
Val Leu Leu Ser Thr Leu	Phe Gly Gly Asn Asn	Asn Ser Asp Phe Ser
	340	345
		350
Gly Phe		

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

aanttcgcgg gatagactcy tcaagggagt ggatcatgcg aatttctcaa tttatatataca	60
ttcagttacct ggtttcgtgt tcaatgaaga aactacacga tcacagtatt tctataatcg	120
ccaattgaac aatagcatta aggtagtatg gggagaatca agcatgattg aagcagaaag	180
attgttgctt gcatctgctt tataggatca ctccaatcaa agatttgctt ttctctctga	240
cagatgtgct ccattatatg actttggcta tatatacaaa tatcttatct cttcaccgag	300
gagttttgtg gatagttttc ttcatactaa agagacacgg tacagtgtga aaatgtctcc	360
tgatcacact gaagagaaat ggcgaaaagg atcccagtggt atagctttga tcagaagtca	420
tgcagagggtc attgtaaatg atggtatcgt attcccagtt ttttaaggaat tctgcaagag	480
atgtccacct ttaggtacca atgaggcatg gttgtttctt aaacagaagc gacgcaactg	540
catccccgat gaacactatg tgcaaacatt gcttacgatg caaggactag agagtgaagt	600
ggaacgaaga acagtgcacat aactgtatg g	

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

Xaa Ser Arg Asp Arg Leu Xaa Lys Gly Val Asp His Ala Asn Phe Ser	
1	5
Ile Tyr Ile His Ser Val Pro Gly Phe Val Phe Asn Glu Glu Thr Thr	10
	15
Arg Ser Gln Tyr Phe Tyr Asn Arg Gln Leu Asn Asn Ser Ile Lys Val	20
	25
Val Trp Gly Glu Ser Ser Met Ile Glu Ala Glu Arg Leu Leu Leu Ala	30
	35
	40
	45

50 55 60  
Ser Ala Leu  
65  
(2) INFORMATION FOR SEQ ID NO:817:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 93 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..93  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499030  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:  
Met Ser Pro Val Ile Pro Glu Glu Lys Trp Arg Lys Gly Ser Gln Trp  
1 5 10 15  
Ile Ala Leu Ile Arg Ser His Ala Glu Val Ile Val Asn Asp Gly Ile  
20 25 30  
Val Phe Pro Val Phe Lys Glu Phe Cys Lys Arg Cys Pro Leu Gly  
35 40 45  
Thr Asn Glu Ala Trp Leu Phe Leu Lys Gln Lys Arg Arg Asn Cys Ile  
50 55 60  
Pro Asp Glu His Tyr Val Gln Thr Leu Leu Thr Met Gln Gly Leu Glu  
65 70 75 80  
Ser Glu Met Glu Arg Arg Thr Val Thr Tyr Thr Val Trp  
85 90

(2) INFORMATION FOR SEQ ID NO:818:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 674 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..674  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499031  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:  
mcccctgctc grgcgcaggg attgttgcat tatgtgccac cagtactact tatgatgaca 60  
ctgaaatagc tactaggatt ctccaaata tcgttgtgct aaccattgac caagacagtg 120  
atgttcggtc aaaggcattt caggccgtag aacagtttct tcagatattg aaacagaact 180  
atgagaagac aaatgctgga gaaataggag ccagcggagg agcctcagct atacctgaaa 240  
ctgctgggtct gatcggatgg gctatgagtt ctttgaccct caagggttaag ccattagaac 300  
aagcgccctct tgcttcttct tcttcagcac catccctagc agctgctgct tcaaattgcta 360  
caagcacagc aacggaggca ccgagtgtca aagccagtca tcatacacgt tccaactcgg 420  
atttcacaga tcaacctgca ccaccatccc caacatcaac agatgggttg ggagatgctg 480  
agaatggcat tagcgaaggt catgagagtg acaaagacgg ttgggatctc gaaccgctgg 540  
atgaacccaaa accttctcca gctcttgcta acattcaagc agctcaaaaa cgacctgtgt 600  
ctcagtcctc tagaccttca gctgcgacaa gctcaagacc aaagattagc acagtgaag 660  
cagctgcgaa aacg

(2) INFORMATION FOR SEQ ID NO:819:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 224 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1499032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

Pro	Cys	Ser	Xaa	Ala	Gly	Ile	Val	Ala	Leu	Cys	Ala	Thr	Ser	Thr	Thr
1			5						10					15	
Tyr	Asp	Asp	Thr	Glu	Ile	Ala	Thr	Arg	Ile	Leu	Pro	Asn	Ile	Val	Val
			20					25					30		
Leu	Thr	Ile	Asp	Gln	Asp	Ser	Asp	Val	Arg	Ser	Lys	Ala	Phe	Gln	Ala
			35					40					45		
Val	Glu	Gln	Phe	Leu	Gln	Ile	Leu	Lys	Gln	Asn	Tyr	Glu	Lys	Thr	Asn
			50					55				60			
Ala	Gly	Glu	Ile	Gly	Ala	Ser	Gly	Gly	Ala	Ser	Ala	Ile	Pro	Glu	Thr
65								70						80	
Ala	Gly	Leu	Ile	Gly	Trp	Ala	Met	Ser	Ser	Leu	Thr	Leu	Lys	Gly	Lys
			85					90						95	
Pro	Leu	Glu	Gln	Ala	Pro	Leu	Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser	Leu
			100					105					110		
Ala	Ala	Ala	Ala	Ser	Asn	Ala	Thr	Ser	Thr	Ala	Thr	Glu	Ala	Pro	Ser
			115					120					125		
Val	Lys	Ala	Ser	His	His	Thr	Arg	Ser	Asn	Ser	Asp	Phe	Thr	Asp	Gln
			130					135						140	
Pro	Ala	Pro	Pro	Ser	Pro	Thr	Ser	Thr	Asp	Gly	Trp	Gly	Asp	Ala	Glu
145								150						160	
Asn	Gly	Ile	Ser	Glu	Gly	His	Glu	Ser	Asp	Lys	Asp	Gly	Trp	Asp	Leu
								165						175	
Glu	Pro	Leu	Asp	Glu	Pro	Lys	Pro	Ser	Pro	Ala	Leu	Ala	Asn	Ile	Gln
								180						190	
Ala	Ala	Gln	Lys	Arg	Pro	Val	Ser	Gln	Ser	Ser	Arg	Pro	Ser	Ala	Ala
			195					200						205	
Thr	Ser	Ser	Arg	Pro	Lys	Ile	Ser	Thr	Val	Lys	Ala	Ala	Ala	Lys	Thr
			210					215						220	

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1499033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

Met	Ser	Ser	Leu	Thr	Leu	Lys	Gly	Lys	Pro	Leu	Glu	Gln	Ala	Pro	Leu
1			5						10					15	
Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser	Leu	Ala	Ala	Ala	Ala	Ser	Asn	Ala
			20					25					30		
Thr	Ser	Thr	Ala	Thr	Glu	Ala	Pro	Ser	Val	Lys	Ala	Ser	His	His	Thr
			35					40					45		
Arg	Ser	Asn	Ser	Asp	Phe	Thr	Asp	Gln	Pro	Ala	Pro	Pro	Ser	Pro	Thr
			50					55					60		
Ser	Thr	Asp	Gly	Trp	Gly	Asp	Ala	Glu	Asn	Gly	Ile	Ser	Glu	Gly	His
65								70						80	
Glu	Ser	Asp	Lys	Asp	Gly	Trp	Asp	Leu	Glu	Pro	Leu	Asp	Glu	Pro	Lys
			85					90						95	
Pro	Ser	Pro	Ala	Leu	Ala	Asn	Ile	Gln	Ala	Ala	Gln	Lys	Arg	Pro	Val
			100					105					110		
Ser	Gln	Ser	Ser	Arg	Pro	Ser	Ala	Ala	Thr	Ser	Ser	Arg	Pro	Lys	Ile
			115					120					125		
Ser	Thr	Val	Lys	Ala	Ala	Ala	Lys	Thr							

130 135

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1639 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1639

(D) OTHER INFORMATION: / Ceres Seq. ID 1499042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

accgggttttg	atctggttgt	ttgtcgtcga	tatggcgagg	atctcgtgtg	acttgagatt	60
tctttctcatc	ccggcagctt	tcatgttcat	ctacatccag	atgaggcttt	tccagacgca	120
atcacagtat	gcagatcgcc	tcagttccgc	tatcgaatct	gagaaccatt	gcactagtca	180
aatgcgaggc	ctcatagatg	aagttagcat	caaacagtcg	cggattgttg	ccctcgaaga	240
tatgaagaac	cgccaggacg	aagaacttgt	gcagcttaag	gatctaatac	agacgtttga	300
aaaaaaagga	atagcaaaac	tcactcaagg	tggacagatg	cctgtggctg	ctgtagtggt	360
tatggcctgc	agtcgtgcag	actatcttga	aaggactgtt	aaatcagttt	taacatatca	420
aactcccgtt	gcttcaaaat	atctcttatt	tatatctcag	gatggatctg	atcaagctgt	480
caagagcaag	tcatttagct	ataatcaatt	aacacatatg	cagcacttgg	attttgaacc	540
agtggctact	gaaaggcctg	gtgaactgac	tgcgtactac	aagattgcac	gtcactacaa	600
gtgggcactg	gaccagttgt	tttacaacaa	caaatttagt	cgagtgatta	tactagaaga	660
tgatatggaa	attgctccag	acttctttga	ttactttgag	gctgcagcta	gtctcatgga	720
tagggataaa	accattatgg	ctgcttcata	atggaatgat	aatggacaga	agcagtttgt	780
gcatgatccc	tatgcgctat	accgatcaga	tttttttcct	ggccttgggt	ggatgctcaa	840
gagatcgact	tgggatgagt	tatcaccaaa	gtggccaaag	gcttactggg	atgattggct	900
gagactaaag	gaaaaccata	aaggccgcca	attcattcga	ccggaagtct	gtagaacata	960
caattttggt	gaacatgggt	ctagtttggg	acagtttttc	agtcagtata	tggaacctat	1020
aaagctaaac	gatgtgacgg	ttgactggaa	agcaaaggac	ctgggatacc	tgacagaggg	1080
aaactatacc	aagtactttt	ctggcttagt	gagacaagca	cgaccaattc	aaggttctga	1140
ccttgtctta	aaggctcaaa	acataaagga	tgatgttcgt	atccggtata	aagaccaagt	1200
agagtttgaa	cgcattgcag	gggaatttgg	tatatttgaa	gaatggaagg	atggtgtgcc	1260
tcgaacagca	tataaaggag	tagtgggtgt	tcgaatccag	acaacaagac	gtgtattcct	1320
ggttggggcca	gattctgtaa	tgcagcttgg	aattcgaaat	tcctgatgca	aaacatatga	1380
aaggaaaaga	agattttgga	ccgcctgcag	cctccttcta	gcagctgtta	agttgtattg	1440
ttatttatgg	atgagtttgt	agagcgggtg	ggttaacttt	aacagcaagg	aagctctggt	1500
gacctggctg	attggcttag	aagttatggg	aacccttga	aagggtcagg	gttaaataata	1560
tttcagttgt	tttattagtg	attatcttgt	gggtaactta	tacgaatgca	aatcattcta	1620
tgcagttttt	cttcgtccc					

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 454 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..454

(D) OTHER INFORMATION: / Ceres Seq. ID 1499043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

Pro	Val	Leu	Ile	Trp	Leu	Phe	Val	Val	Asp	Met	Ala	Arg	Ile	Ser	Cys
1				5					10					15	
Asp	Leu	Arg	Phe	Leu	Leu	Ile	Pro	Ala	Ala	Phe	Met	Phe	Ile	Tyr	Ile
				20				25					30		
Gln	Met	Arg	Leu	Phe	Gln	Thr	Gln	Ser	Gln	Tyr	Ala	Asp	Arg	Leu	Ser
				35				40					45		
Ser	Ala	Ile	Glu	Ser	Glu	Asn	His	Cys	Thr	Ser	Gln	Met	Arg	Gly	Leu
				50				55						60	

Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg	Ile	Val	Ala	Leu	Glu	Asp
65					70					75					80
Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val	Gln	Leu	Lys	Asp	Leu	Ile
				85					90					95	
Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys	Leu	Thr	Gln	Gly	Gly	Gln
			100					105					110		
Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala	Cys	Ser	Arg	Ala	Asp	Tyr
		115					120					125			
Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr	Tyr	Gln	Thr	Pro	Val	Ala
	130					135					140				
Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp	Gly	Ser	Asp	Gln	Ala	Val
145				150						155					160
Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu	Thr	His	Met	Gln	His	Leu
				165				170						175	
Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro	Gly	Glu	Leu	Thr	Ala	Tyr
			180					185					190		
Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala	Leu	Asp	Gln	Leu	Phe	Tyr
	195					200						205			
Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu	Glu	Asp	Asp	Met	Glu	Ile
	210					215					220				
Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala	Ala	Ser	Leu	Met	Asp	
225				230					235					240	
Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser	Trp	Asn	Asp	Asn	Gly	Gln
				245				250						255	
Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu	Tyr	Arg	Ser	Asp	Phe	Phe
			260					265					270		
Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser	Thr	Trp	Asp	Glu	Leu	Ser
	275					280						285			
Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp	Trp	Leu	Arg	Leu	Lys	Glu
	290					295					300				
Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro	Glu	Val	Cys	Arg	Thr	Tyr
305				310						315					320
Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly	Gln	Phe	Phe	Ser	Gln	Tyr
				325				330						335	
Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr	Val	Asp	Trp	Lys	Ala	Lys
		340						345					350		
Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr	Thr	Lys	Tyr	Phe	Ser	Gly
	355					360						365			
Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly	Ser	Asp	Leu	Val	Leu	Lys
	370					375					380				
Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile	Arg	Tyr	Lys	Asp	Gln	Val
385				390					395						400
Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly	Ile	Phe	Glu	Glu	Trp	Lys
				405				410						415	
Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly	Val	Val	Val	Phe	Arg	Ile
			420				425						430		
Gln	Thr	Thr	Arg	Arg	Val	Phe	Leu	Val	Gly	Pro	Asp	Ser	Val	Met	Gln
	435						440					445			
Leu	Gly	Ile	Arg	Asn	Ser										
	450														

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499044



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

Met	Ala	Arg	Ile	Ser	Cys	Asp	Leu	Arg	Phe	Leu	Leu	Ile	Pro	Ala	Ala
1				5				10					15		
Phe	Met	Phe	Ile	Tyr	Ile	Gln	Met	Arg	Leu	Phe	Gln	Thr	Gln	Ser	Gln
			20					25					30		
Tyr	Ala	Asp	Arg	Leu	Ser	Ser	Ala	Ile	Glu	Ser	Glu	Asn	His	Cys	Thr
		35					40					45			
Ser	Gln	Met	Arg	Gly	Leu	Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg
		50				55					60				
Ile	Val	Ala	Leu	Glu	Asp	Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val
65					70				75					80	
Gln	Leu	Lys	Asp	Leu	Ile	Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys
			85					90						95	
Leu	Thr	Gln	Gly	Gly	Gln	Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala
			100					105					110		
Cys	Ser	Arg	Ala	Asp	Tyr	Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr
		115					120					125			
Tyr	Gln	Thr	Pro	Val	Ala	Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp
	130					135					140				
Gly	Ser	Asp	Gln	Ala	Val	Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu
145					150					155				160	
Thr	His	Met	Gln	His	Leu	Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro
			165					170						175	
Gly	Glu	Leu	Thr	Ala	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala
			180					185					190		
Leu	Asp	Gln	Leu	Phe	Tyr	Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu
		195					200					205			
Glu	Asp	Asp	Met	Glu	Ile	Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala
	210					215					220				
Ala	Ala	Ser	Leu	Met	Asp	Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser
225					230					235				240	
Trp	Asn	Asp	Asn	Gly	Gln	Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu
			245					250						255	
Tyr	Arg	Ser	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser
		260						265					270		
Thr	Trp	Asp	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp
		275					280						285		
Trp	Leu	Arg	Leu	Lys	Glu	Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro
	290					295					300				
Glu	Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly
305					310					315				320	
Gln	Phe	Phe	Ser	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr
			325						330					335	
Val	Asp	Trp	Lys	Ala	Lys	Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr
			340					345					350		
Thr	Lys	Tyr	Phe	Ser	Gly	Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly
		355					360					365			
Ser	Asp	Leu	Val	Leu	Lys	Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile
	370					375					380				
Arg	Tyr	Lys	Asp	Gln	Val	Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly
385					390					395				400	
Ile	Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly
			405					410						415	
Val	Val	Val	Phe	Arg	Ile	Gln	Thr	Thr	Arg	Arg	Val	Phe	Leu	Val	Gly
			420					425					430		
Pro	Asp	Ser	Val	Met	Gln	Leu	Gly	Ile	Arg	Asn	Ser				
		435					440								

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..427  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499045  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

Met	Phe	Ile	Tyr	Ile	Gln	Met	Arg	Leu	Phe	Gln	Thr	Gln	Ser	Gln	Tyr
1			5						10					15	
Ala	Asp	Arg	Leu	Ser	Ser	Ala	Ile	Glu	Ser	Glu	Asn	His	Cys	Thr	Ser
			20					25					30		
Gln	Met	Arg	Gly	Leu	Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg	Ile
			35				40					45			
Val	Ala	Leu	Glu	Asp	Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val	Gln
			50				55				60				
Leu	Lys	Asp	Leu	Ile	Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys	Leu
65					70					75				80	
Thr	Gln	Gly	Gly	Gln	Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala	Cys
				85					90					95	
Ser	Arg	Ala	Asp	Tyr	Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr	Tyr
			100					105					110		
Gln	Thr	Pro	Val	Ala	Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp	Gly
			115				120					125			
Ser	Asp	Gln	Ala	Val	Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu	Thr
			130				135				140				
His	Met	Gln	His	Leu	Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro	Gly
145					150					155				160	
Glu	Leu	Thr	Ala	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala	Leu
				165					170					175	
Asp	Gln	Leu	Phe	Tyr	Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu	Glu
			180					185					190		
Asp	Asp	Met	Glu	Ile	Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala	Ala
			195				200					205			
Ala	Ser	Leu	Met	Asp	Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser	Trp
			210				215				220				
Asn	Asp	Asn	Gly	Gln	Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu	Tyr
225					230					235				240	
Arg	Ser	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser	Thr
				245					250					255	
Trp	Asp	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp	Trp
			260					265					270		
Leu	Arg	Leu	Lys	Glu	Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro	Glu
			275				280					285			
Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly	Gln
			290				295				300				
Phe	Phe	Ser	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr	Val
305					310					315				320	
Asp	Trp	Lys	Ala	Lys	Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr	Thr
				325					330					335	
Lys	Tyr	Phe	Ser	Gly	Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly	Ser
			340					345					350		
Asp	Leu	Val	Leu	Lys	Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile	Arg
			355				360					365			
Tyr	Lys	Asp	Gln	Val	Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly	Ile
			370				375				380				
Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly	Val
385					390					395				400	
Val	Val	Phe	Arg	Ile	Gln	Thr	Thr	Arg	Arg	Val	Phe	Leu	Val	Gly	Pro
				405				410						415	
Asp	Ser	Val	Met	Gln	Leu	Gly	Ile	Arg	Asn	Ser					

420 425

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1499046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

agcgattgtc	cttttttgac	tcacttggtc	ttcttctaaa	gaaagcgaag	tttctttctct	60
ccagaataat	gttgattctc	tgtgttgga	tcctccatag	gataaatccc	tagacaatcc	120
tcttgatcgc	gcttttcgtt	tcgaaaaatt	taaacttttt	aactccgttg	atcgagatgg	180
tacagtcagc	ggtggaagtt	ctattaccgt	cggcggtgga	gattgaggtc	gcgggtggtcg	240
cttctgtgtt	tttaatcgct	tcctattggc	tattcgctta	cagaggaggc	ggagatgacg	300
atgtcgtcgg	tggtggattt	gatcgggtctc	gtctcatgca	gaatctcgat	tccggtgacg	360
cctttgacaa	agacaagata	ggacacttga	gaggagacac	tcaactaat	gctgcttata	420
tagtcaaggt	ggaactcttg	gctgctaaga	atctaattgg	tgctaactta	aatgggaacat	480
cagatcctta	tgctattggt	aattgtggat	cagaaaagcg	attcagttct	atgggtccctg	540
gctcgagaaa	tccaatgtgg	ggtgaagagt	tcaattttcc	cacagatgaa	cttcctgcta	600
agattaatgt	aacaattcat	gattgggata	tcatttgga	aagtactgtt	cttggctcag	660
taactattaa	tggtgaacgt	gaaggccaaa	cgggtccagt	gtggcactca	ttagacagcc	720
cgtctgggca	ggtttgccct	aacattaatg	caatcaaact	acccgtgaat	gctcctaggg	780
ctgtaactgg	atatgctgga	gccggtagaa	gaagggtcac	attggatcag	caaggcccaa	840
caattgtaca	tcaaaagcca	ggcctctgc	agacgatatt	tgatctcctc	ccggatgagg	900
ttgtcgagca	cagttattca	tgtgccctgg	agaggtcatt	cctgtatcat	ggcgaatgt	960
atgtttccgc	gtggcacata	tgtttccact	ccaatgtttt	ctctaagcaa	atgaaggttg	1020
ttgtccctct	cggagatata	gatgagattc	gtagaagtca	acacgcattg	ataaaccag	1080
ctataacaat	catactacgg	atgggtgctg	gtggacatgg	tgttccccct	cttgggactc	1140
ctgatggtag	agtgaggtag	aaatttgcac	cgttttggaa	caggaaccat	acactaaaag	1200
cattgcaacg	tgcggtgaat					

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1499047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

Met	Val	Gln	Ser	Ala	Val	Glu	Val	Leu	Leu	Pro	Ser	Ala	Trp	Glu	Ile
1					5				10					15	
Glu	Val	Ala	Val	Val	Ala	Ser	Val	Phe	Leu	Ile	Ala	Ser	Tyr	Trp	Leu
			20					25					30		
Phe	Ala	Tyr	Arg	Gly	Gly	Gly	Asp	Asp	Val	Val	Gly	Val	Gly	Phe	
		35				40					45				
Asp	Arg	Ser	Arg	Leu	Met	Gln	Asn	Leu	Asp	Ser	Gly	Asp	Ala	Phe	Asp
		50				55				60					
Lys	Asp	Lys	Ile	Gly	His	Leu	Arg	Gly	Asp	Thr	Gln	Thr	Asn	Ala	Ala
		65			70				75					80	
Tyr	Ile	Val	Lys	Val	Glu	Leu	Leu	Ala	Ala	Lys	Asn	Leu	Ile	Gly	Ala
			85					90						95	
Asn	Leu	Asn	Gly	Thr	Ser	Asp	Pro	Tyr	Ala	Ile	Val	Asn	Cys	Gly	Ser
		100						105					110		
Glu	Lys	Arg	Phe	Ser	Ser	Met	Val	Pro	Gly	Ser	Arg	Asn	Pro	Met	Trp

	115		120		125										
Gly	Glu	Glu	Phe	Asn	Phe	Pro	Thr	Asp	Glu	Leu	Pro	Ala	Lys	Ile	Asn
	130				135						140				
Val	Thr	Ile	His	Asp	Trp	Asp	Ile	Ile	Trp	Lys	Ser	Thr	Val	Leu	Gly
145					150					155					160
Ser	Val	Thr	Ile	Asn	Val	Glu	Arg	Glu	Gly	Gln	Thr	Gly	Pro	Val	Trp
				165					170					175	
His	Ser	Leu	Asp	Ser	Pro	Ser	Gly	Gln	Val	Cys	Leu	Asn	Ile	Asn	Ala
			180					185					190		
Ile	Lys	Leu	Pro	Val	Asn	Ala	Pro	Arg	Ala	Val	Thr	Gly	Tyr	Ala	Gly
	195						200					205			
Ala	Gly	Arg	Arg	Arg	Val	Thr	Leu	Asp	Gln	Gln	Gly	Pro	Thr	Ile	Val
	210						215				220				
His	Gln	Lys	Pro	Gly	Pro	Leu	Gln	Thr	Ile	Phe	Asp	Leu	Leu	Pro	Asp
225					230					235					240
Glu	Val	Val	Glu	His	Ser	Tyr	Ser	Cys	Ala	Leu	Glu	Arg	Ser	Phe	Leu
				245					250					255	
Tyr	His	Gly	Arg	Met	Tyr	Val	Ser	Ala	Trp	His	Ile	Cys	Phe	His	Ser
			260					265					270		
Asn	Val	Phe	Ser	Lys	Gln	Met	Lys	Val	Val	Val	Pro	Leu	Gly	Asp	Ile
	275						280					285			
Asp	Glu	Ile	Arg	Arg	Ser	Gln	His	Ala	Leu	Ile	Asn	Pro	Ala	Ile	Thr
	290					295					300				
Ile	Ile	Leu	Arg	Met	Gly	Ala	Gly	Gly	His	Gly	Val	Pro	Pro	Leu	Gly
305					310					315					320
Thr	Pro	Asp	Gly	Arg	Val	Arg	Tyr	Lys	Phe	Ala	Ser	Phe	Trp	Asn	Arg
				325					330					335	
Asn	His	Thr	Leu	Lys	Ala	Leu	Gln	Arg	Ala	Val	Asn				
			340					345							

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

Met	Gln	Asn	Leu	Asp	Ser	Gly	Asp	Ala	Phe	Asp	Lys	Asp	Lys	Ile	Gly
1			5					10						15	
His	Leu	Arg	Gly	Asp	Thr	Gln	Thr	Asn	Ala	Ala	Tyr	Ile	Val	Lys	Val
			20					25					30		
Glu	Leu	Leu	Ala	Ala	Lys	Asn	Leu	Ile	Gly	Ala	Asn	Leu	Asn	Gly	Thr
		35					40					45			
Ser	Asp	Pro	Tyr	Ala	Ile	Val	Asn	Cys	Gly	Ser	Glu	Lys	Arg	Phe	Ser
	50						55				60				
Ser	Met	Val	Pro	Gly	Ser	Arg	Asn	Pro	Met	Trp	Gly	Glu	Glu	Phe	Asn
65					70					75				80	
Phe	Pro	Thr	Asp	Glu	Leu	Pro	Ala	Lys	Ile	Asn	Val	Thr	Ile	His	Asp
			85					90						95	
Trp	Asp	Ile	Ile	Trp	Lys	Ser	Thr	Val	Leu	Gly	Ser	Val	Thr	Ile	Asn
			100					105					110		
Val	Glu	Arg	Glu	Gly	Gln	Thr	Gly	Pro	Val	Trp	His	Ser	Leu	Asp	Ser
			115				120					125			
Pro	Ser	Gly	Gln	Val	Cys	Leu	Asn	Ile	Asn	Ala	Ile	Lys	Leu	Pro	Val
		130					135					140			
Asn	Ala	Pro	Arg	Ala	Val	Thr	Gly	Tyr	Ala	Gly	Ala	Gly	Arg	Arg	Arg
145					150					155					160

Val Thr Leu Asp Gln Gln Gly Pro Thr Ile Val His Gln Lys Pro Gly  
165 170 175  
Pro Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp Glu Val Val Glu His  
180 185 190  
Ser Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu Tyr His Gly Arg Met  
195 200 205  
Tyr Val Ser Ala Trp His Ile Cys Phe His Ser Asn Val Phe Ser Lys  
210 215 220  
Gln Met Lys Val Val Val Pro Leu Gly Asp Ile Asp Glu Ile Arg Arg  
225 230 235 240  
Ser Gln His Ala Leu Ile Asn Pro Ala Ile Thr Ile Ile Leu Arg Met  
245 250 255  
Gly Ala Gly Gly His Gly Val Pro Pro Leu Gly Thr Pro Asp Gly Arg  
260 265 270  
Val Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg Asn His Thr Leu Lys  
275 280 285  
Ala Leu Gln Arg Ala Val Asn  
290 295

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..230
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

Met Val Pro Gly Ser Arg Asn Pro Met Trp Gly Glu Glu Phe Asn Phe  
1 5 10 15  
Pro Thr Asp Glu Leu Pro Ala Lys Ile Asn Val Thr Ile His Asp Trp  
20 25 30  
Asp Ile Ile Trp Lys Ser Thr Val Leu Gly Ser Val Thr Ile Asn Val  
35 40 45  
Glu Arg Glu Gly Gln Thr Gly Pro Val Trp His Ser Leu Asp Ser Pro  
50 55 60  
Ser Gly Gln Val Cys Leu Asn Ile Asn Ala Ile Lys Leu Pro Val Asn  
65 70 75 80  
Ala Pro Arg Ala Val Thr Gly Tyr Ala Gly Ala Gly Arg Arg Arg Val  
85 90 95  
Thr Leu Asp Gln Gln Gly Pro Thr Ile Val His Gln Lys Pro Gly Pro  
100 105 110  
Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp Glu Val Val Glu His Ser  
115 120 125  
Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu Tyr His Gly Arg Met Tyr  
130 135 140  
Val Ser Ala Trp His Ile Cys Phe His Ser Asn Val Phe Ser Lys Gln  
145 150 155 160  
Met Lys Val Val Val Pro Leu Gly Asp Ile Asp Glu Ile Arg Arg Ser  
165 170 175  
Gln His Ala Leu Ile Asn Pro Ala Ile Thr Ile Ile Leu Arg Met Gly  
180 185 190  
Ala Gly Gly His Gly Val Pro Pro Leu Gly Thr Pro Asp Gly Arg Val  
195 200 205  
Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg Asn His Thr Leu Lys Ala  
210 215 220  
Leu Gln Arg Ala Val Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1226 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1226  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499050  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

gacgagacaa	aagatagaga	agcaaaagta	agctgataag	gtttgatata	gtagaaaata	60
cactctctta	acttcttctt	cttcttcttc	ttcttctcct	atctttgaaa	atggcgatga	120
ctccggtgcg	gtcatcatct	ccagtttcaa	cctgcagact	ctttcgctgc	aatctcctcc	180
ctgatctctt	acctaagcct	ctgtttctct	ccctccccaa	acgaaacaga	attgcctcgt	240
gccgcttcac	tgtacgtgcc	tccgcgaatg	ctaccgtcga	atcccctaac	gggtgtccctg	300
cctccacatc	agatacggat	acggagacgg	ataccacctc	ctatggccga	cagtttttcc	360
ctttggccgc	agttgttggc	caggaaggca	taaaaactgc	tcttttactt	ggcgcggttg	420
atcgtgaaat	cggagggatt	gccatttcag	gtcgtagagg	cactgcaaaa	acagtcattg	480
cgcgagggct	tcatgaaatc	ctccctccta	ttgaagttgt	tgtaggctca	atatcaaatg	540
ctgacccagc	ttgtccagat	gagtggaag	atgacttaga	tgagcgcata	gagtacaatg	600
ctgacaatac	cattaagact	gagattgtca	aatctccttt	cattcagatt	ccactaggag	660
ttacagaaga	cagactcatt	gggtctgttg	atgttgagga	gtctgtgaaa	agggggacaa	720
ctgttttcca	acctggctct	ttggctgaag	cccatagagg	agtgttgtat	gttgatgaaa	780
taaatctctt	agatgagggg	attagtaatt	tgcttctcaa	tgtattgacg	gatgggtgta	840
atatagttga	aagagaagga	atcagcttta	ggcacccgtg	caaaccactt	ttaattgcaa	900
cctataaccc	tgaagaaggt	gctgttcgag	agcacttgct	agaccgtgtt	gcggttgctt	960
ctgtctacatc	tggaggtgga	ggaggtgggt	gtgctcctgc	tgttgagtcc	aagaaagaag	1020
agaagaagga	agaaaaggaa	gaatccgatg	atgacatggg	tttcagtcta	ttcgagtaag	1080
ctggtagtag	catgaaaagt	ccggttttgt	tgctctcttt	taatatgkq	accttttgaa	1140
atctatatgt	tgttgttggt	tagtttgtat	tcgatcatct	tttttagaca	ttgctgaaat	1200
tctcaagagt	ttttgacccg	aatgcc				

(2) INFORMATION FOR SEQ ID NO:830:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 322 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..322  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499051  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met	Ala	Met	Thr	Pro	Val	Ala	Ser	Ser	Ser	Pro	Val	Ser	Thr	Cys	Arg
1				5					10					15	
Leu	Phe	Arg	Cys	Asn	Leu	Leu	Pro	Asp	Leu	Leu	Pro	Lys	Pro	Leu	Phe
			20					25					30		
Leu	Ser	Leu	Pro	Lys	Arg	Asn	Arg	Ile	Ala	Ser	Cys	Arg	Phe	Thr	Val
		35				40					45				
Arg	Ala	Ser	Ala	Asn	Ala	Thr	Val	Glu	Ser	Pro	Asn	Gly	Val	Pro	Ala
	50				55						60				
Ser	Thr	Ser	Asp	Thr	Asp	Thr	Glu	Thr	Asp	Thr	Thr	Ser	Tyr	Gly	Arg
65			70					75					80		
Gln	Phe	Phe	Pro	Leu	Ala	Ala	Val	Val	Gly	Gln	Glu	Gly	Ile	Lys	Thr
			85				90						95		
Ala	Leu	Leu	Leu	Gly	Ala	Val	Asp	Arg	Glu	Ile	Gly	Gly	Ile	Ala	Ile
		100					105						110		
Ser	Gly	Arg	Arg	Gly	Thr	Ala	Lys	Thr	Val	Met	Ala	Arg	Gly	Leu	His
		115				120						125			
Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val	Gly	Ser	Ile	Ser	Asn	Ala

130	135	140
Asp Pro Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile		
145	150	155
Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro		160
	165	170
Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser		175
	180	185
Val Asp Val Glu Glu Ser Val Lys Arg Gly Thr Thr Val Phe Gln Pro		190
	195	200
Gly Leu Leu Ala Glu Ala His Arg Gly Val Leu Tyr Val Asp Glu Ile		205
210	215	220
Asn Leu Leu Asp Glu Gly Ile Ser Asn Leu Leu Leu Asn Val Leu Thr		
225	230	235
Asp Gly Val Asn Ile Val Glu Arg Glu Gly Ile Ser Phe Arg His Pro		240
	245	250
Cys Lys Pro Leu Leu Ile Ala Thr Tyr Asn Pro Glu Glu Gly Ala Val		255
	260	265
Arg Glu His Leu Leu Asp Arg Val Ala Val Ala Ser Ala Thr Ser Gly		270
	275	280
Gly Gly Gly Gly Gly Gly Ala Pro Ala Ala Glu Ser Lys Lys Glu Glu		285
290	295	300
Lys Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser Leu		
305	310	315
Phe Glu		320

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1499052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Met Thr Pro Val Ala Ser Ser Ser Pro Val Ser Thr Cys Arg Leu Phe		
1	5	10
Arg Cys Asn Leu Leu Pro Asp Leu Leu Pro Lys Pro Leu Phe Leu Ser		15
	20	25
Leu Pro Lys Arg Asn Arg Ile Ala Ser Cys Arg Phe Thr Val Arg Ala		30
	35	40
Ser Ala Asn Ala Thr Val Glu Ser Pro Asn Gly Val Pro Ala Ser Thr		45
	50	55
Ser Asp Thr Asp Thr Glu Thr Asp Thr Thr Ser Tyr Gly Arg Gln Phe		60
65	70	75
Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr Ala Leu		80
	85	90
Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile Ser Gly		95
	100	105
Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His Glu Ile		110
	115	120
Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala Asp Pro		125
	130	135
Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile Glu Tyr		140
145	150	155
Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro Phe Ile		160
	165	170
Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser Val Asp		175
	180	185
		190

Val	Glu	Glu	Ser	Val	Lys	Arg	Gly	Thr	Thr	Val	Phe	Gln	Pro	Gly	Leu
	195						200					205			
Leu	Ala	Glu	Ala	His	Arg	Gly	Val	Leu	Tyr	Val	Asp	Glu	Ile	Asn	Leu
	210					215					220				
Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu	Leu	Leu	Asn	Val	Leu	Thr	Asp	Gly
225					230					235				240	
Val	Asn	Ile	Val	Glu	Arg	Glu	Gly	Ile	Ser	Phe	Arg	His	Pro	Cys	Lys
				245					250					255	
Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn	Pro	Glu	Glu	Gly	Ala	Val	Arg	Glu
			260				265						270		
His	Leu	Leu	Asp	Arg	Val	Ala	Val	Ala	Ser	Ala	Thr	Ser	Gly	Gly	Gly
	275						280					285			
Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala	Glu	Ser	Lys	Lys	Glu	Glu	Lys	Lys
	290					295					300				
Glu	Glu	Lys	Glu	Glu	Ser	Asp	Asp	Asp	Met	Gly	Phe	Ser	Leu	Phe	Glu
305					310					315				320	

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1499053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

Met	Ala	Arg	Gly	Leu	His	Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val
1				5					10					15	
Gly	Ser	Ile	Ser	Asn	Ala	Asp	Pro	Ala	Cys	Pro	Asp	Glu	Trp	Glu	Asp
			20					25					30		
Asp	Leu	Asp	Glu	Arg	Ile	Glu	Tyr	Asn	Ala	Asp	Asn	Thr	Ile	Lys	Thr
	35					40						45			
Glu	Ile	Val	Lys	Ser	Pro	Phe	Ile	Gln	Ile	Pro	Leu	Gly	Val	Thr	Glu
	50					55					60				
Asp	Arg	Leu	Ile	Gly	Ser	Val	Asp	Val	Glu	Glu	Ser	Val	Lys	Arg	Gly
65				70					75					80	
Thr	Thr	Val	Phe	Gln	Pro	Gly	Leu	Leu	Ala	Glu	Ala	His	Arg	Gly	Val
			85					90						95	
Leu	Tyr	Val	Asp	Glu	Ile	Asn	Leu	Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu
	100						105						110		
Leu	Leu	Asn	Val	Leu	Thr	Asp	Gly	Val	Asn	Ile	Val	Glu	Arg	Glu	Gly
	115						120					125			
Ile	Ser	Phe	Arg	His	Pro	Cys	Lys	Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn
	130					135					140				
Pro	Glu	Glu	Gly	Ala	Val	Arg	Glu	His	Leu	Leu	Asp	Arg	Val	Ala	Val
145					150					155				160	
Ala	Ser	Ala	Thr	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala
			165					170						175	
Glu	Ser	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Glu	Lys	Glu	Glu	Ser	Asp	Asp
			180					185					190		
Asp	Met	Gly	Phe	Ser	Leu	Phe	Glu								
	195						200								

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..540
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

acatctgtcg ccgcccgtga gaccgccact taaggccgctc tcctccgctc tatccatatac	60
caaaacagct ataaagataa acttccagag cttggtgaag gacgagcaac cctagttttc	120
aatccctaaa gatattagtt ctccagcgag ttgacacaaa acccgattac gtttcatccg	180
gcgactcgct ttgatattcc atggattctc agttgaatcc ttccaagaga cgcaagataa	240
gtgtcaggca cagatgcggt gcgtgctata agatgttcaa tagacgagaa cacctcgttg	300
agcacatgaa gatttccctac cactcacttc accagcctcg ctgtggggtt tgccctcaagc	360
actgtaaatc cttcgaatcc gtgagggaac accttaacgt tccagaccat ctttccaaag	420
gaaactgcaa agccattttc actaaacgag gctgtactct ctgtcttcaa atctttgagg	480
aggcctttgc tctcgccgag cataaaaaca agtgtcacct ctccccamct cgctctcttg	540

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..113
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Met Asp Ser Gln Leu Asn Pro Ser Lys Arg Arg Lys Ile Ser Val Arg	
1 5 10 15	
His Arg Cys Val Ala Cys Tyr Lys Met Phe Asn Arg Arg Glu His Leu	
20 25 30	
Val Glu His Met Lys Ile Ser Tyr His Ser Leu His Gln Pro Arg Cys	
35 40 45	
Gly Val Cys Leu Lys His Cys Lys Ser Phe Glu Ser Val Arg Glu His	
50 55 60	
Leu Asn Val Pro Asp His Leu Ser Lys Gly Asn Cys Lys Ala Ile Phe	
65 70 75 80	
Thr Lys Arg Gly Cys Thr Leu Cys Leu Gln Ile Phe Glu Glu Ala Phe	
85 90 95	
Ala Leu Ala Glu His Lys Asn Lys Cys His Leu Ser Pro Xaa Arg Pro	
100 105 110	
Leu	

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..89
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met Phe Asn Arg Arg Glu His Leu Val Glu His Met Lys Ile Ser Tyr	
1 5 10 15	
His Ser Leu His Gln Pro Arg Cys Gly Val Cys Leu Lys His Cys Lys	
20 25 30	

Ser Phe Glu Ser Val Arg Glu His Leu Asn Val Pro Asp His Leu Ser  
35 40 45  
Lys Gly Asn Cys Lys Ala Ile Phe Thr Lys Arg Gly Cys Thr Leu Cys  
50 55 60  
Leu Gln Ile Phe Glu Glu Ala Phe Ala Leu Ala Glu His Lys Asn Lys  
65 70 75 80  
Cys His Leu Ser Pro Xaa Arg Pro Leu  
85

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1499057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

Met Lys Ile Ser Tyr His Ser Leu His Gln Pro Arg Cys Gly Val Cys  
1 5 10 15  
Leu Lys His Cys Lys Ser Phe Glu Ser Val Arg Glu His Leu Asn Val  
20 25 30  
Pro Asp His Leu Ser Lys Gly Asn Cys Lys Ala Ile Phe Thr Lys Arg  
35 40 45  
Gly Cys Thr Leu Cys Leu Gln Ile Phe Glu Glu Ala Phe Ala Leu Ala  
50 55 60  
Glu His Lys Asn Lys Cys His Leu Ser Pro Xaa Arg Pro Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1347 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1347

(D) OTHER INFORMATION: / Ceres Seq. ID 1499066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

acaaacccta agaagcttct catcttcctc acaaacccta agaagcttct catcttctct 60  
ttctctcgaa gattccgatt tgctcttttg aaacttccga tgacgaagaa actcgatcca 120  
ccaacggcac cttcaagcga cgaagatgac gtcgagactt ccgaagatga ttctcttcca 180  
tctgaagaag acgaaccaat caaatccctt cccgccacaa ccgccgctgc tcttgctaaa 240  
tccaccgccg tctccgccgc tactccagct aaatccaccg ccgtctccgc cgctgctcct 300  
tctaaatcca ccgccgtctc cgccgctgct gattcagatt ctgggttcga gagtgaataa 360  
gattcggatt ctgaatcgac ggatcctccg aaatctggat ccggtaaaac aatcgcttca 420  
aagaagaaag aggatccgct gtcgtcgtct gctactttag ctttaccggc ggtgaaatct 480  
ggagcaaaga gggcagcgag tgaagctgcg acgacttcaa cgaaacgagt caagaagat 540  
gaagagagtg taaagaagcc agcacttttt caaagactat ggagtgacga tgacgaaatc 600  
tctatgttac aaggaatgat agattatcat gctgatacag ggaagtctcc ttccgcagat 660  
actaatgctt tttacgagtt ccagaagaaa tctatcagct ttgaggttag taagagtcaa 720  
ttctcgata aggttaggag ttttaaggaag aagtaccgtg cttaagaagg aaaggacgaa 780  
cctagggttg tgaaagctca tgataagaaa gcttttgtat tgtcaaagt tatttgggga 840  
cctaaaggaa tagctcttga ttctaattgct aagtccaacg gtgtgtcgaa aaagaatgcg 900  
agtaagacga aggagaagct tgattctgta aagcaagact tggcgtttgt tgggtgttct 960  
tcaactaagt gagatgattg gtttgagaag tcgtctcttg ctaggatgat tgctgggtcg 1020  
ggattatgat agtattatgt gaggcagaaa tggagttcgt ttactcttga gactaagaag 1080  
attgttgaag agaagtttca gttgatgcaa gctaaagagc ttgaggctaa gttggagaag 1140

aatgtgcgtt tgactgacct tacgtcttac ttcgttgatg cttcgaagaa ctagagctat 1200  
tagttactta gatttgcgg ttttttgat cggaatgcta tgcataatgc tttcttttgt 1260  
ttttcggatt taggatttga ttctttctgg ttgtttttt tggggttgaa agattctcta 1320  
ccttataata tttatttttt tattcgt

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1499067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

Thr	Asn	Pro	Lys	Lys	Leu	Leu	Ile	Phe	Leu	Thr	Asn	Pro	Lys	Lys	Leu
1			5						10					15	
Leu	Ile	Phe	Ser	Phe	Ser	Arg	Arg	Phe	Arg	Phe	Ala	Leu	Leu	Lys	Leu
			20						25				30		
Pro	Met	Thr	Lys	Lys	Leu	Asp	Pro	Pro	Thr	Ala	Pro	Ser	Ser	Asp	Glu
			35				40					45			
Asp	Asp	Val	Glu	Thr	Ser	Glu	Asp	Asp	Ser	Ser	Ser	Ser	Glu	Glu	Asp
			50				55					60			
Glu	Pro	Ile	Lys	Ser	Leu	Pro	Ala	Thr	Thr	Ala	Ala	Ala	Pro	Ala	Lys
65					70				75					80	
Ser	Thr	Ala	Val	Ser	Ala	Ala	Thr	Pro	Ala	Lys	Ser	Thr	Ala	Val	Ser
			85						90					95	
Ala	Ala	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Val	Ser	Ala	Ala	Ala	Asp	Ser
			100					105					110		
Asp	Ser	Gly	Ser	Glu	Ser	Glu	Thr	Asp	Ser	Asp	Ser	Glu	Ser	Thr	Asp
			115				120					125			
Pro	Pro	Lys	Ser	Gly	Ser	Gly	Lys	Thr	Ile	Ala	Ser	Lys	Lys	Lys	Glu
			130				135					140			
Asp	Pro	Ser	Ser	Ser	Ser	Ala	Thr	Leu	Ala	Leu	Pro	Ala	Val	Lys	Ser
145					150					155				160	
Gly	Ala	Lys	Arg	Ala	Ala	Ser	Glu	Ala	Ala	Thr	Thr	Ser	Thr	Lys	Arg
			165						170					175	
Val	Lys	Lys	Asp	Glu	Glu	Ser	Val	Lys	Lys	Pro	Ala	Leu	Phe	Gln	Arg
			180					185					190		
Leu	Trp	Ser	Asp	Asp	Asp	Glu	Ile	Ser	Met	Leu	Gln	Gly	Met	Ile	Asp
			195				200					205			
Tyr	His	Ala	Asp	Thr	Gly	Lys	Ser	Pro	Ser	Ala	Asp	Thr	Asn	Ala	Phe
			210			215					220				
Tyr	Glu	Phe	Gln	Lys	Lys	Ser	Ile	Ser	Phe	Glu	Val	Ser	Lys	Ser	Gln
225				230						235				240	
Phe	Ser	Asp	Lys	Val	Arg	Ser	Leu	Arg	Lys	Lys	Tyr	Arg	Ala	Lys	Glu
			245						250					255	
Gly	Lys	Asp	Glu	Pro	Arg	Phe	Val	Lys	Ala	His	Asp	Lys	Lys	Ala	Phe
			260					265					270		
Val	Leu	Ser	Lys	Phe	Ile	Trp	Gly	Pro	Lys	Gly	Ile	Ala	Leu	Asp	Ser
			275				280					285			
Asn	Ala	Lys	Ser	Asn	Gly	Val	Ser	Lys	Lys	Asn	Ala	Ser	Lys	Thr	Lys
			290			295					300				
Glu	Lys	Leu	Asp	Ser	Val	Lys	Gln	Asp	Leu	Ala	Phe	Val	Gly	Val	Ser
305				310						315				320	
Ser	Thr	Asn	Gly	Asp	Trp	Phe	Glu	Lys	Ser	Ser	Leu	Ala	Arg	Met	
			325					330					335		
Ile	Ala	Gly	Ser	Gly	Ile	Asp	Glu	Tyr	Tyr	Val	Arg	Gln	Lys	Trp	Ser
			340					345					350		
Ser	Phe	Thr	Leu	Glu	Thr	Lys	Lys	Ile	Val	Glu	Glu	Lys	Phe	Gln	Leu

355	360	365
Met Gln Ala Lys Glu Leu	Glu Ala Lys Leu Glu	Lys Asn Val Arg Leu
370	375	380
Thr Asp Leu Thr Ser Tyr	Phe Val Asp Ala Ser	Lys Asn
385	390	395

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1499068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

Met	Thr	Lys	Lys	Leu	Asp	Pro	Pro	Thr	Ala	Pro	Ser	Ser	Asp	Glu	Asp
1			5					10						15	
Asp	Val	Glu	Thr	Ser	Glu	Asp	Asp	Ser	Ser	Ser	Ser	Glu	Glu	Asp	Glu
			20					25					30		
Pro	Ile	Lys	Ser	Leu	Pro	Ala	Thr	Thr	Ala	Ala	Ala	Pro	Ala	Lys	Ser
			35				40					45			
Thr	Ala	Val	Ser	Ala	Ala	Thr	Pro	Ala	Lys	Ser	Thr	Ala	Val	Ser	Ala
			50				55				60				
Ala	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Val	Ser	Ala	Ala	Ala	Asp	Ser	Asp
65					70					75				80	
Ser	Gly	Ser	Glu	Ser	Glu	Thr	Asp	Ser	Asp	Ser	Glu	Ser	Thr	Asp	Pro
			85					90					95		
Pro	Lys	Ser	Gly	Ser	Gly	Lys	Thr	Ile	Ala	Ser	Lys	Lys	Lys	Glu	Asp
			100					105					110		
Pro	Ser	Ser	Ser	Ser	Ala	Thr	Leu	Ala	Leu	Pro	Ala	Val	Lys	Ser	Gly
			115				120					125			
Ala	Lys	Arg	Ala	Ala	Ser	Glu	Ala	Ala	Thr	Thr	Ser	Thr	Lys	Arg	Val
			130				135					140			
Lys	Lys	Asp	Glu	Glu	Ser	Val	Lys	Lys	Pro	Ala	Leu	Phe	Gln	Arg	Leu
145					150					155				160	
Trp	Ser	Asp	Asp	Asp	Glu	Ile	Ser	Met	Leu	Gln	Gly	Met	Ile	Asp	Tyr
			165					170						175	
His	Ala	Asp	Thr	Gly	Lys	Ser	Pro	Ser	Ala	Asp	Thr	Asn	Ala	Phe	Tyr
			180					185					190		
Glu	Phe	Gln	Lys	Lys	Ser	Ile	Ser	Phe	Glu	Val	Ser	Lys	Ser	Gln	Phe
			195				200					205			
Ser	Asp	Lys	Val	Arg	Ser	Leu	Arg	Lys	Lys	Tyr	Arg	Ala	Lys	Glu	Gly
			210				215					220			
Lys	Asp	Glu	Pro	Arg	Phe	Val	Lys	Ala	His	Asp	Lys	Lys	Ala	Phe	Val
225					230					235				240	
Leu	Ser	Lys	Phe	Ile	Trp	Gly	Pro	Lys	Gly	Ile	Ala	Leu	Asp	Ser	Asn
			245						250					255	
Ala	Lys	Ser	Asn	Gly	Val	Ser	Lys	Lys	Asn	Ala	Ser	Lys	Thr	Lys	Glu
			260					265					270		
Lys	Leu	Asp	Ser	Val	Lys	Gln	Asp	Leu	Ala	Phe	Val	Gly	Val	Ser	Ser
			275				280					285			
Thr	Asn	Gly	Asp	Asp	Trp	Phe	Glu	Lys	Ser	Ser	Leu	Ala	Arg	Met	Ile
			290				295					300			
Ala	Gly	Ser	Gly	Ile	Asp	Glu	Tyr	Tyr	Val	Arg	Gln	Lys	Trp	Ser	Ser
305					310					315				320	
Phe	Thr	Leu	Glu	Thr	Lys	Lys	Ile	Val	Glu	Glu	Lys	Phe	Gln	Leu	Met
			325						330					335	
Gln	Ala	Lys	Glu	Leu	Glu	Ala	Lys	Leu	Glu	Lys	Asn	Val	Arg	Leu	Thr
			340					345						350	

Asp Leu Thr Ser Tyr Phe Val Asp Ala Ser Lys Asn  
355 360

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1565
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

```
atggttccag tcgtctttgt tcccttattg atagaataat caaaaatccg agtcggagac      60
gacgaagacc cgagttccag ctattaacta tgcagatacc atcaagagag catagtttca      120
ttctatttct cttcatatct gcttttgtaa ttggtgctgc gtctgtacct gtacctgatt      180
ctaattgcta cgctctcgac aattcaagtc gtcttgctga ttttagcagc tggatcggtc      240
atccatttga atatgatggc aaggaatttg atttggtggg tagattttgc aaggatgtgg      300
aaacaagagg gcaggcgagg tatgttgatt ttggacgatt tgaccggtta agctactttg      360
tttctagttc tgaaaatttc gatttcgtgc aagggtttta ccatggcgac ctgtcaaatt      420
gtgaacagag ttatgacaaa cttggacgta cagcacaggt taatattatt tgtgggaact      480
gtagtgatgg acggtgtaaa ggtggacttg gatgcatatg tagtgtcacc caagattcaa      540
ctttagagat tactgtcgac ttggctattc catgtgagaa acctggtccg cgggtgttta      600
agggatttac agtcggtttg catcctcgct catgggaaat tatctataat gggatgacac      660
agtttgattt tgataagccc cgctcgtgag tttagcttcaa gaccgagcag actcatctca      720
ctctctatat gactgcaatt gcttctcttt caacattggg agggaaagcct atcatcaagg      780
tttccccaga gaatggtctt gatgttaaga tagctgggtt ttccttgact gggaatcatc      840
caacaacttt atcacctgca acttttagtac tggattggaa ttgtgagaaa tctcggcgaa      900
ctccatatga agtcaatgtc accatcccag tggatggtta tgatcctgtt cagtttttcc      960
ttacaaaact ctgcgaatac aatcaaggta acgaaggagg atcagcgaaa ggatgggcta      1020
tatttgagat tttttcctgc gtattcctcg ttgcatctgc acttttctgc tgtgggggct      1080
ttatttataa aacaagagta gagcgtgtgc gtggaactga tgcattgccg gggatgtcac      1140
ttctatcggg ctactagaa actgtgagtg gaagtggaca aagctactca agaactgaag      1200
acatcaacaa tgcttttgcc aatgaagtct catgggaccg ctcttcgca tcttctactc      1260
aagcgacaac aacacagaga ccaagtgaac gaacatatgg tgcgatctaa tttgtcaag      1320
tgctcacaac gaggtacttt ttcaagccat ggtatggcac gcttgtgata tgcgatttct      1380
ggattttgct ttgtatgttt attttctacc ttctagaaag aggtcaaaaa gttaatatgt      1440
tcaccgtgag aatgttggtt tcaccagatt catgtgctat gatagaaaaa gacaaagcaa      1500
acaagagttc tttctttgct taggttacaa gaacaagagt atcgttataa agtcaacaaa      1560
gattg
```

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

```
Gly Ser Ser Arg Leu Cys Ser Leu Ile Asp Arg Ile Ile Lys Asn Pro
1      5      10      15
Ser Arg Arg Arg Arg Pro Glu Phe Gln Leu Leu Thr Met Gln Ile
20      25      30
Pro Ser Arg Glu His Ser Phe Ile Leu Phe Leu Phe Ile Ser Ala Phe
35      40      45
Val Ile Gly Ala Ala Ser Val Pro Val Pro Asp Ser Asn Cys Tyr Ala
50      55      60
```

Leu	Asp	Asn	Ser	Ser	Arg	Leu	Val	Asp	Phe	Ser	Ser	Trp	Ile	Gly	His
65					70					75					80
Pro	Phe	Glu	Tyr	Asp	Gly	Lys	Glu	Phe	Asp	Leu	Val	Val	Arg	Phe	Cys
				85					90					95	
Lys	Asp	Val	Glu	Thr	Arg	Gly	Gln	Ala	Gly	Tyr	Val	Asp	Phe	Gly	Arg
			100					105					110		
Phe	Asp	Pro	Leu	Ser	Tyr	Phe	Val	Ser	Ser	Ser	Glu	Asn	Phe	Asp	Phe
			115				120					125			
Val	Gln	Gly	Phe	Tyr	His	Gly	Asp	Leu	Ser	Asn	Cys	Glu	Gln	Ser	Tyr
			130				135				140				
Asp	Lys	Leu	Gly	Arg	Thr	Ala	Gln	Val	Asn	Ile	Ile	Cys	Gly	Asn	Cys
145				150						155					160
Ser	Asp	Gly	Arg	Cys	Lys	Gly	Gly	Leu	Gly	Cys	Ile	Cys	Ser	Val	Thr
				165					170					175	
Gln	Asp	Ser	Thr	Cys	Arg	Val	Thr	Val	Asp	Leu	Ala	Ile	Pro	Cys	Glu
			180					185					190		
Lys	Pro	Gly	Pro	Arg	Val	Phe	Lys	Gly	Phe	Thr	Val	Gly	Leu	His	Pro
			195				200					205			
Arg	Ser	Trp	Glu	Ile	Ile	Tyr	Asn	Gly	Met	Thr	Gln	Phe	Gly	Phe	Asp
			210				215					220			
Lys	Pro	Arg	Arg	Glu	Phe	Ser	Phe	Lys	Thr	Glu	Gln	Thr	His	Leu	Thr
225				230						235					240
Leu	Tyr	Met	Thr	Ala	Ile	Ala	Ser	Leu	Ser	Thr	Leu	Val	Gly	Lys	Pro
				245					250					255	
Ile	Ile	Lys	Val	Ser	Pro	Glu	Asn	Gly	Leu	Asp	Val	Lys	Ile	Ala	Gly
			260					265					270		
Ser	Ser	Leu	Thr	Gly	Asn	His	Pro	Thr	Thr	Leu	Ser	Pro	Ser	Thr	Leu
			275				280					285			
Val	Leu	Asp	Trp	Asn	Cys	Glu	Lys	Ser	Arg	Arg	Thr	Pro	Tyr	Glu	Val
			290				295				300				
Asn	Val	Thr	Ile	Pro	Val	Asp	Gly	Tyr	Asp	Pro	Val	Gln	Phe	Phe	Leu
305				310						315					320
Thr	Lys	Leu	Cys	Glu	Tyr	Asn	Gln	Gly	Asn	Glu	Gly	Gly	Ser	Ala	Lys
				325					330					335	
Gly	Trp	Ala	Ile	Phe	Gly	Val	Phe	Ser	Cys	Val	Phe	Leu	Val	Ala	Ser
			340					345					350		
Ala	Leu	Phe	Cys	Cys	Gly	Gly	Phe	Ile	Tyr	Lys	Thr	Arg	Val	Glu	Arg
			355				360					365			
Val	Arg	Gly	Thr	Asp	Ala	Leu	Pro	Gly	Met	Ser	Leu	Leu	Ser	Gly	Leu
			370				375				380				
Leu	Glu	Thr	Val	Ser	Gly	Ser	Gly	Gln	Ser	Tyr	Ser	Arg	Thr	Glu	Asp
385				390						395					400
Ile	Asn	Asn	Ala	Phe	Ala	Asn	Glu	Val	Ser	Trp	Asp	Arg	Ser	Ser	Ala
				405					410					415	
Ser	Ser	Thr	Gln	Ala	Thr	Thr	Thr	Gln	Arg	Pro	Ser	Glu	Arg	Thr	Tyr
			420					425					430		
Gly	Ala	Ile													
			435												

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1499075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met Gln Ile Pro Ser Arg Glu His Ser Phe Ile Leu Phe Leu Phe Ile

1	5	10	15
Ser Ala Phe Val Ile Gly Ala Ala Ser Val Pro Val Pro Asp Ser Asn			
20	25	30	
Cys Tyr Ala Leu Asp Asn Ser Ser Arg Leu Val Asp Phe Ser Ser Trp			
35	40	45	
Ile Gly His Pro Phe Glu Tyr Asp Gly Lys Glu Phe Asp Leu Val Val			
50	55	60	
Arg Phe Cys Lys Asp Val Glu Thr Arg Gly Gln Ala Gly Tyr Val Asp			
65	70	75	80
Phe Gly Arg Phe Asp Pro Leu Ser Tyr Phe Val Ser Ser Ser Glu Asn			
85	90	95	
Phe Asp Phe Val Gln Gly Phe Tyr His Gly Asp Leu Ser Asn Cys Glu			
100	105	110	
Gln Ser Tyr Asp Lys Leu Gly Arg Thr Ala Gln Val Asn Ile Ile Cys			
115	120	125	
Gly Asn Cys Ser Asp Gly Arg Cys Lys Gly Gly Leu Gly Cys Ile Cys			
130	135	140	
Ser Val Thr Gln Asp Ser Thr Cys Arg Val Thr Val Asp Leu Ala Ile			
145	150	155	160
Pro Cys Glu Lys Pro Gly Pro Arg Val Phe Lys Gly Phe Thr Val Gly			
165	170	175	
Leu His Pro Arg Ser Trp Glu Ile Ile Tyr Asn Gly Met Thr Gln Phe			
180	185	190	
Gly Phe Asp Lys Pro Arg Arg Glu Phe Ser Phe Lys Thr Glu Gln Thr			
195	200	205	
His Leu Thr Leu Tyr Met Thr Ala Ile Ala Ser Leu Ser Thr Leu Val			
210	215	220	
Gly Lys Pro Ile Ile Lys Val Ser Pro Glu Asn Gly Leu Asp Val Lys			
225	230	235	240
Ile Ala Gly Ser Ser Leu Thr Gly Asn His Pro Thr Thr Leu Ser Pro			
245	250	255	
Ser Thr Leu Val Leu Asp Trp Asn Cys Glu Lys Ser Arg Arg Thr Pro			
260	265	270	
Tyr Glu Val Asn Val Thr Ile Pro Val Asp Gly Tyr Asp Pro Val Gln			
275	280	285	
Phe Phe Leu Thr Lys Leu Cys Glu Tyr Asn Gln Gly Asn Glu Gly Gly			
290	295	300	
Ser Ala Lys Gly Trp Ala Ile Phe Gly Val Phe Ser Cys Val Phe Leu			
305	310	315	320
Val Ala Ser Ala Leu Phe Cys Cys Gly Gly Phe Ile Tyr Lys Thr Arg			
325	330	335	
Val Glu Arg Val Arg Gly Thr Asp Ala Leu Pro Gly Met Ser Leu Leu			
340	345	350	
Ser Gly Leu Leu Glu Thr Val Ser Gly Ser Gly Gln Ser Tyr Ser Arg			
355	360	365	
Thr Glu Asp Ile Asn Asn Ala Phe Ala Asn Glu Val Ser Trp Asp Arg			
370	375	380	
Ser Ser Ala Ser Ser Thr Gln Ala Thr Thr Thr Gln Arg Pro Ser Glu			
385	390	395	400
Arg Thr Tyr Gly Ala Ile			
405			

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1499076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

Met Thr Gln Phe Gly Phe Asp Lys Pro Arg Arg Glu Phe Ser Phe Lys  
1 5 10 15  
Thr Glu Gln Thr His Leu Thr Leu Tyr Met Thr Ala Ile Ala Ser Leu  
20 25 30  
Ser Thr Leu Val Gly Lys Pro Ile Ile Lys Val Ser Pro Glu Asn Gly  
35 40 45  
Leu Asp Val Lys Ile Ala Gly Ser Ser Leu Thr Gly Asn His Pro Thr  
50 55 60  
Thr Leu Ser Pro Ser Thr Leu Val Leu Asp Trp Asn Cys Glu Lys Ser  
65 70 75 80  
Arg Arg Thr Pro Tyr Glu Val Asn Val Thr Ile Pro Val Asp Gly Tyr  
85 90 95  
Asp Pro Val Gln Phe Phe Leu Thr Lys Leu Cys Glu Tyr Asn Gln Gly  
100 105 110  
Asn Glu Gly Gly Ser Ala Lys Gly Trp Ala Ile Phe Gly Val Phe Ser  
115 120 125  
Cys Val Phe Leu Val Ala Ser Ala Leu Phe Cys Cys Gly Gly Phe Ile  
130 135 140  
Tyr Lys Thr Arg Val Glu Arg Val Arg Gly Thr Asp Ala Leu Pro Gly  
145 150 155 160  
Met Ser Leu Leu Ser Gly Leu Leu Glu Thr Val Ser Gly Ser Gly Gln  
165 170 175  
Ser Tyr Ser Arg Thr Glu Asp Ile Asn Asn Ala Phe Ala Asn Glu Val  
180 185 190  
Ser Trp Asp Arg Ser Ser Ala Ser Ser Thr Gln Ala Thr Thr Thr Gln  
195 200 205  
Arg Pro Ser Glu Arg Thr Tyr Gly Ala Ile  
210 215

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1358

(D) OTHER INFORMATION: / Ceres Seq. ID 1499077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

agcacataa tactgtctaa atgcttctct actttctcat cacttgctctc tctttctttt 60  
tctttaccaa atctcttttct cttcctccat gggcatctga aacccaaaacc ttgctctcct 120  
tctacttcat caagaatccc tttatgaaca ccctacatca gaccaaacac gatccagcct 180  
ctccggtgat cgaccaaagt tgggttcttg acctccctga gctggtctct gactgcattc 240  
ttgaccttct tccacctctt ggactctgca gcatggctag ggtttgtagc tccttgaggg 300  
agagatgtgt tagtgatcat ctatgggaga aacatttgaa gaccaaagtg ggcaaaatcc 360  
ttggccctgc tgctcacaga gagtggcaat gctatatctc ctcttcacaca tatcatcttg 420  
attctcctca tcatcaaact gggaatcttg gttttgcaa aatcatctct ctgatccgat 480  
ctctttcatc cgttttccga gaggataaac aaaggagggg atatgcatct tctctgccac 540  
ttgattccag catgagctgc tacctctccc ttgaaacagg tcgttttttg ttcccagctc 600  
aagtttacaa ccgtgagaat ggacatgtag ggttcatgtt gtcatgctat gatgcggagc 660  
tcagctatga tactcacacg gatacgttcc aagccaggta tccaccacat ggtagacgag 720  
catctgcgat tgaaaagggg gtgacatggg atagaataag agcagctccc attgatgcat 780  
cacctcatct tctccatgta tcagattctt taaaagagtt gaaacctgga gatcacatcg 840  
aatccagtg gagaaggaac aaagagttcc catatggatg gtggtatggt cttgttcgcc 900  
acttggaatc ctgtgatgga gatcataacc attgccattg ccatcttagt gagacggtag 960  
tgttggaatt caaccagtac acagtcggat caagtgagg aagaacgatg atcatgagag 1020  
atcataaaga ggaaggtaac gaagaagacg ggttctatgg aggaatccga aagctaaatt 1080  
gtaaagaaga gattgcaatg tggaacgctc actggccttg ctccatcttg gaatagcatt 1140



aaagaagctt tgcttaaaca catggggaaa gatattacac atcactatac tgagagtagg 1200  
ttgttaaatt tagacgtcta ttctctttta tccaatgtat ggttgatcgt gaattatttg 1260  
ttgggaataa agtctatacg tgaaattatt gtgtcacttc gatttgagaa atattgtgtt 1320  
gtatagggaa aacttaatac aattgatttg aatactcc

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1499078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

Met	Leu	Leu	Tyr	Phe	Leu	Ile	Thr	Cys	Leu	Ser	Phe	Phe	Phe	Phe	Thr
1			5						10					15	
Lys	Ser	Leu	Ser	Leu	Pro	Pro	Trp	Ala	Ser	Glu	Thr	Lys	Thr	Leu	Leu
			20					25					30		
Ser	Phe	Tyr	Phe	Ile	Lys	Asn	Pro	Phe	Met	Asn	Thr	Leu	His	Gln	Thr
			35				40					45			
Lys	His	Asp	Pro	Ala	Ser	Pro	Val	Ile	Asp	Gln	Met	Ser	Val	Leu	Asp
			50				55				60				
Leu	Pro	Glu	Leu	Ala	Leu	Asp	Cys	Ile	Leu	Asp	Leu	Leu	Pro	Pro	Ser
65					70					75					80
Gly	Leu	Cys	Ser	Met	Ala	Arg	Val	Cys	Ser	Ser	Leu	Arg	Glu	Arg	Cys
				85					90					95	
Val	Ser	Asp	His	Leu	Trp	Glu	Lys	His	Leu	Lys	Thr	Lys	Trp	Gly	Lys
			100					105					110		
Ile	Leu	Gly	Pro	Ala	Ala	His	Arg	Glu	Trp	Gln	Cys	Tyr	Ile	Ser	Ser
			115				120					125			
Ser	Thr	Tyr	His	Leu	Asp	Ser	Pro	His	His	Gln	Thr	Gly	Asn	Leu	Gly
			130				135					140			
Phe	Ala	Lys	Ile	Ile	Ser	Leu	Ile	Arg	Ser	Leu	Ser	Ser	Val	Phe	Arg
145					150					155					160
Glu	Asp	Lys	Gln	Arg	Arg	Gly	Tyr	Ala	Ser	Ser	Leu	Pro	Leu	Asp	Ser
				165					170					175	
Ser	Met	Ser	Cys	Tyr	Leu	Ser	Leu	Glu	Thr	Gly	Arg	Phe	Trp	Phe	Pro
			180					185					190		
Ala	Gln	Val	Tyr	Asn	Arg	Glu	Asn	Gly	His	Val	Gly	Phe	Met	Leu	Ser
			195				200					205			
Cys	Tyr	Asp	Ala	Glu	Leu	Ser	Tyr	Asp	Thr	His	Thr	Asp	Thr	Phe	Gln
			210				215					220			
Ala	Arg	Tyr	Pro	Pro	His	Gly	Arg	Arg	Ala	Ser	Ala	Ile	Glu	Lys	Gly
225					230					235					240
Val	Thr	Trp	Asp	Arg	Ile	Arg	Ala	Ala	Pro	Ile	Asp	Ala	Ser	Pro	His
				245					250					255	
Leu	Leu	His	Val	Ser	Asp	Ser	Leu	Lys	Glu	Leu	Lys	Pro	Gly	Asp	His
			260					265					270		
Ile	Glu	Ile	Gln	Trp	Arg	Arg	Asn	Lys	Glu	Phe	Pro	Tyr	Gly	Trp	Trp
			275				280						285		
Tyr	Gly	Leu	Val	Arg	His	Leu	Glu	Ser	Cys	Asp	Gly	Asp	His	Asn	His
			290				295				300				
Cys	His	Cys	His	Leu	Ser	Glu	Thr	Val	Val	Leu	Glu	Phe	Asn	Gln	Tyr
305					310					315					320
Thr	Val	Gly	Ser	Arg	Trp	Arg	Arg	Thr	Met	Ile	Met	Arg	Asp	His	Lys
				325					330					335	
Glu	Glu	Gly	Asn	Glu	Glu	Asp	Gly	Phe	Tyr	Gly	Gly	Ile	Arg	Lys	Leu
			340					345					350		
Asn	Cys	Lys	Glu	Glu	Ile	Ala	Met	Trp	Lys	Arg	His	Trp	Pro	Cys	Ser

355 360 365  
Ile Leu Glu  
370

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

Met	Asn	Thr	Leu	His	Gln	Thr	Lys	His	Asp	Pro	Ala	Ser	Pro	Val	Ile
1				5					10					15	
Asp	Gln	Met	Ser	Val	Leu	Asp	Leu	Pro	Glu	Leu	Ala	Leu	Asp	Cys	Ile
		20						25					30		
Leu	Asp	Leu	Leu	Pro	Pro	Ser	Gly	Leu	Cys	Ser	Met	Ala	Arg	Val	Cys
		35					40					45			
Ser	Ser	Leu	Arg	Glu	Arg	Cys	Val	Ser	Asp	His	Leu	Trp	Glu	Lys	His
		50				55					60				
Leu	Lys	Thr	Lys	Trp	Gly	Lys	Ile	Leu	Gly	Pro	Ala	Ala	His	Arg	Glu
65					70					75				80	
Trp	Gln	Cys	Tyr	Ile	Ser	Ser	Ser	Thr	Tyr	His	Leu	Asp	Ser	Pro	His
			85						90					95	
His	Gln	Thr	Gly	Asn	Leu	Gly	Phe	Ala	Lys	Ile	Ile	Ser	Leu	Ile	Arg
			100						105					110	
Ser	Leu	Ser	Ser	Val	Phe	Arg	Glu	Asp	Lys	Gln	Arg	Arg	Gly	Tyr	Ala
		115					120						125		
Ser	Ser	Leu	Pro	Leu	Asp	Ser	Ser	Met	Ser	Cys	Tyr	Leu	Ser	Leu	Glu
		130					135					140			
Thr	Gly	Arg	Phe	Trp	Phe	Pro	Ala	Gln	Val	Tyr	Asn	Arg	Glu	Asn	Gly
145					150					155				160	
His	Val	Gly	Phe	Met	Leu	Ser	Cys	Tyr	Asp	Ala	Glu	Leu	Ser	Tyr	Asp
			165						170					175	
Thr	His	Thr	Asp	Thr	Phe	Gln	Ala	Arg	Tyr	Pro	Pro	His	Gly	Arg	Arg
			180					185						190	
Ala	Ser	Ala	Ile	Glu	Lys	Gly	Val	Thr	Trp	Asp	Arg	Ile	Arg	Ala	Ala
		195					200							205	
Pro	Ile	Asp	Ala	Ser	Pro	His	Leu	Leu	His	Val	Ser	Asp	Ser	Leu	Lys
		210				215						220			
Glu	Leu	Lys	Pro	Gly	Asp	His	Ile	Glu	Ile	Gln	Trp	Arg	Arg	Asn	Lys
225				230						235				240	
Glu	Phe	Pro	Tyr	Gly	Trp	Trp	Tyr	Gly	Leu	Val	Arg	His	Leu	Glu	Ser
			245						250					255	
Cys	Asp	Gly	Asp	His	Asn	His	Cys	His	Cys	His	Leu	Ser	Glu	Thr	Val
			260				265							270	
Val	Leu	Glu	Phe	Asn	Gln	Tyr	Thr	Val	Gly	Ser	Arg	Trp	Arg	Arg	Thr
		275					280							285	
Met	Ile	Met	Arg	Asp	His	Lys	Glu	Glu	Gly	Asn	Glu	Glu	Asp	Gly	Phe
		290				295					300				
Tyr	Gly	Gly	Ile	Arg	Lys	Leu	Asn	Cys	Lys	Glu	Glu	Ile	Ala	Met	Trp
305				310						315				320	
Lys	Arg	His	Trp	Pro	Cys	Ser	Ile	Leu	Glu						
				325					330						

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..312  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499080  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:  
Met Ser Val Leu Asp Leu Pro Glu Leu Ala Leu Asp Cys Ile Leu Asp  
1                  5                  10                  15  
Leu Leu Pro Pro Ser Gly Leu Cys Ser Met Ala Arg Val Cys Ser Ser  
          20                  25                  30  
Leu Arg Glu Arg Cys Val Ser Asp His Leu Trp Glu Lys His Leu Lys  
          35                  40                  45  
Thr Lys Trp Gly Lys Ile Leu Gly Pro Ala Ala His Arg Glu Trp Gln  
          50                  55                  60  
Cys Tyr Ile Ser Ser Ser Thr Tyr His Leu Asp Ser Pro His His Gln  
65                  70                  75                  80  
Thr Gly Asn Leu Gly Phe Ala Lys Ile Ile Ser Leu Ile Arg Ser Leu  
          85                  90                  95  
Ser Ser Val Phe Arg Glu Asp Lys Gln Arg Arg Gly Tyr Ala Ser Ser  
          100                  105                  110  
Leu Pro Leu Asp Ser Ser Met Ser Cys Tyr Leu Ser Leu Glu Thr Gly  
          115                  120                  125  
Arg Phe Trp Phe Pro Ala Gln Val Tyr Asn Arg Glu Asn Gly His Val  
130                  135                  140  
Gly Phe Met Leu Ser Cys Tyr Asp Ala Glu Leu Ser Tyr Asp Thr His  
145                  150                  155                  160  
Thr Asp Thr Phe Gln Ala Arg Tyr Pro Pro His Gly Arg Arg Ala Ser  
          165                  170                  175  
Ala Ile Glu Lys Gly Val Thr Trp Asp Arg Ile Arg Ala Ala Pro Ile  
          180                  185                  190  
Asp Ala Ser Pro His Leu Leu His Val Ser Asp Ser Leu Lys Glu Leu  
          195                  200                  205  
Lys Pro Gly Asp His Ile Glu Ile Gln Trp Arg Arg Asn Lys Glu Phe  
210                  215                  220  
Pro Tyr Gly Trp Trp Tyr Gly Leu Val Arg His Leu Glu Ser Cys Asp  
225                  230                  235                  240  
Gly Asp His Asn His Cys His Cys His Leu Ser Glu Thr Val Val Leu  
          245                  250                  255  
Glu Phe Asn Gln Tyr Thr Val Gly Ser Arg Trp Arg Arg Thr Met Ile  
          260                  265                  270  
Met Arg Asp His Lys Glu Glu Gly Asn Glu Glu Asp Gly Phe Tyr Gly  
275                  280                  285  
Gly Ile Arg Lys Leu Asn Cys Lys Glu Glu Ile Ala Met Trp Lys Arg  
290                  295                  300  
His Trp Pro Cys Ser Ile Leu Glu  
305                  310

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1499085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

aaaacattac tcattcaciaa aaccatctta aagcaactac acaaatcttg aaattttctc

```
atatttttcta tttactatat aaacttttaa tcaaatacaag attaactatg gctgaggagt 120
acaagaacaa cgttcccag caccagacac caacggctgc aacagaggaa tcaccagcga 180
cgacaacaga ggttacggat cgtggattgt ttgatttctt ggggaagaag gaagaggaag 240
tgaaacctca agagacaacg acgctcgagt ctgagtgtcg atcataaggc tcagatctct 300
gaaccggagt tagctgcgga sacgaggaag taaaggagaa caagattact ctgctagagg 360
agcttcaaga aaagaccgag gaagatgagg agaacaagcc tagtgtcatc gaaaagcttc 420
accgatccaa cagctcttct tccctcttcg agcgatgaag aagagctgtt
```

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1499086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

```
Asn Ile Thr His Ser Gln Asn His Leu Lys Ala Thr Thr Gln Ile Leu
1           5           10           15
Lys Phe Ser His Ile Phe Tyr Leu Leu Tyr Lys Leu Leu Ile Lys Ser
20           25           30
Arg Leu Thr Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu
35           40           45
Thr Pro Thr Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val
50           55           60
Thr Asp Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val
65           70           75           80
Lys Pro Gln Glu Thr Thr Thr Leu Glu Ser Glu Cys Arg Ser
85           90
```

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1499087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

```
Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu Thr Pro Thr
1           5           10           15
Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val Thr Asp Arg
20           25           30
Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val Lys Pro Gln
35           40           45
Glu Thr Thr Thr Leu Glu Ser Glu Cys Arg Ser
50           55
```

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1499088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

cggkgtgataa	aggaaatatt	aastccatgc	caaacagaag	catgccagct	tctccttatc	60
ctactccagg	ggctctgtta	atgggagatg	catttaacat	gcgtcatcct	ttgacgggtg	120
gaggaatgac	ggttgacatta	gctgacattg	ttgtcctgcg	taatctcctt	agaccgctgc	180
gtgatcttag	tgacggcgct	agtctctgca	aatatcttga	atcattttac	actctgcgaa	240
agccagtggc	agcaacaatc	aacacccttg	cgaatgctct	ttaccaagtt	ttctgttcac	300
cagaaaatga	agcaagaaac	gagatgaggg	aagcttgctt	cgattatctg	ggactcgggg	360
gtatgtgcac	aagtggacca	gtatctttgc	tttcgggttt	gaaccctcga	ccattaacac	420
ttgtctgcca	tttctttgcg	gttgcggttt	atggagtcac	acgggttgta	atccccattcc	480
cttccccaaa	acgaatctgg	cttggagcta	aattgatctc	gggagcatcg	gggataatat	540
ttccaataat	aaaagcggaa	ggagtttaggc	agatgttttt	cccagcaact	gtacctgcat	600
actactacaa	agctcctaca	gttggagaaa	ccaaatgttc	atagttccaa	ataaattctg	660
tcacgagaaa	tgccatac					

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1499089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

Xaa	Asp	Lys	Gly	Asn	Ile	Xaa	Ser	Met	Pro	Asn	Arg	Ser	Met	Pro	Ala
1			5					10					15		
Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala	Leu	Leu	Met	Gly	Asp	Ala	Phe	Asn
			20					25					30		
Met	Arg	His	Pro	Leu	Thr	Gly	Gly	Gly	Met	Thr	Val	Ala	Leu	Ala	Asp
			35				40					45			
Ile	Val	Val	Leu	Arg	Asn	Leu	Arg	Pro	Leu	Arg	Asp	Leu	Ser	Asp	
			50			55				60					
Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu	Glu	Ser	Phe	Tyr	Thr	Leu	Arg	Lys
65					70					75				80	
Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr	Leu	Ala	Asn	Ala	Leu	Tyr	Gln	Val
				85					90					95	
Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala	Arg	Asn	Glu	Met	Arg	Glu	Ala	Cys
			100				105					110			
Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly	Met	Cys	Thr	Ser	Gly	Pro	Val	Ser
			115				120					125			
Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg	Pro	Leu	Thr	Leu	Val	Cys	His	Phe
			130				135					140			
Phe	Ala	Val	Ala	Val	Tyr	Gly	Val	Ile	Arg	Leu	Leu	Ile	Pro	Phe	Pro
145					150					155				160	
Ser	Pro	Lys	Arg	Ile	Trp	Leu	Gly	Ala	Lys	Leu	Ile	Ser	Gly	Ala	Ser
				165					170					175	
Gly	Ile	Ile	Phe	Pro	Ile	Ile	Lys	Ala	Glu	Gly	Val	Arg	Gln	Met	Phe
			180				185						190		
Phe	Pro	Ala	Thr	Val	Pro	Ala	Tyr	Tyr	Lys	Ala	Pro	Thr	Val	Gly	
			195				200								
Glu	Thr	Lys	Cys	Ser											
															210

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

Met	Pro	Asn	Arg	Ser	Met	Pro	Ala	Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala
1				5					10					15	
Leu	Leu	Met	Gly	Asp	Ala	Phe	Asn	Met	Arg	His	Pro	Leu	Thr	Gly	Gly
			20					25					30		
Gly	Met	Thr	Val	Ala	Leu	Ala	Asp	Ile	Val	Val	Leu	Arg	Asn	Leu	Leu
		35					40					45			
Arg	Pro	Leu	Arg	Asp	Leu	Ser	Asp	Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu
	50					55					60				
Glu	Ser	Phe	Tyr	Thr	Leu	Arg	Lys	Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr
65					70					75				80	
Leu	Ala	Asn	Ala	Leu	Tyr	Gln	Val	Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala
				85					90					95	
Arg	Asn	Glu	Met	Arg	Glu	Ala	Cys	Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly
		100						105					110		
Met	Cys	Thr	Ser	Gly	Pro	Val	Ser	Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg
	115						120					125			
Pro	Leu	Thr	Leu	Val	Cys	His	Phe	Phe	Ala	Val	Ala	Val	Tyr	Gly	Val
	130					135					140				
Ile	Arg	Leu	Leu	Ile	Pro	Phe	Pro	Ser	Pro	Lys	Arg	Ile	Trp	Leu	Gly
145					150					155				160	
Ala	Lys	Leu	Ile	Ser	Gly	Ala	Ser	Gly	Ile	Ile	Phe	Pro	Ile	Ile	Lys
			165					170						175	
Ala	Glu	Gly	Val	Arg	Gln	Met	Phe	Phe	Pro	Ala	Thr	Val	Pro	Ala	Tyr
			180					185					190		
Tyr	Tyr	Lys	Ala	Pro	Thr	Val	Gly	Glu	Thr	Lys	Cys	Ser			
	195					200						205			

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met	Pro	Ala	Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala	Leu	Leu	Met	Gly	Asp
1				5					10					15	
Ala	Phe	Asn	Met	Arg	His	Pro	Leu	Thr	Gly	Gly	Gly	Met	Thr	Val	Ala
			20					25					30		
Leu	Ala	Asp	Ile	Val	Val	Leu	Arg	Asn	Leu	Leu	Arg	Pro	Leu	Arg	Asp
		35					40					45			
Leu	Ser	Asp	Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu	Glu	Ser	Phe	Tyr	Thr
	50					55					60				
Leu	Arg	Lys	Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr	Leu	Ala	Asn	Ala	Leu
65				70						75				80	
Tyr	Gln	Val	Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala	Arg	Asn	Glu	Met	Arg
			85					90					95		
Glu	Ala	Cys	Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly	Met	Cys	Thr	Ser	Gly
		100					105					110			
Pro	Val	Ser	Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg	Pro	Leu	Thr	Leu	Val
	115					120						125			
Cys	His	Phe	Phe	Ala	Val	Ala	Val	Tyr	Gly	Val	Ile	Arg	Leu	Leu	Ile
	130					135					140				

Pro Phe Pro Ser Pro Lys Arg Ile Trp Leu Gly Ala Lys Leu Ile Ser  
145 150 155 160  
Gly Ala Ser Gly Ile Ile Phe Pro Ile Ile Lys Ala Glu Gly Val Arg  
165 170 175  
Gln Met Phe Phe Pro Ala Thr Val Pro Ala Tyr Tyr Tyr Lys Ala Pro  
180 185 190  
Thr Val Gly Glu Thr Lys Cys Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

aattgcaaat caaatggatc gtcttaagct ttatttctcc gttttcgttt tgtctttctt 60  
tatcgctctcg gtttcgctcg ctgatgtcaa cgacggcgat gatctcgtga tccgctcaggt 120  
ggttgggtgga gccgagcctc aggttttgac ctcagaggat cacttttctc tcttcaagcg 180  
gaagttcggg aaggtctacg cttccaacga ggagcatgac tatagattct cggtttgagt 240  
tccgtaagaa gcacttgggg gttagaagtg gctttaagct tcctaaagat gccacaaggg 300  
ctccgattct ccctaccgaa aatctccctg aggtatttga ttggagagat catggcgccg 360  
ttactcccggt caaaaatcag ggatcttgcg gctcttgctg gagtttcagc gccactggag 420  
ctttggaagg tgctaacttc ctcgctaccg gcagactcgt cagcctcagc gaacaacagc 480  
tcgctgactg tgatcacgag tgtgatcccg aggaggcaga tttcctgcga ctctggttgc 540  
aatgggtgggc taatgaacag cgcttttgaa tacaccctca aaaccggagg gctcatgaaa 600  
gaagaagact atccttacac cggaaggac ggcaagacct gcaagctaga caagtccaag 660  
atcgttgcct ctgtctccaa cttcagtggt atctccattg atgaagaaca gattgctgca 720  
aaccttgta agaacggacc tcttgctgta gccatcaacg ctggctatat gcagacttac 780  
attggaggag tctcatgccc ttacatatgc accaggaggc tcaaccacgg tgtcttattg 840  
gttggtatg gagcggcagg ttacgctccg gctaggttca aggagaagcc ttactggatc 900  
atcaagaact cgtggggaga gacttgggtt gaaaatgggt tctacaaaat ctgcaaaggg 960  
cgtaacattt gtggtgttga cagtatggtc tccactgttg cagccaccgt ctcaaccacc 1020  
gcccattaag catctcgtca ataagtttta attacttttg tgatttgbat gagcgagctc 1080  
tctttgcgct gctgactctc tctatttatc tctgcttctt gcttgtaaat aaaatgcggt 1140  
ctattg

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

Met Pro Thr Arg Leu Arg Phe Ser Leu Pro Lys Ile Ser Leu Arg Ile  
1 5 10 15  
Leu Ile Gly Glu Ile Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp  
20 25 30  
Leu Ala Ala Leu Ala Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val  
35 40 45  
Leu Thr Ser Ser Leu Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser  
50 55 60  
Ser Ser Thr Val Ile Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys

(2) INFORMATION FOR SEQ ID NO:857:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

```
{A) NAME/KEY: peptide
```

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1499094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

Met	Ala	Pro	Leu	Leu	Pro	Ser	Lys	Ile	Arg	Asp	Leu	Ala	Ala	Leu	Ala
1				5					10					15	
Gly	Val	Ser	Ala	Pro	Leu	Glu	Leu	Trp	Lys	Val	Leu	Thr	Ser	Ser	Leu
			20					25					30		
Pro	Ala	Asp	Ser	Ser	Ala	Ser	Ala	Asn	Asn	Ser	Ser	Ser	Thr	Val	Ile
		35					40					45			
Thr	Ser	Val	Ile	Pro	Arg	Arg	Gln	Ile	Ser	Cys	Asp	Ser	Gly	Cys	Asn
	50					55					60				
Gly	Gly	Leu	Met	Asn	Ser	Ala	Phe	Glu	Tyr	Thr	Leu	Lys	Thr	Gly	Gly
65				70						75					80
Leu	Met	Lys	Glu	Glu	Asp	Tyr	Pro	Tyr	Thr	Gly	Lys	Asp	Gly	Lys	Thr
			85						90					95	
Cys	Lys	Leu	Asp	Lys	Ser	Lys	Ile	Val	Ala	Ser	Val	Ser	Asn	Phe	Ser
			100					105					110		
Val	Ile	Ser	Ile	Asp	Glu	Glu	Gln	Ile	Ala	Ala	Asn	Leu	Val	Lys	Asn
		115					120					125			
Gly	Pro	Leu	Ala	Val	Ala	Ile	Asn	Ala	Gly	Tyr	Met	Gln	Thr	Tyr	Ile
	130					135					140				
Gly	Gly	Val	Ser	Cys	Pro	Tyr	Ile	Cys	Thr	Arg	Arg	Leu	Asn	His	Gly
145				150						155				160	
Val	Leu	Leu	Val	Gly	Tyr	Gly	Ala	Ala	Gly	Tyr	Ala	Pro	Ala	Arg	Phe
			165						170					175	
Lys	Glu	Lys	Pro	Tyr	Trp	Ile	Ile	Lys	Asn	Ser	Trp	Gly	Glu	Thr	Trp
			180					185					190		
Gly	Glu	Asn	Gly	Phe	Tyr	Lys	Ile	Cys	Lys	Gly	Arg	Asn	Ile	Cys	Gly
		195					200					205			



Val Asp Ser Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala  
210 215 220

His  
225

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly Leu Met Lys  
1 5 10 15  
Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr Cys Lys Leu  
20 25 30  
Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser Val Ile Ser  
35 40 45  
Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn Gly Pro Leu  
50 55 60  
Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile Gly Gly Val  
65 70 75 80  
Ser Cys Pro Tyr Ile Cys Thr Arg Arg Leu Asn His Gly Val Leu Leu  
85 90 95  
Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe Lys Glu Lys  
100 105 110  
Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp Gly Glu Asn  
115 120 125  
Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly Val Asp Ser  
130 135 140  
Met Val Ser Thr Val Ala Thr Val Ser Thr Thr Ala His  
145 150 155

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1854
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

aattcacctt cctccgtccc ctccccctaa tccccaaaac acacagataa aaatctctcc 60  
ttttttcatc gaagcatata acacaacacc gacaaggaga ttcctttaac tatggcgaag 120  
aaagcaagaa ttgttataat cggagctgga atggctggtc tcacggcggc gaacaagctc 180  
tacacaagct ccaacaacac ctccgagctc tcagtcgtcg aaggcggttc tagaatcggc 240  
ggtaggatca atacctctga gttctcatca gagaagattg agatgggtgc cacgtggatc 300  
cacggaatcg gtggaagccc tgtttataga atcgctaaag agactggttc tttagtctct 360  
gatgagccat gggagtgtat ggattccacc attgataaag ctaagacctt tgctgaaggt 420  
gggttcgaga ttgagccttc cattgttgaa tccatctctg gtttgttcac tgctctcatg 480  
gaattagctc aggggaaaga gatctctcaa tccgacgccg atttgagtgc tttggctcat 540  
atttacgaaa ctgccactag gggttgctct aagggaagta gtactagtgt tgggtcgttt 600  
ttgaaatctg ggtttgatgc ttattgggat tcaatcagca atggaggaga agaaggagtt 660  
aaagggtagt ggaaatggag taggaagtca cttgaagaag ccatttttac gatgtttagt 720  
aacacacaga ggacttacac atctgctgat gaactctcga cgcttgattt cgcggcggag 780

agtgagtatc	agatgtttcc	aggagaagaa	atcactatag	ctaaaggcta	tcttagtggt	840
attcatcatt	tggcatctgt	gcttcctcaa	ggtgttatcc	aattgaatcg	aaaggtcacg	900
aagatcgagt	ggcagagtaa	tgaagtgaag	ctgcatttct	cagatgggtc	tggtgttttt	960
gcagatcatg	ttattgttac	tgtctcttta	ggtgtgctta	aagcagggat	tgagactgat	1020
gctgaattgt	ttagtcctcc	tttgctgat	ttcaaatacag	acgctattag	aagactaggc	1080
tatggagttg	tcaacaagct	gttcgtcgag	atgtctcaaa	gaaagttccc	ctctttgcag	1140
cttgtgtttg	accgggagga	ttccgagttt	aggttcgtga	aaattccatg	gtggatgaga	1200
agaaccgcga	ccattacccc	aatccatagc	aattcaaagg	tcttgctttc	ttggtttgca	1260
ggcaaagaag	ctctcgagct	tgagaaactt	accgatgagg	agatcaaaga	cgctgtcatg	1320
accactatct	cttgcttgac	aggcaaggaa	gttaagaatg	ataccgcaaa	gcccttgacc	1380
aatggctcat	tgaatgatga	tgatgaagcc	atgaagatta	caaaggctct	gaagagcaaa	1440
tggggaagtg	atcctctgtt	cagaggctcc	tattcgtatg	tagcgggttg	atcaagcggg	1500
gatgacctag	acgcaatggc	tgagccattg	ccaaagatta	ataagaagg	tggtcagggtc	1560
aatggtcattg	atcaagccaa	ggttcatgag	cttcaagtca	tggttgccagg	ggaagcaaca	1620
catagaaccc	attactccac	aactcatggt	gcctactata	gtggtttaag	ggaagccaat	1680
aggcttctca	agcattacaa	atgtaatttt	tgagtgttaa	tttttaaaat	atgttctggt	1740
tttttttttt	ggggtaattg	gtttagagaa	gcataattag	ttttgtaaga	tttttaatt	1800
gtttaacttc	aatttttttt	ttactgtttt	ttactttttc	ttactacaaa	attc	

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Met	Ala	Lys	Lys	Ala	Arg	Ile	Val	Ile	Ile	Gly	Ala	Gly	Met	Ala	Gly
1			5						10					15	
Leu	Thr	Ala	Ala	Asn	Lys	Leu	Tyr	Thr	Ser	Ser	Asn	Asn	Thr	Phe	Glu
			20					25					30		
Leu	Ser	Val	Val	Glu	Gly	Gly	Ser	Arg	Ile	Gly	Gly	Arg	Ile	Asn	Thr
		35				40					45				
Ser	Glu	Phe	Ser	Ser	Glu	Lys	Ile	Glu	Met	Gly	Ala	Thr	Trp	Ile	His
	50					55				60					
Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	Ile	Ala	Lys	Glu	Thr	Gly	Ser
65				70					75					80	
Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	Met	Asp	Ser	Thr	Ile	Asp	Lys
			85					90					95		
Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	Glu	Ile	Glu	Pro	Ser	Ile	Val
		100					105					110			
Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala	Leu	Met	Glu	Leu	Ala	Gln	Gly
	115					120					125				
Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Ala	His	Ile
	130				135					140					
Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser	Lys	Gly	Ser	Ser	Thr	Ser	Val
145				150					155					160	
Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp	Ala	Tyr	Trp	Asp	Ser	Ile	Ser
		165					170						175		
Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly	Tyr	Gly	Lys	Trp	Ser	Arg	Lys
		180				185					190				
Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met	Phe	Ser	Asn	Thr	Gln	Arg	Thr
	195					200					205				
Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr	Leu	Asp	Phe	Ala	Ala	Glu	Ser
	210				215						220				
Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu	Ile	Thr	Ile	Ala	Lys	Gly	Tyr
225				230					235					240	
Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser	Val	Leu	Pro	Gln	Gly	Val	Ile

															245																250																255	
Gln	Leu	Asn	Arg	Lys	Val	Thr	Lys	Ile	Glu	Trp	Gln	Ser	Asn	Glu	Val																																	
															260																265																270	
Lys	Leu	His	Phe	Ser	Asp	Gly	Ser	Val	Val	Phe	Ala	Asp	His	Val	Ile																																	
															275																280																285	
Val	Thr	Val	Ser	Leu	Gly	Val	Leu	Lys	Ala	Gly	Ile	Glu	Thr	Asp	Ala																																	
															290																295																300	
Glu	Leu	Phe	Ser	Pro	Pro	Leu	Pro	Asp	Phe	Lys	Ser	Asp	Ala	Ile	Arg																																	
305																310																315																320
Arg	Leu	Gly	Tyr	Gly	Val	Val	Asn	Lys	Leu	Phe	Val	Glu	Met	Ser	Gln																																	
															325																330																335	
Arg	Lys	Phe	Pro	Ser	Leu	Gln	Leu	Val	Phe	Asp	Arg	Glu	Asp	Ser	Glu																																	
															340																345																350	
Phe	Arg	Phe	Val	Lys	Ile	Pro	Trp	Trp	Met	Arg	Arg	Thr	Ala	Thr	Ile																																	
															355																360																365	
Thr	Pro	Ile	His	Ser	Asn	Ser	Lys	Val	Leu	Leu	Ser	Trp	Phe	Ala	Gly																																	
															370																375																380	
Lys	Glu	Ala	Leu	Glu	Leu	Glu	Lys	Leu	Thr	Asp	Glu	Glu	Ile	Lys	Asp																																	
385																390																395																400
Ala	Val	Met	Thr	Thr	Ile	Ser	Cys	Leu	Thr	Gly	Lys	Glu	Val	Lys	Asn																																	
															405																410																415	
Asp	Thr	Ala	Lys	Pro	Leu	Thr	Asn	Gly	Ser	Leu	Asn	Asp	Asp	Asp	Glu																																	
															420																425																430	
Ala	Met	Lys	Ile	Thr	Lys	Val	Leu	Lys	Ser	Lys	Trp	Gly	Ser	Asp	Pro																																	
															435																440																445	
Leu	Phe	Arg	Gly	Ser	Tyr	Ser	Tyr	Val	Ala	Val	Gly	Ser	Ser	Gly	Asp																																	
															450																455																460	
Asp	Leu	Asp	Ala	Met	Ala	Glu	Pro	Leu	Pro	Lys	Ile	Asn	Lys	Lys	Val																																	
465																470																475																480
Gly	Gln	Val	Asn	Gly	His	Asp	Gln	Ala	Lys	Val	His	Glu	Leu	Gln	Val																																	
															485																490																495	
Met	Phe	Ala	Gly	Glu	Ala	Thr	His	Arg	Thr	His	Tyr	Ser	Thr	Thr	His																																	
															500																505																510	
Gly	Ala	Tyr	Tyr	Ser	Gly	Leu	Arg	Glu	Ala	Asn	Arg	Leu	Leu	Lys	His																																	
															515																520																525	
Tyr	Lys	Cys	Asn	Phe																																												
															530																																	

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..520  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

Met	Ala	Gly	Leu	Thr	Ala	Ala	Asn	Lys	Leu	Tyr	Thr	Ser	Ser	Asn	Asn
1				5					10					15	
Thr	Phe	Glu	Leu	Ser	Val	Val	Glu	Gly	Gly	Ser	Arg	Ile	Gly	Gly	Arg
			20					25					30		
Ile	Asn	Thr	Ser	Glu	Phe	Ser	Ser	Glu	Lys	Ile	Glu	Met	Gly	Ala	Thr
		35					40					45			
Trp	Ile	His	Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	Ile	Ala	Lys	Glu
	50					55					60				
Thr	Gly	Ser	Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	Met	Asp	Ser	Thr
65					70					75				80	
Ile	Asp	Lys	Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	Glu	Ile	Glu	Pro
				85					90					95	

Ser	Ile	Val	Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala	Leu	Met	Glu	Leu
			100					105					110		
Ala	Gln	Gly	Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp	Leu	Ser	Arg	Leu
			115				120					125			
Ala	His	Ile	Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser	Lys	Gly	Ser	Ser
			130				135				140				
Thr	Ser	Val	Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp	Ala	Tyr	Trp	Asp
			145			150				155					160
Ser	Ile	Ser	Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly	Tyr	Gly	Lys	Trp
			165						170						175
Ser	Arg	Lys	Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met	Phe	Ser	Asn	Thr
			180					185					190		
Gln	Arg	Thr	Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr	Leu	Asp	Phe	Ala
			195				200					205			
Ala	Glu	Ser	Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu	Ile	Thr	Ile	Ala
			210			215					220				
Lys	Gly	Tyr	Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser	Val	Leu	Pro	Gln
			225			230				235					240
Gly	Val	Ile	Gln	Leu	Asn	Arg	Lys	Val	Thr	Lys	Ile	Glu	Trp	Gln	Ser
			245						250						255
Asn	Glu	Val	Lys	Leu	His	Phe	Ser	Asp	Gly	Ser	Val	Val	Phe	Ala	Asp
			260					265					270		
His	Val	Ile	Val	Thr	Val	Ser	Leu	Gly	Val	Leu	Lys	Ala	Gly	Ile	Glu
			275				280					285			
Thr	Asp	Ala	Glu	Leu	Phe	Ser	Pro	Pro	Leu	Pro	Asp	Phe	Lys	Ser	Asp
			290			295					300				
Ala	Ile	Arg	Arg	Leu	Gly	Tyr	Gly	Val	Val	Asn	Lys	Leu	Phe	Val	Glu
			305			310				315					320
Met	Ser	Gln	Arg	Lys	Phe	Pro	Ser	Leu	Gln	Leu	Val	Phe	Asp	Arg	Glu
			325					330							335
Asp	Ser	Glu	Phe	Arg	Phe	Val	Lys	Ile	Pro	Trp	Trp	Met	Arg	Arg	Thr
			340					345				350			
Ala	Thr	Ile	Thr	Pro	Ile	His	Ser	Asn	Ser	Lys	Val	Leu	Leu	Ser	Trp
			355				360					365			
Phe	Ala	Gly	Lys	Glu	Ala	Leu	Glu	Leu	Glu	Lys	Leu	Thr	Asp	Glu	Glu
			370			375					380				
Ile	Lys	Asp	Ala	Val	Met	Thr	Thr	Ile	Ser	Cys	Leu	Thr	Gly	Lys	Glu
			385		390					395					400
Val	Lys	Asn	Asp	Thr	Ala	Lys	Pro	Leu	Thr	Asn	Gly	Ser	Leu	Asn	Asp
			405						410						415
Asp	Asp	Glu	Ala	Met	Lys	Ile	Thr	Lys	Val	Leu	Lys	Ser	Lys	Trp	Gly
			420					425					430		
Ser	Asp	Pro	Leu	Phe	Arg	Gly	Ser	Tyr	Ser	Tyr	Val	Ala	Val	Gly	Ser
			435				440					445			
Ser	Gly	Asp	Asp	Leu	Asp	Ala	Met	Ala	Glu	Pro	Leu	Pro	Lys	Ile	Asn
			450			455					460				
Lys	Lys	Val	Gly	Gln	Val	Asn	Gly	His	Asp	Gln	Ala	Lys	Val	His	Glu
			465			470				475					480
Leu	Gln	Val	Met	Phe	Ala	Gly	Glu	Ala	Thr	His	Arg	Thr	His	Tyr	Ser
			485						490						495
Thr	Thr	His	Gly	Ala	Tyr	Tyr	Ser	Gly	Leu	Arg	Glu	Ala	Asn	Arg	Leu
			500					505					510		
Leu	Lys	His	Tyr	Lys	Cys	Asn	Phe								
			515				520								

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..476

(D) OTHER INFORMATION: / Ceres Seq. ID 1499103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Met	Gly	Ala	Thr	Trp	Ile	His	Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg
1				5				10						15	
Ile	Ala	Lys	Glu	Thr	Gly	Ser	Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys
			20					25					30		
Met	Asp	Ser	Thr	Ile	Asp	Lys	Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe
		35				40					45				
Glu	Ile	Glu	Pro	Ser	Ile	Val	Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala
	50					55					60				
Leu	Met	Glu	Leu	Ala	Gln	Gly	Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp
65					70					75					80
Leu	Ser	Arg	Leu	Ala	His	Ile	Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser
			85						90					95	
Lys	Gly	Ser	Ser	Thr	Ser	Val	Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp
			100					105					110		
Ala	Tyr	Trp	Asp	Ser	Ile	Ser	Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly
		115					120						125		
Tyr	Gly	Lys	Trp	Ser	Arg	Lys	Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met
	130					135					140				
Phe	Ser	Asn	Thr	Gln	Arg	Thr	Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr
145				150						155					160
Leu	Asp	Phe	Ala	Ala	Glu	Ser	Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu
			165						170					175	
Ile	Thr	Ile	Ala	Lys	Gly	Tyr	Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser
			180					185					190		
Val	Leu	Pro	Gln	Gly	Val	Ile	Gln	Leu	Asn	Arg	Lys	Val	Thr	Lys	Ile
		195					200						205		
Glu	Trp	Gln	Ser	Asn	Glu	Val	Lys	Leu	His	Phe	Ser	Asp	Gly	Ser	Val
	210					215						220			
Val	Phe	Ala	Asp	His	Val	Ile	Val	Thr	Val	Ser	Leu	Gly	Val	Leu	Lys
225				230						235					240
Ala	Gly	Ile	Glu	Thr	Asp	Ala	Glu	Leu	Phe	Ser	Pro	Pro	Leu	Pro	Asp
			245						250					255	
Phe	Lys	Ser	Asp	Ala	Ile	Arg	Arg	Leu	Gly	Tyr	Gly	Val	Val	Asn	Lys
		260						265					270		
Leu	Phe	Val	Glu	Met	Ser	Gln	Arg	Lys	Phe	Pro	Ser	Leu	Gln	Leu	Val
	275						280						285		
Phe	Asp	Arg	Glu	Asp	Ser	Glu	Phe	Arg	Phe	Val	Lys	Ile	Pro	Trp	Trp
290					295						300				
Met	Arg	Arg	Thr	Ala	Thr	Ile	Thr	Pro	Ile	His	Ser	Asn	Ser	Lys	Val
305					310					315					320
Leu	Leu	Ser	Trp	Phe	Ala	Gly	Lys	Glu	Ala	Leu	Glu	Leu	Glu	Lys	Leu
			325						330					335	
Thr	Asp	Glu	Glu	Ile	Lys	Asp	Ala	Val	Met	Thr	Thr	Ile	Ser	Cys	Leu
		340						345					350		
Thr	Gly	Lys	Glu	Val	Lys	Asn	Asp	Thr	Ala	Lys	Pro	Leu	Thr	Asn	Gly
	355						360						365		
Ser	Leu	Asn	Asp	Asp	Asp	Glu	Ala	Met	Lys	Ile	Thr	Lys	Val	Leu	Lys
	370					375					380				
Ser	Lys	Trp	Gly	Ser	Asp	Pro	Leu	Phe	Arg	Gly	Ser	Tyr	Ser	Tyr	Val
385					390					395					400
Ala	Val	Gly	Ser	Ser	Gly	Asp	Asp	Leu	Asp	Ala	Met	Ala	Glu	Pro	Leu
			405						410					415	
Pro	Lys	Ile	Asn	Lys	Lys	Val	Gly	Gln	Val	Asn	Gly	His	Asp	Gln	Ala
		420						425					430		
Lys	Val	His	Glu	Leu	Gln	Val	Met	Phe	Ala	Gly	Glu	Ala	Thr	His	Arg
		435					440						445		

Thr His Tyr Ser Thr Thr His Gly Ala Tyr Tyr Ser Gly Leu Arg Glu  
450 455 460  
Ala Asn Arg Leu Leu Lys His Tyr Lys Cys Asn Phe  
465 470 475

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1618
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```
aaatacagag cagaaacctt taagagaaga tctaataaga aagaagagga aaaaaagga 60
tggttttctc agtttccatt tttgcctctc tcgctccgta cttagtctct tcgttactac 120
tcttctttct catcgagcag ctctcttacc tcgtcaagaa acgtaacctc cctggtcctc 180
tctttgtccc tccgatcatc ggaaacgcc a tttcactcgt ccgtgatcct acttcttctt 240
ggttcaagca atccgacacg gcaggcactt cccctggcct cgctgctaac tacctcatcg 300
gcaaattcat catctacatc agagacacag agctttctca tcaaattatc tccaacgttc 360
gtcttgaagc ttttcacctt ctaggacatc cttttggcaa acaactattc ggtgatcata 420
gcctaatacta cttgttttgt gaggatcaca aaactgttcg ccgtcacctt gctcctaact 480
tcaccccaaa ggcactctcc acttactctg atctccaaca aatagtattg ctccgtcatc 540
tacgacagtg ggaggaaagt ttctccggcg gaactaagcc ggtttctatg cgagaccttg 600
tccgtgaact caatcttgag acttctcaaa cggttttcgt tggacctac cttgacaagg 660
aagctaggaa cacgttctgt actgattaca atctgttcaa tctcggtatc atggcgctcc 720
cgatcaacct gcccggttt cgttcaaca aggcctgcgc gccggtaatg aacctggaga 780
agacgtcttc cgtctgtgcg gaaaaatcaa aaaagaggat ggctacagga gaggagccaa 840
catgcttaat cgattttttg atgcatgcat tcgtcacgga gatagaatcc ggtaatccac 900
cgccgcttca ctccgaagac gaagccatcg gcggtttgct cttcgatttt ctctttgccg 960
cacaagacgc gtcgacgtca tcaactcttt gggcggtgac gtttctagaa tctcatccga 1020
aagtgtgag caaagtgagg gaggaagtgg ccaagatttg gtcacctcag tctggccatc 1080
tgatcacggc cgatcagctc gcggagatga agtatactcg cgctgtggca cgtgaggttg 1140
tgagatatac accaccgca actatgggtc cacacattgc tactaatgat ttccctctta 1200
cagaatcgta cactatccca aaaggtacaa tagtgtttcc ctcggttttc gagcctcgt 1260
ttcaagggtt tactgaaccg aaccggttcg atccggaccg gtttagtgag acaaggcaag 1320
aggatcaagt gttcaaacga aactacctag cttttggatg ggggtgcacac caatgcgtag 1380
gccagcgtaa cgcattgaac cacctcgtgc tcttcatcgc tatgttctca tcgttgtttg 1440
atttcaagag acttcaatcg gacggttgcg atgacatcat atactgtccc acgatatcgc 1500
caaaggacgg gtgcacggtg ttcttgtcta agcgcacatc aacgtatccg aacctctgat 1560
ttggattttt gttacaaatt attggtgatc aaagtcaata ctcatgagtg tgattact
```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..499
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

```
Met Val Phe Ser Val Ser Ile Phe Ala Ser Leu Ala Pro Tyr Leu Val
1 5 10 15
Ser Ser Leu Leu Leu Phe Phe Leu Ile Glu Gln Leu Ser Tyr Leu Val
20 25 30
Lys Lys Arg Asn Leu Pro Gly Pro Leu Phe Val Pro Pro Ile Ile Gly
35 40 45
```

Asn	Ala	Ile	Ser	Leu	Val	Arg	Asp	Pro	Thr	Ser	Phe	Trp	Phe	Lys	Gln
50						55					60				
Ser	Asp	Thr	Ala	Gly	Thr	Ser	Pro	Gly	Leu	Ala	Ala	Asn	Tyr	Leu	Ile
65					70					75					80
Gly	Lys	Phe	Ile	Ile	Tyr	Ile	Arg	Asp	Thr	Glu	Leu	Ser	His	Gln	Ile
			85						90					95	
Phe	Ser	Asn	Val	Arg	Leu	Glu	Ala	Phe	His	Pro	Leu	Gly	His	Pro	Phe
			100					105					110		
Gly	Lys	Gln	Leu	Phe	Gly	Asp	His	Ser	Leu	Ile	Tyr	Leu	Phe	Gly	Glu
		115				120						125			
Asp	His	Lys	Thr	Val	Arg	Arg	His	Leu	Ala	Pro	Asn	Phe	Thr	Pro	Lys
	130					135					140				
Ala	Leu	Ser	Thr	Tyr	Ser	Asp	Leu	Gln	Gln	Ile	Val	Met	Leu	Arg	His
145					150					155					160
Leu	Arg	Gln	Trp	Glu	Glu	Ser	Phe	Ser	Gly	Gly	Thr	Lys	Pro	Val	Ser
			165						170					175	
Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr	Ser	Gln	Thr	Val
		180						185					190		
Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn	Thr	Phe	Cys	Thr
	195					200						205			
Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu	Pro	Ile	Asn	Leu
	210				215						220				
Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val	Met	Asn	Leu	Glu
225					230					235					240
Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys	Arg	Met	Ala	Thr
			245						250					255	
Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met	His	Ala	Phe	Val
		260						265					270		
Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His	Ser	Glu	Asp	Glu
		275				280							285		
Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala	Ala	Gln	Asp	Ala
	290					295					300				
Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu	Glu	Ser	His	Pro
305				310						315					320
Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys	Ile	Trp	Ser	Pro
			325						330					335	
Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala	Glu	Met	Lys	Tyr
		340						345					350		
Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg	Pro	Pro	Ala	Thr
		355				360						365			
Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu	Thr	Glu	Ser	Tyr
	370				375						380				
Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val	Phe	Asp	Ala	Ser
385				390						395					400
Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro	Asp	Arg	Phe	Ser
			405						410					415	
Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn	Tyr	Leu	Ala	Phe
		420				425						430			
Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr	Ala	Leu	Asn	His
		435				440						445			
Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe	Asp	Phe	Lys	Arg
	450					455					460				
Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys	Pro	Thr	Ile	Ser
465				470						475					480
Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg	Ile	Val	Thr	Tyr
			485						490					495	
Pro	Asn	Leu													

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..343
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

Met	Leu	Arg	His	Leu	Arg	Gln	Trp	Glu	Glu	Ser	Phe	Ser	Gly	Gly	Thr
1			5					10						15	
Lys	Pro	Val	Ser	Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr
			20				25					30			
Ser	Gln	Thr	Val	Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn
		35				40					45				
Thr	Phe	Cys	Thr	Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu
	50				55					60					
Pro	Ile	Asn	Leu	Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val
65				70						75					80
Met	Asn	Leu	Glu	Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys
			85					90					95		
Arg	Met	Ala	Thr	Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met
		100					105					110			
His	Ala	Phe	Val	Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His
	115				120						125				
Ser	Glu	Asp	Glu	Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala
	130				135					140					
Ala	Gln	Asp	Ala	Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu
145				150						155					160
Glu	Ser	His	Pro	Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys
			165					170						175	
Ile	Trp	Ser	Pro	Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala
	180						185					190			
Glu	Met	Lys	Tyr	Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg
	195				200							205			
Pro	Pro	Ala	Thr	Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu
	210				215						220				
Thr	Glu	Ser	Tyr	Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val
225				230						235					240
Phe	Asp	Ala	Ser	Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro
		245						250						255	
Asp	Arg	Phe	Ser	Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn
		260					265						270		
Tyr	Leu	Ala	Phe	Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr
	275				280							285			
Ala	Leu	Asn	His	Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe
	290				295						300				
Asp	Phe	Lys	Arg	Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys
305				310						315					320
Pro	Thr	Ile	Ser	Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg
			325					330						335	
Ile	Val	Thr	Tyr	Pro	Asn	Leu									
			340												

- (2) INFORMATION FOR SEQ ID NO:866:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 323 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:



(A) NAME/KEY: peptide  
(B) LOCATION: 1..323  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr	Ser	Gln	Thr	Val
1			5					10					15		
Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn	Thr	Phe	Cys	Thr
		20						25					30		
Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu	Pro	Ile	Asn	Leu
		35					40					45			
Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val	Met	Asn	Leu	Glu
	50					55					60				
Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys	Arg	Met	Ala	Thr
65					70					75				80	
Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met	His	Ala	Phe	Val
				85					90					95	
Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His	Ser	Glu	Asp	Glu
			100					105					110		
Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala	Ala	Gln	Asp	Ala
	115						120						125		
Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu	Glu	Ser	His	Pro
	130					135					140				
Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys	Ile	Trp	Ser	Pro
145					150					155				160	
Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala	Glu	Met	Lys	Tyr
			165					170						175	
Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg	Pro	Pro	Ala	Thr
		180						185					190		
Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu	Thr	Glu	Ser	Tyr
	195						200					205			
Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val	Phe	Asp	Ala	Ser
	210					215					220				
Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro	Asp	Arg	Phe	Ser
225					230					235				240	
Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn	Tyr	Leu	Ala	Phe
			245						250					255	
Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr	Ala	Leu	Asn	His
		260						265					270		
Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe	Asp	Phe	Lys	Arg
	275					280						285			
Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys	Pro	Thr	Ile	Ser
	290					295					300				
Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg	Ile	Val	Thr	Tyr
305					310					315				320	
Pro	Asn	Leu													

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1451 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1451  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

actcaactta	aactcttitta	gtaacaatgg	tttcttcttc	tttaaccaag	cttgtgttct	60
ttggttgctc	cctcctgctc	acattcacgg	acaaccttgt	ggctggaaaa	tctggcaaag	120
tgaagctcaa	tccttactac	gaatcacttt	gtcccggttg	tcaggaattc	atogtcgatg	180

acctaggtaa aatctttgac tacgatctct acacaatcac tgatctcaag ctgtttccat	240
ttggtaatgc cgaactctcc gataatctga ctgtcacttt tttttttttt ttttttgaga	300
gaaacaaagg caatggatat gaacagacaa gcacaccaca tgagcttggt gattacaaac	360
acaagcttct ttttcgcctt ctgctcaatc acaacaactg aagtcctgcac cacaacaaca	420
gctaaggata taaacagtgc caagctgtca aagatgaaga agaccagaaa cgggtgcttg	480
tttgctatat gagcttgctc tagcaactct cttttcgacc ggtcctcttc gtactgaccg	540
ggtattgtga agattgctgc gaaagccact gtggcaataa gcactgccac aacagttgct	600
gagtttatag cgttggtttag accactaatg tgtagcttct tgagtctttt tgctatcttc	660
tggaactctta cacctgtttg tctggattgc tgaagctgag attgtacttc atgtttgatg	720
tcgctgactg tttgcttcag ttgcttagct gggttctgag gctttccgag atcttttagct	780
gtagcagctc ctgcttcctt cagaactgac acaagctctg cgtttcctat cttctcagag	840
acatcgagtg gcgtatctcc agctttgttt attgggttga ggtttatgcc ttcaaaagat	900
accaaacacc gtactatctt aatacgcccc ttgtttgtgg caataagaac ttggcccgat	960
cagaaatcac aatactcggt catacggtgc gtcgaaagcg atacgaaagg ctgggaatca	1020
tgtgttaaaa actctggacg tgagaaagca atcaatgatt gttacaatgg tgatctttct	1080
agaaagctga tacttgggta cgcaacaaaa accaagaatt tgaagccgcc acatgaatac	1140
gtaccatggg tcacactcaa cggcaagcca ctogatgaca gcgtacaaaag tacggatgat	1200
ctcgtagctc aaatctgcaa agcatacaaa ggaaagggtg ctctcccaaa agtttgcaat	1260
tcatccgcct caatgtctaa gtcgcctgag aggaaatgga agcttcaagt ctcttatgcc	1320
aataaagcta ccaattatta agttaactat caaacttcgt attgaactaa gatggattta	1380
agctttatgt tataagtgga atgatgaata aaggcctggt ctaaactttt atggttacga	1440
attgatgtat t	

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

Met Val Ser Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu	
1 5 10 15	
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val	
20 25 30	
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Gln Glu Phe	
35 40 45	
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile	
50 55 60	
Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn	
65 70 75 80	
Leu Thr Val Thr Phe Phe Phe Phe Phe Glu Arg Asn Lys Gly Asn	
85 90 95	
Gly Tyr Glu Gln Thr Ser Thr Pro His Glu Leu Val Asp Tyr Lys His	
100 105 110	
Lys Leu Leu Phe Arg Leu Leu Leu Asn His Asn Asn	
115 120	

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

Met	Pro	Ser	Lys	Asp	Thr	Lys	His	Arg	Thr	Ile	Leu	Ile	Arg	Pro	Leu
1			5						10					15	
Phe	Val	Ala	Ile	Arg	Thr	Trp	Pro	Asp	Gln	Lys	Ser	Gln	Tyr	Ser	Phe
		20						25				30			
Ile	Arg	Cys	Val	Glu	Ser	Asp	Thr	Lys	Gly	Trp	Glu	Ser	Cys	Val	Lys
		35					40					45			
Asn	Ser	Gly	Arg	Glu	Lys	Ala	Ile	Asn	Asp	Cys	Tyr	Asn	Gly	Asp	Leu
		50				55					60				
Ser	Arg	Lys	Leu	Ile	Leu	Gly	Tyr	Ala	Thr	Lys	Thr	Lys	Asn	Leu	Lys
65					70					75				80	
Pro	Pro	His	Glu	Tyr	Val	Pro	Trp	Val	Thr	Leu	Asn	Gly	Lys	Pro	Leu
			85						90					95	
Asp	Asp	Ser	Val	Gln	Ser	Thr	Asp	Asp	Leu	Val	Ala	Gln	Ile	Cys	Lys
			100					105					110		
Ala	Tyr	Lys	Gly	Lys	Val	Ala	Leu	Pro	Lys	Val	Cys	Asn	Ser	Ser	Ala
		115					120					125			
Ser	Met	Ser	Lys	Ser	Pro	Glu	Arg	Lys	Trp	Lys	Leu	Gln	Val	Ser	Tyr
	130					135					140				
Ala	Asn	Lys	Ala	Thr	Asn	Tyr									
145					150										

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1905
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

acacaaaccg	acccgacccg	aatctggccg	gtgagaaaat	ggaggtccaa	agcagcagca	60
acaatggtgg	tcaactttct	ttctccagtc	tccgcgtcta	cctcaactct	ctttccgcga	120
cgccttctcg	cttatcccg	cgcgtatatt	ccgtctccac	ctcttccgac	gagatgagtc	180
gcgtccgcgc	cgtctccggc	gaacagatgc	gccgtactct	ccggtggtac	gatctcattg	240
gactcggaat	cgggggaatg	gtcggcgccg	gtgtctttgt	caccaaccggc	cgtgctagtc	300
gtctcgacgc	cggctccttca	attgtcgtct	cttacgccat	cgcggggctc	tgcgtctctc	360
tctccgcttt	ctgttacacc	gaattcgccg	tccatctccc	ggtcgccggc	ggtgccttca	420
gctacatccg	tatcacattc	ggtgaatttc	cagcattttt	caccggagca	aatcttgtaa	480
tggattacgt	aatgtcaaac	gcggccggtt	cgagaagctt	caccgcttat	ttaggaacag	540
ctttcgggat	ctcaacttcc	aagtggcgat	tcgtcgtctc	cggtttaccg	aaaggattca	600
acgagattga	tccagtcgca	gttctcgtcg	tcctcgtaat	cacagtcatc	atctgttgca	660
gtacaagaga	gagttccaaa	gtgaacatga	taatgactgc	atttcacatc	gcattcatat	720
tcttcgtgat	cgtgatggga	ttcataaaag	gagattcaaa	gaatctatcc	tcaccggcga	780
atccagagca	cccctcggga	ttttttccgt	tcggcgccgc	gggagttttc	aacggagctg	840
ccatgggtta	cttaagctac	ataggatacg	acgccgtttc	aaccatggcg	gaagaagttg	900
aaaatccggg	caaagatatc	cccgctcggg	tttccggctc	cgtcgcaatc	gtcaccgttc	960
tttactgtct	catggcagtc	tctatgtcaa	tgettctgcc	atacgatctg	atagatccgg	1020
aggcgccggt	ttccgcggcg	ttcagaggat	cgaacggctg	ggaatgggtg	acgaaagtgg	1080
tggggatagg	agcaagcttt	gggatattaa	catcactttt	ggtaggcaatg	ttaggtcagg	1140
ctcgctacat	gtgtgtcatc	ggacgggtcca	gagtggtccc	cttttggttc	gctaagattc	1200
atcccaaaac	atctacgcca	gtcaacgcct	ccacttttct	tggcattttc	acggcggttc	1260
ttgcgctttt	caccgacctc	aacgtcctcc	taaacctcgt	atccattgga	acactatttg	1320
tcttctacat	ggtcgcaaac	gctctcatct	tcagacgtta	cgtcccggtt	ggaccacca	1380
agccgtggcc	cacactctgc	ttcctcacac	tattctccat	aacctctctc	gtcttcaccc	1440
tcacttgga	acttggtgcg	gaaggtaagc	ctaaagcttt	catgctcggg	gccagtgcgg	1500
tgggtgctat	agccatcgtg	ctgagctttc	agtcgctggg	tcccagggtc	aggaaacctg	1560
agttgtgggg	agtcctcggt	atgcctgga	ccccgtgcgt	gtcgatatcc	ttgaacattt	1620
ttttgcttgg	ttcgttggac	gcaccctctt	acgtccggtt	tggattcttc	tccggtttga	1680

tcgtgctcgt gtatttggtt tatggcggtc atgcgaggtc tgatgctgaa gcgaatggat 1740  
cttttggtgt gaaagatgga caagtcataa aagagctaata tgaagtgtga aaagtattta 1800  
tttagtttag ttttctaaag catcatgaac caaaatgtaa ttaaactctc taattttttt 1860  
tctacatgag ggggtttgaa atattaatga gaaaatatta aatgc

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1499116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

Thr	Asn	Arg	Pro	Asp	Pro	Asn	Leu	Ala	Gly	Glu	Lys	Met	Glu	Val	Gln
1				5					10					15	
Ser	Ser	Ser	Asn	Asn	Gly	Gly	His	Ser	Ser	Phe	Ser	Ser	Leu	Arg	Val
			20					25					30		
Tyr	Leu	Asn	Ser	Leu	Ser	Ala	Thr	Pro	Ser	Arg	Leu	Ser	Arg	Arg	Ala
		35					40					45			
Ile	Ser	Val	Ser	Thr	Ser	Ser	Asp	Glu	Met	Ser	Arg	Val	Arg	Ala	Val
	50					55					60				
Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu	Arg	Trp	Tyr	Asp	Leu	Ile	Gly
65					70					75				80	
Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala	Gly	Val	Phe	Val	Thr	Thr	Gly
				85					90					95	
Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro	Ser	Ile	Val	Val	Ser	Tyr	Ala
			100					105					110		
Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser	Ala	Phe	Cys	Tyr	Thr	Glu	Phe
	115						120					125			
Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly	Ala	Phe	Ser	Tyr	Ile	Arg	Ile
	130					135					140				
Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe	Thr	Gly	Ala	Asn	Leu	Val	Met
145					150					155					160
Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val	Ser	Arg	Ser	Phe	Thr	Ala	Tyr
			165						170					175	
Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr	Ser	Lys	Trp	Arg	Phe	Val	Val
		180						185					190		
Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu	Ile	Asp	Pro	Val	Ala	Val	Leu
	195						200					205			
Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile	Cys	Cys	Ser	Thr	Arg	Glu	Ser
	210					215					220				
Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala	Phe	His	Ile	Ala	Phe	Ile	Phe
225				230						235				240	
Phé	Val	Ile	Val	Met	Gly	Phe	Ile	Lys	Gly	Asp	Ser	Lys	Asn	Leu	Ser
			245						250					255	
Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser	Gly	Phe	Phe	Pro	Phe	Gly	Ala
		260						265					270		
Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met	Val	Tyr	Leu	Ser	Tyr	Ile	Gly
	275					280						285			
Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu	Glu	Val	Glu	Asn	Pro	Val	Lys
	290					295					300				
Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser	Val	Ala	Ile	Val	Thr	Val	Leu
305				310						315					320
Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser	Met	Leu	Leu	Pro	Tyr	Asp	Leu
			325						330					335	
Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala	Ala	Phe	Arg	Gly	Ser	Asn	Gly
		340						345					350		
Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly	Ile	Gly	Ala	Ser	Phe	Gly	Ile

355 360 365  
Leu Thr Ser Leu Leu Val Ala Met Leu Gly Gln Ala Arg Tyr Met Cys  
370 375 380  
Val Ile Gly Arg Ser Arg Val Val Pro Phe Trp Phe Ala Lys Ile His  
385 390 395 400  
Pro Lys Thr Ser Thr Pro Val Asn Ala Ser Thr Phe Leu Gly Ile Phe  
405 410 415  
Thr Ala Ala Leu Ala Leu Phe Thr Asp Leu Asn Val Leu Leu Asn Leu  
420 425 430  
Val Ser Ile Gly Thr Leu Phe Val Phe Tyr Met Val Ala Asn Ala Leu  
435 440 445  
Ile Phe Arg Arg Tyr Val Pro Val Gly Pro Thr Lys Pro Trp Pro Thr  
450 455 460  
Leu Cys Phe Leu Thr Leu Phe Ser Ile Thr Ser Leu Val Phe Thr Leu  
465 470 475 480  
Ile Trp Lys Leu Val Pro Glu Gly Lys Pro Lys Ala Phe Met Leu Gly  
485 490 495  
Ala Ser Ala Val Val Ala Ile Ala Ile Val Leu Ser Phe Gln Cys Val  
500 505 510  
Val Pro Gln Ala Arg Lys Pro Glu Leu Trp Gly Val Pro Phe Met Pro  
515 520 525  
Trp Thr Pro Cys Val Ser Ile Phe Leu Asn Ile Phe Leu Leu Gly Ser  
530 535 540  
Leu Asp Ala Pro Ser Tyr Val Arg Phe Gly Phe Phe Ser Gly Leu Ile  
545 550 555 560  
Val Leu Val Tyr Leu Phe Tyr Gly Val His Ala Ser Ser Asp Ala Glu  
565 570 575  
Ala Asn Gly Ser Phe Gly Val Lys Asp Gly Gln Val Met Lys Glu Leu  
580 585 590  
Ile Glu Val  
595

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..583
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

Met Glu Val Gln Ser Ser Asn Asn Gly Gly His Ser Ser Phe Ser  
1 5 10 15  
Ser Leu Arg Val Tyr Leu Asn Ser Leu Ser Ala Thr Pro Ser Arg Leu  
20 25 30  
Ser Arg Arg Ala Ile Ser Val Ser Thr Ser Ser Asp Glu Met Ser Arg  
35 40 45  
Val Arg Ala Val Ser Gly Glu Gln Met Arg Arg Thr Leu Arg Trp Tyr  
50 55 60  
Asp Leu Ile Gly Leu Gly Ile Gly Gly Met Val Gly Ala Gly Val Phe  
65 70 75 80  
Val Thr Thr Gly Arg Ala Ser Arg Leu Asp Ala Gly Pro Ser Ile Val  
85 90 95  
Val Ser Tyr Ala Ile Ala Gly Leu Cys Ala Leu Leu Ser Ala Phe Cys  
100 105 110  
Tyr Thr Glu Phe Ala Val His Leu Pro Val Ala Gly Gly Ala Phe Ser  
115 120 125  
Tyr Ile Arg Ile Thr Phe Gly Glu Phe Pro Ala Phe Phe Thr Gly Ala  
130 135 140

Asn	Leu	Val	Met	Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val	Ser	Arg	Ser
145					150					155					160
Phe	Thr	Ala	Tyr	Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr	Ser	Lys	Trp
				165					170					175	
Arg	Phe	Val	Val	Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu	Ile	Asp	Pro
				180				185						190	
Val	Ala	Val	Leu	Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile	Cys	Cys	Ser
				195			200					205			
Thr	Arg	Glu	Ser	Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala	Phe	His	Ile
							215					220			
Ala	Phe	Ile	Phe	Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys	Gly	Asp	Ser
225					230					235					240
Lys	Asn	Leu	Ser	Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser	Gly	Phe	Phe
				245					250					255	
Pro	Phe	Gly	Ala	Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met	Val	Tyr	Leu
				260				265					270		
Ser	Tyr	Ile	Gly	Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu	Glu	Val	Glu
				275			280					285			
Asn	Pro	Val	Lys	Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser	Val	Ala	Ile
290							295				300				
Val	Thr	Val	Leu	Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser	Met	Leu	Leu
305					310					315					320
Pro	Tyr	Asp	Leu	Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala	Ala	Phe	Arg
				325					330					335	
Gly	Ser	Asn	Gly	Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly	Ile	Gly	Ala
				340				345					350		
Ser	Phe	Gly	Ile	Leu	Thr	Ser	Leu	Leu	Val	Ala	Met	Leu	Gly	Gln	Ala
				355			360					365			
Arg	Tyr	Met	Cys	Val	Ile	Gly	Arg	Ser	Arg	Val	Val	Pro	Phe	Trp	Phe
						375					380				
Ala	Lys	Ile	His	Pro	Lys	Thr	Ser	Thr	Pro	Val	Asn	Ala	Ser	Thr	Phe
385					390					395					400
Leu	Gly	Ile	Phe	Thr	Ala	Ala	Leu	Ala	Leu	Phe	Thr	Asp	Leu	Asn	Val
				405					410					415	
Leu	Leu	Asn	Leu	Val	Ser	Ile	Gly	Thr	Leu	Phe	Val	Phe	Tyr	Met	Val
				420				425					430		
Ala	Asn	Ala	Leu	Ile	Phe	Arg	Arg	Tyr	Val	Pro	Val	Gly	Pro	Thr	Lys
				435			440					445			
Pro	Trp	Pro	Thr	Leu	Cys	Phe	Leu	Thr	Leu	Phe	Ser	Ile	Thr	Ser	Leu
				450			455				460				
Val	Phe	Thr	Leu	Ile	Trp	Lys	Leu	Val	Pro	Glu	Gly	Lys	Pro	Lys	Ala
465					470					475					480
Phe	Met	Leu	Gly	Ala	Ser	Ala	Val	Val	Ala	Ile	Ala	Ile	Val	Leu	Ser
				485					490					495	
Phe	Gln	Cys	Val	Val	Pro	Gln	Ala	Arg	Lys	Pro	Glu	Leu	Trp	Gly	Val
				500				505					510		
Pro	Phe	Met	Pro	Trp	Thr	Pro	Cys	Val	Ser	Ile	Phe	Leu	Asn	Ile	Phe
				515			520					525			
Leu	Leu	Gly	Ser	Leu	Asp	Ala	Pro	Ser	Tyr	Val	Arg	Phe	Gly	Phe	Phe
				530			535				540				
Ser	Gly	Leu	Ile	Val	Leu	Val	Tyr	Leu	Phe	Tyr	Gly	Val	His	Ala	Ser
545					550					555					560
Ser	Asp	Ala	Glu	Ala	Asn	Gly	Ser	Phe	Gly	Val	Lys	Asp	Gly	Gln	Val
				565					570					575	
Met	Lys	Glu	Leu	Ile	Glu	Val									
				580											

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..538  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499118  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

Met	Ser	Arg	Val	Arg	Ala	Val	Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu
1			5					10						15	
Arg	Trp	Tyr	Asp	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala
			20				25						30		
Gly	Val	Phe	Val	Thr	Thr	Gly	Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro
		35				40					45				
Ser	Ile	Val	Val	Ser	Tyr	Ala	Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser
	50				55					60					
Ala	Phe	Cys	Tyr	Thr	Glu	Phe	Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly
65				70					75					80	
Ala	Phe	Ser	Tyr	Ile	Arg	Ile	Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe
				85				90						95	
Thr	Gly	Ala	Asn	Leu	Val	Met	Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val
			100					105					110		
Ser	Arg	Ser	Phe	Thr	Ala	Tyr	Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr
		115				120						125			
Ser	Lys	Trp	Arg	Phe	Val	Val	Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu
	130				135						140				
Ile	Asp	Pro	Val	Ala	Val	Leu	Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile
145				150					155					160	
Cys	Cys	Ser	Thr	Arg	Glu	Ser	Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala
				165				170						175	
Phe	His	Ile	Ala	Phe	Ile	Phe	Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys
			180					185					190		
Gly	Asp	Ser	Lys	Asn	Leu	Ser	Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser
		195				200						205			
Gly	Phe	Phe	Pro	Phe	Gly	Ala	Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met
	210				215							220			
Val	Tyr	Leu	Ser	Tyr	Ile	Gly	Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu
225				230						235				240	
Glu	Val	Glu	Asn	Pro	Val	Lys	Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser
			245					250						255	
Val	Ala	Ile	Val	Thr	Val	Leu	Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser
			260					265					270		
Met	Leu	Leu	Pro	Tyr	Asp	Leu	Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala
	275					280							285		
Ala	Phe	Arg	Gly	Ser	Asn	Gly	Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly
	290				295							300			
Ile	Gly	Ala	Ser	Phe	Gly	Ile	Leu	Thr	Ser	Leu	Leu	Val	Ala	Met	Leu
305				310						315				320	
Gly	Gln	Ala	Arg	Tyr	Met	Cys	Val	Ile	Gly	Arg	Ser	Arg	Val	Val	Pro
				325					330					335	
Phe	Trp	Phe	Ala	Lys	Ile	His	Pro	Lys	Thr	Ser	Thr	Pro	Val	Asn	Ala
			340					345						350	
Ser	Thr	Phe	Leu	Gly	Ile	Phe	Thr	Ala	Ala	Leu	Ala	Leu	Phe	Thr	Asp
		355				360						365			
Leu	Asn	Val	Leu	Leu	Asn	Leu	Val	Ser	Ile	Gly	Thr	Leu	Phe	Val	Phe
	370				375						380				
Tyr	Met	Val	Ala	Asn	Ala	Leu	Ile	Phe	Arg	Arg	Tyr	Val	Pro	Val	Gly
385				390						395				400	
Pro	Thr	Lys	Pro	Trp	Pro	Thr	Leu	Cys	Phe	Leu	Thr	Leu	Phe	Ser	Ile
				405					410					415	
Thr	Ser	Leu	Val	Phe	Thr	Leu	Ile	Trp	Lys	Leu	Val	Pro	Glu	Gly	Lys
			420					425					430		

Pro Lys Ala Phe Met Leu Gly Ala Ser Ala Val Val Ala Ile Ala Ile  
435 440 445  
Val Leu Ser Phe Gln Cys Val Val Pro Gln Ala Arg Lys Pro Glu Leu  
450 455 460  
Trp Gly Val Pro Phe Met Pro Trp Thr Pro Cys Val Ser Ile Phe Leu  
465 470 475 480  
Asn Ile Phe Leu Leu Gly Ser Leu Asp Ala Pro Ser Tyr Val Arg Phe  
485 490 495  
Gly Phe Phe Ser Gly Leu Ile Val Leu Val Tyr Leu Phe Tyr Gly Val  
500 505 510  
His Ala Ser Ser Asp Ala Glu Ala Asn Gly Ser Phe Gly Val Lys Asp  
515 520 525  
Gly Gln Val Met Lys Glu Leu Ile Glu Val  
530 535

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

aactgaattt	gaaagaaaaa	aaaaaaagaa	atcataaaat	gagaatcaat	atgttattca	60
tagtggcatt	ctcattttta	gtctctgttc	ggtcattacc	gatgagacca	actctaaagt	120
acgagtcaat	ctttaatttt	ggcgattctt	taagcgatac	cggaaacttt	ttattatccg	180
gtgatgttga	ctctccgaac	attggaagac	taccgtacgg	acaaaccttt	tttaaccggt	240
ccaccggtcg	ttgtcttgac	ggacgtctca	tcacgtattt	catcgtgag	gctagtggac	300
taccgtacat	tccaccgtat	ctccaaagct	tacggacgaa	tgattcggta	gatttcaaga	360
gaggtgcaaa	ttttgcggtg	gctggagcaa	cagcgaacga	atttagcttc	tttaaaaaca	420
gaggtctttc	agtaacattg	ttgacaaaaca	agacactgga	tattcaactt	gatttggttca	480
agaagttgaa	acotttctctg	tgtaaaaacca	agccagaatg	tgagcgatat	tttagaaaat	540
ctctatttct	cgtcggagaa	attagtggaa	acgattataa	ctaccctctt	ttggcattcc	600
gaagtttcaa	acatgctatg	gatttggtag	catttgttat	taacaaaatc	atggacgtca	660
caagtgcatt	gatagaggaa	ggtgccatga	cactaatagt	tccaggaaac	cttccaatcg	720
gttggttctgc	ggctctacta	gagcggttta	atgataatag	tggtatggctt	tatgactcga	780
ggaaccaatg	ctacatgccca	ttgaacaatt	tggctaagct	tcacaatgat	aagctcaaga	840
aaggcctcgc	ggctctaaga	aaaaagttacc	cttatgccaa	aattatatat	gctgattatt	900
acagttctgc	catgcaattc	ttcaactcac	cttccaaata	cggtttccact	ggaagtgtcc	960
taaaggcatg	ttgtggagga	ggagatggaa	gatacaacgt	gcaaccaaac	gtgcggtgcg	1020
gagaaaaggg	ttcaaccact	tgcggaagtc	catcaacgta	cgcaaattgg	gacggaattc	1080
acctcactga	agcggccttac	cgccacattg	caactggctc	catctccggc	cgtttcacca	1140
tgcctactta	taattaataa	caattaagtt	actcataagt	tgtaactttt	tttttaaacac	1200
acaaactttt	catataactc	ctaattgaaa	acctataaat	cgatcatatt	tatatcaagc	1260
tcgttcgaga	gcataagcc					

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

Leu Asn Leu Lys Glu Lys Lys Lys Arg Asn His Lys Met Arg Ile Asn



1	5	10	15
Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser Val Arg Ser Leu			
20	25	30	
Pro Met Arg Pro Thr Leu Lys Tyr Glu Ser Ile Phe Asn Phe Gly Asp			
35	40	45	
Ser Leu Ser Asp Thr Gly Asn Phe Leu Leu Ser Gly Asp Val Asp Ser			
50	55	60	
Pro Asn Ile Gly Arg Leu Pro Tyr Gly Gln Thr Phe Phe Asn Arg Ser			
65	70	75	80
Thr Gly Arg Cys Ser Asp Gly Arg Leu Ile Asp Phe Ile Ala Glu			
85	90	95	
Ala Ser Gly Leu Pro Tyr Ile Pro Pro Tyr Leu Gln Ser Leu Arg Thr			
100	105	110	
Asn Asp Ser Val Asp Phe Lys Arg Gly Ala Asn Phe Ala Val Ala Gly			
115	120	125	
Ala Thr Ala Asn Glu Phe Ser Phe Phe Lys Asn Arg Gly Leu Ser Val			
130	135	140	
Thr Leu Leu Thr Asn Lys Thr Leu Asp Ile Gln Leu Asp Trp Phe Lys			
145	150	155	160
Lys Leu Lys Pro Ser Leu Cys Lys Thr Lys Pro Glu Cys Glu Arg Tyr			
165	170	175	
Phe Arg Lys Ser Leu Phe Leu Val Gly Glu Ile Ser Gly Asn Asp Tyr			
180	185	190	
Asn Tyr Pro Leu Leu Ala Phe Arg Ser Phe Lys His Ala Met Asp Leu			
195	200	205	
Val Pro Phe Val Ile Asn Lys Ile Met Asp Val Thr Ser Ala Leu Ile			
210	215	220	
Glu Glu Gly Ala Met Thr Leu Ile Val Pro Gly Asn Leu Pro Ile Gly			
225	230	235	240
Cys Ser Ala Ala Leu Leu Glu Arg Phe Asn Asp Asn Ser Gly Trp Leu			
245	250	255	
Tyr Asp Ser Arg Asn Gln Cys Tyr Met Pro Leu Asn Asn Leu Ala Lys			
260	265	270	
Leu His Asn Asp Lys Leu Lys Lys Gly Leu Ala Ala Leu Arg Lys Lys			
275	280	285	
Tyr Pro Tyr Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr Ser Ser Ala Met			
290	295	300	
Gln Phe Phe Asn Ser Pro Ser Lys Tyr Gly Phe Thr Gly Ser Val Leu			
305	310	315	320
Lys Ala Cys Cys Gly Gly Gly Asp Gly Arg Tyr Asn Val Gln Pro Asn			
325	330	335	
Val Arg Cys Gly Glu Lys Gly Ser Thr Thr Cys Glu Asp Pro Ser Thr			
340	345	350	
Tyr Ala Asn Trp Asp Gly Ile His Leu Thr Glu Ala Ala Tyr Arg His			
355	360	365	
Ile Ala Thr Gly Leu Ile Ser Gly Arg Phe Thr Met Pro Thr Tyr Asn			
370	375	380	

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1499121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

Met	Arg	Ile	Asn	Met	Leu	Phe	Ile	Val	Ala	Phe	Ser	Phe	Leu	Val	Ser
1			5						10					15	
Val	Arg	Ser	Leu	Pro	Met	Arg	Pro	Thr	Leu	Lys	Tyr	Glu	Ser	Ile	Phe
			20					25						30	
Asn	Phe	Gly	Asp	Ser	Leu	Ser	Asp	Thr	Gly	Asn	Phe	Leu	Leu	Ser	Gly
			35				40						45		
Asp	Val	Asp	Ser	Pro	Asn	Ile	Gly	Arg	Leu	Pro	Tyr	Gly	Gln	Thr	Phe
			50			55					60				
Phe	Asn	Arg	Ser	Thr	Gly	Arg	Cys	Ser	Asp	Gly	Arg	Leu	Ile	Ile	Asp
65					70					75					80
Phe	Ile	Ala	Glu	Ala	Ser	Gly	Leu	Pro	Tyr	Ile	Pro	Pro	Tyr	Leu	Gln
				85					90					95	
Ser	Leu	Arg	Thr	Asn	Asp	Ser	Val	Asp	Phe	Lys	Arg	Gly	Ala	Asn	Phe
			100					105						110	
Ala	Val	Ala	Gly	Ala	Thr	Ala	Asn	Glu	Phe	Ser	Phe	Phe	Lys	Asn	Arg
			115				120						125		
Gly	Leu	Ser	Val	Thr	Leu	Leu	Thr	Asn	Lys	Thr	Leu	Asp	Ile	Gln	Leu
			130			135						140			
Asp	Trp	Phe	Lys	Lys	Leu	Lys	Pro	Ser	Leu	Cys	Lys	Thr	Lys	Pro	Glu
145					150					155					160
Cys	Glu	Arg	Tyr	Phe	Arg	Lys	Ser	Leu	Phe	Leu	Val	Gly	Glu	Ile	Ser
				165					170					175	
Gly	Asn	Asp	Tyr	Asn	Tyr	Pro	Leu	Leu	Ala	Phe	Arg	Ser	Phe	Lys	His
			180					185						190	
Ala	Met	Asp	Leu	Val	Pro	Phe	Val	Ile	Asn	Lys	Ile	Met	Asp	Val	Thr
			195				200						205		
Ser	Ala	Leu	Ile	Glu	Glu	Gly	Ala	Met	Thr	Leu	Ile	Val	Pro	Gly	Asn
			210			215						220			
Leu	Pro	Ile	Gly	Cys	Ser	Ala	Ala	Leu	Leu	Glu	Arg	Phe	Asn	Asp	Asn
225					230					235					240
Ser	Gly	Trp	Leu	Tyr	Asp	Ser	Arg	Asn	Gln	Cys	Tyr	Met	Pro	Leu	Asn
				245					250					255	
Asn	Leu	Ala	Lys	Leu	His	Asn	Asp	Lys	Leu	Lys	Lys	Gly	Leu	Ala	Ala
			260					265						270	
Leu	Arg	Lys	Lys	Tyr	Pro	Tyr	Ala	Lys	Ile	Ile	Tyr	Ala	Asp	Tyr	Tyr
			275				280						285		
Ser	Ser	Ala	Met	Gln	Phe	Phe	Asn	Ser	Pro	Ser	Lys	Tyr	Gly	Phe	Thr
			290				295					300			
Gly	Ser	Val	Leu	Lys	Ala	Cys	Cys	Gly	Gly	Gly	Asp	Gly	Arg	Tyr	Asn
305					310					315					320
Val	Gln	Pro	Asn	Val	Arg	Cys	Gly	Glu	Lys	Gly	Ser	Thr	Thr	Cys	Glu
				325						330				335	
Asp	Pro	Ser	Thr	Tyr	Ala	Asn	Trp	Asp	Gly	Ile	His	Leu	Thr	Glu	Ala
			340					345					350		
Ala	Tyr	Arg	His	Ile	Ala	Thr	Gly	Leu	Ile	Ser	Gly	Arg	Phe	Thr	Met
			355				360						365		
Pro	Thr	Tyr	Asn												
			370												

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1499122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser Val Arg Ser Leu

1	5	10	15
Pro Met Arg	Pro Thr Leu Lys Tyr Glu Ser Ile Phe Asn Phe Gly Asp		
	20	25	30
Ser Leu Ser	Asp Thr Gly Asn Phe Leu Leu Ser Gly Asp Val Asp Ser		
	35	40	45
Pro Asn Ile	Gly Arg Leu Pro Tyr Gly Gln Thr Phe Phe Asn Arg Ser		
	50	55	60
Thr Gly Arg	Cys Ser Asp Gly Arg Leu Ile Ile Asp Phe Ile Ala Glu		
65	70	75	80
Ala Ser Gly	Leu Pro Tyr Ile Pro Pro Tyr Leu Gln Ser Leu Arg Thr		
	85	90	95
Asn Asp Ser	Val Asp Phe Lys Arg Gly Ala Asn Phe Ala Val Ala Gly		
	100	105	110
Ala Thr Ala	Asn Glu Phe Ser Phe Phe Lys Asn Arg Gly Leu Ser Val		
	115	120	125
Thr Leu Leu	Thr Asn Lys Thr Leu Asp Ile Gln Leu Asp Trp Phe Lys		
	130	135	140
Lys Leu Lys	Pro Ser Leu Cys Lys Thr Lys Pro Glu Cys Glu Arg Tyr		
145	150	155	160
Phe Arg Lys	Ser Leu Phe Leu Val Gly Glu Ile Ser Gly Asn Asp Tyr		
	165	170	175
Asn Tyr Pro	Leu Leu Ala Phe Arg Ser Phe Lys His Ala Met Asp Leu		
	180	185	190
Val Pro Phe	Val Ile Asn Lys Ile Met Asp Val Thr Ser Ala Leu Ile		
	195	200	205
Glu Glu Gly	Ala Met Thr Leu Ile Val Pro Gly Asn Leu Pro Ile Gly		
	210	215	220
Cys Ser Ala	Ala Leu Leu Glu Arg Phe Asn Asp Asn Ser Gly Trp Leu		
225	230	235	240
Tyr Asp Ser	Arg Asn Gln Cys Tyr Met Pro Leu Asn Asn Leu Ala Lys		
	245	250	255
Leu His Asn	Asp Lys Leu Lys Lys Gly Leu Ala Ala Leu Arg Lys Lys		
	260	265	270
Tyr Pro Tyr	Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr Ser Ser Ala Met		
	275	280	285
Gln Phe Phe	Asn Ser Pro Ser Lys Tyr Gly Phe Thr Gly Ser Val Leu		
	290	295	300
Lys Ala Cys	Cys Gly Gly Gly Asp Gly Arg Tyr Asn Val Gln Pro Asn		
305	310	315	320
Val Arg Cys	Gly Glu Lys Gly Ser Thr Thr Cys Glu Asp Pro Ser Thr		
	325	330	335
Tyr Ala Asn	Trp Asp Gly Ile His Leu Thr Glu Ala Ala Tyr Arg His		
	340	345	350
Ile Ala Thr	Gly Leu Ile Ser Gly Arg Phe Thr Met Pro Thr Tyr Asn		
	355	360	365

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

ctctgcctct catctctgt tctctccgcc catctctgct ctcttttatt ttcccagaaa	60
gttttttttt tttcccgaat tccgttaatc tcattggggg ttccattgat agcaatggcg	120

acggcttttcg	ctcccactaa	gtcactgcc	acggttcctc	tgcattggatc	ccatgagaat	180
cgtctcttgc	tcccgatccg	attggctcct	ccttcttctt	tcctcggatc	caccggttcc	240
ctctcccttc	gcagactcaa	tcactccaac	gccaccgcgc	gatctcccg	cgtctctgtc	300
caggaagtgtg	tcaaggagaa	gcaatccacc	aataatacca	gcctgttgat	aaccaaagag	360
gaaggattgg	agttgtatga	agatatgata	ctaggttagat	ctttcgaaga	catgtgtgct	420
caaattgtatt	accgaggcaa	gatgttttgt	tttgttcact	tgtacaatgg	ccaagaggct	480
gtttctactg	gctttatcaa	gctccttacc	aagtctgact	ctgtcgttag	tacctaccgt	540
gacctgtgcc	atgccctcag	caaagggtgc	tctgctcgtg	ctggttatgag	cgagctcttc	600
ggcaagggtta	ctggatgctg	cagaggccaa	ggtggatcca	tgcacatggt	ctccaaagaa	660
cacaacatgc	ttggtggctt	tgcttttatt	ggtgaaggca	ttcctgtcgc	cactggtgct	720
gccttttagct	ccaagtacag	gagggaagtc	ttgaaacagg	attgtgatga	tgtcactgtc	780
gccttttttcg	gagatggaac	ttgtaacaac	ggacagttct	tcgagtgtct	caacatggct	840
gctctctata	aactgcctat	tatctttgtt	gtcgagaata	acttgtgggc	cattgggatg	900
tctcacttga	gagccacttc	tgaccccgag	atttggaaag	aaggtcctgc	atttgggatg	960
cctggtgttc	atgttgacgg	tatggatgtc	ttgaaggcca	gggaagtcgc	taaagaggct	1020
gtcactagag	ctagaagagg	agaagggtcca	accttggttg	aatgtgagac	ttatagattt	1080
agaggacact	ccttggctga	tcccgatgag	ctccgtgatg	ctgctgagaa	agccaaatac	1140
gcggtctagag	acccaatcgc	agcattgaag	aagtatttga	tagagaacaa	gcttgcaaag	1200
gaagcagagc	taaagtcaat	agagaaaaag	atagacagtt	ggtggaggaa	gcggttgagt	1260
ttgcagacgc	tatgccacag	cccgttcgca	gtcagttgct	agagaatgtg	tttgctgac	1320
caaaaggatt	tgggaattgga	cctgatggac	ggtacagatg	tgaggacccc	aagtttaccg	1380
aaggcacagc	tcaagtctga	gaagacaagt	ttaaccataa	gctgtctact	gtctcttcga	1440
tgtttctata	tatcttatta	agttaaatgc	tacagagaat	cagtttgaat	catttgcact	1500
ttttgctttt	tgtttggtgt	tactaaatta	tcacaagggt	cttctttag	ttcgttgggt	1560
tttcattggt	taccacttac	cagagaattg	tatttttttt	tttaaagata	attattttgc	1620

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1499124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

Leu	Cys	Leu	Ser	Ser	Leu	Val	Leu	Ser	Ala	His	Leu	Cys	Ser	Leu	Leu
1				5					10					15	
Phe	Ser	Gln	Lys	Val	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu
		20						25					30		
Gly	Phe	Pro	Leu	Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu
		35					40					45			
Thr	Ala	Thr	Val	Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu
	50					55					60				
Pro	Ile	Arg	Leu	Ala	Pro	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser
65				70					75					80	
Leu	Ser	Leu	Arg	Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro
			85						90					95	
Val	Val	Ser	Val	Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn
		100						105					110		
Thr	Ser	Leu	Leu	Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp
		115				120					125				
Met	Ile	Leu	Gly	Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr
		130				135					140				
Arg	Gly	Lys	Met	Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala
145				150					155					160	
Val	Ser	Thr	Gly	Phe	Ile	Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val
			165					170						175	
Ser	Thr	Tyr	Arg	Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala

Arg	Ala	Val	Met	Ser	Glu	Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg
		195					200					205			
Gly	Gln	Gly	Gly	Ser	Met	His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu
	210					215					220				
Gly	Gly	Phe	Ala	Phe	Ile	Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala
225					230					235					240
Ala	Phe	Ser	Ser	Lys	Tyr	Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp
				245					250					255	
Asp	Val	Thr	Val	Ala	Phe	Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln
			260					265						270	
Phe	Phe	Glu	Cys	Leu	Asn	Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile
		275					280					285			
Phe	Val	Val	Glu	Asn	Asn	Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg
	290					295					300				
Ala	Thr	Ser	Asp	Pro	Glu	Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met
305					310					315					320
Pro	Gly	Val	His	Val	Asp	Gly	Met	Asp	Val	Leu	Lys	Val	Arg	Glu	Val
				325					330					335	
Ala	Lys	Glu	Ala	Val	Thr	Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu
			340					345					350		
Val	Glu	Cys	Glu	Thr	Tyr	Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro
		355					360					365			
Asp	Glu	Leu	Arg	Asp	Ala	Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp
	370					375					380				
Pro	Ile	Ala	Ala	Leu	Lys	Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys
385					390					395					400
Glu	Ala	Glu	Leu	Lys	Ser	Ile	Glu	Lys	Lys	Ile	Asp	Ser	Trp	Trp	Arg
				405					410					415	
Lys	Arg	Leu	Ser	Leu	Gln	Thr	Leu	Val	His	Ser	Pro	Val	Ala	Val	Ser
			420				425						430		

Cys

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1499125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val	Pro	Leu
1			5						10					15	
His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu	Ala	Pro
			20					25					30		
Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg	Arg	Leu
		35					40					45			
Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val	Gln	Glu
		50				55					60				
Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	Ile	Thr
65					70				75					80	
Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	Arg	Ser
			85					90					95		
Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	Phe	Gly
			100					105					110		
Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	Phe	Ile
			115				120						125		

Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	Ser	Thr	Tyr	Arg	Asp	His
130					135					140					
Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala	Arg	Ala	Val	Met	Ser	Glu
145					150					155					160
Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg	Gly	Gln	Gly	Gly	Ser	Met
				165					170					175	
His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu	Gly	Gly	Phe	Ala	Phe	Ile
				180				185					190		
Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala	Ala	Phe	Ser	Ser	Lys	Tyr
				195			200					205			
Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp	Asp	Val	Thr	Val	Ala	Phe
				210		215					220				
Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln	Phe	Phe	Glu	Cys	Leu	Asn
225					230					235					240
Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile	Phe	Val	Val	Glu	Asn	Asn
				245					250					255	
Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg	Ala	Thr	Ser	Asp	Pro	Glu
				260				265					270		
Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met	Pro	Gly	Val	His	Val	Asp
				275			280					285			
Gly	Met	Asp	Val	Leu	Lys	Val	Arg	Glu	Val	Ala	Lys	Glu	Ala	Val	Thr
				290		295				300					
Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu	Val	Glu	Cys	Glu	Thr	Tyr
305					310					315					320
Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro	Asp	Glu	Leu	Arg	Asp	Ala
				325					330					335	
Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp	Pro	Ile	Ala	Ala	Leu	Lys
				340			345					350			
Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys	Glu	Ala	Glu	Leu	Lys	Ser
				355			360					365			
Ile	Glu	Lys	Lys	Ile	Asp	Ser	Trp	Trp	Arg	Lys	Arg	Leu	Ser	Leu	Gln
				370		375					380				
Thr	Leu	Val	His	Ser	Pro	Val	Ala	Val	Ser	Cys					
385				390						395					

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

Met	Ile	Leu	Gly	Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr
1				5					10					15	
Arg	Gly	Lys	Met	Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala
				20			25					30			
Val	Ser	Thr	Gly	Phe	Ile	Lys	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	
				35		40					45				
Ser	Thr	Tyr	Arg	Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala
				50		55					60				
Arg	Ala	Val	Met	Ser	Glu	Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg
65					70				75						80
Gly	Gln	Gly	Gly	Ser	Met	His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu
				85					90				95		
Gly	Gly	Phe	Ala	Phe	Ile	Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala
				100			105					110			
Ala	Phe	Ser	Ser	Lys	Tyr	Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp

115	120	125
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln		
130	135	140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile		
145	150	155
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg		
165	170	175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met		
180	185	190
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val		
195	200	205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu		
210	215	220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro		
225	230	235
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp		
245	250	255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys		
260	265	270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Ser Trp Trp Arg		
275	280	285
Lys Arg Leu Ser Leu Gln Thr Leu Val His Ser Pro Val Ala Val Ser		
290	295	300

Cys  
305

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

aaacacatga cccctaaatc gagaggcttc gttaggagaa ggagaagcag aagagtgttg	60
gttctcgatt gtcgatctca acaatggcgt agtctcccca aaatgcgtca acctcgagct	120
tctcctgccg cgtatgttaa gtaggtcttg atcattgtga ttggaggttg caggtccaag	180
aatatcgaga cttggggaga gatttatgat cttaaagacca atacttgggg gcgaatactg	240
ctccaatcac atgatccac agttcaaaat gcttacttga atcgctttaa acctaaactg	300
cagacgaatg cttgctatgt agagattgac aaggtgtcgt gcctgatatt tttatccgat	360
gggaagctat tttggcgtga aacaaagcaa ggttttgaga ggtgtagtgt tatattggga	420
gatgatgagc aagtgtcctc ttatcaactt gtttcgggtg caaacgccgc cggaggagga	480
agagtgcacg tttgggtgaa gtcgggggta aaagtctctg atctcttaag tggcactgag	540
acttgggaat gttacacaaa tagtcggtgt gcagagattt cgtttgagag aagagggtta	600
agagagcttt ggggattcgt tgaatggtct agagaggtgt ttaccgttga tggatatgac	660
gatacttacg atttcttttt aaattctgct attgtgacct attgatcagt gggactttat	720
cttacttgta ctgtgggaat tttgagtatg attttaatag ataaataaat gtgatttgct	780
aacaacatta caacatagat ctaagcattc aaggttggtg tgggtgcctga tggcctttga	840
tgaaggggag gttttctact ttgtatcaga cttttgcttg ctagtgaaag agagaataat	900
gggcacaaca tttttgttac tccatgggaa agataatgta gagtggctctc aaggaaaaaa	960
tgggtgtggg agtgggtcaag ggacttggat tgccaaacat tgtgtttcag tttgggtggg	1020
tacaatgttg gatcaccctt atggtcgtaa agtgcagatt tcgcagagct ttccaagggg	1080
atcatagaat cgtcaacgga gttgtgtttc gaaccaaagg atgtatatat cgttccactt	1140
tcttcttgca ctctgctaca gtaacacatg gatttgtatg ctctcatggg agtgtacaaa	1200
ctcctagtga ttgggtgttt ttttgcct ttggaatgct taaagaatga tat	

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..234  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499128  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:  
Lys His Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser  
1                  5                  10                  15  
Arg Arg Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu  
                  20                  25                  30  
Pro Lys Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp  
                  35                  40                  45  
Gly Leu Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr  
50                  55                  60  
Trp Gly Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu  
65                  70                  75                  80  
Leu Gln Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe  
                  85                  90                  95  
Lys Pro Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val  
                  100                  105                  110  
Ser Cys Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr  
                  115                  120                  125  
Lys Gln Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln  
130                  135                  140  
Val Ser Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly  
145                  150                  155                  160  
Arg Val Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu  
                  165                  170                  175  
Ser Gly Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu  
                  180                  185                  190  
Ile Ser Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu  
195                  200                  205  
Trp Ser Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp  
210                  215                  220  
Phe Phe Leu Asn Ser Ala Ile Val Thr Tyr  
225                  230  
(2) INFORMATION FOR SEQ ID NO:884:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 232 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..232  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499129  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:  
Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser Arg Arg  
1                  5                  10                  15  
Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu Pro Lys  
                  20                  25                  30  
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu  
35                  40                  45  
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly  
50                  55                  60  
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln  
65                  70                  75                  80



Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro  
85 90 95  
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys  
100 105 110  
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln  
115 120 125  
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser  
130 135 140  
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val  
145 150 155 160  
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly  
165 170 175  
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser  
180 185 190  
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser  
195 200 205  
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe  
210 215 220  
Leu Asn Ser Ala Ile Val Thr Tyr  
225 230

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu  
1 5 10 15  
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly  
20 25 30  
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln  
35 40 45  
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro  
50 55 60  
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys  
65 70 75 80  
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln  
85 90 95  
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser  
100 105 110  
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val  
115 120 125  
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly  
130 135 140  
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser  
145 150 155 160  
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser  
165 170 175  
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe  
180 185 190  
Leu Asn Ser Ala Ile Val Thr Tyr  
195 200

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1636  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499135  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```
ggagagtaac atcgagacaa agaagaaaag ctaaaaaaga gaaccccaaa gaatcgaata      60
tttattatatt cgccccgaag attctatttc tgatcattta caccctataa aagagtagag      120
ctttcgtgaa gccaccatgt gtggaggagc tataatctcc gatttcatac ctccgccgag      180
gtccctccgc gtcactaacg agtttatctg gccggatctg aaaaacaaag tgaaagcttc      240
aaagaagaga tcgaataagc gatccgattt cttcgatctt gacgatgatt tcgaagctga      300
tttccaaggg tttaaggatg actcggcttt tgactgcgaa gacgatgatg atgtcttcgt      360
caatgttaag cttttcgtct tcaccgcaac tactaagccc gtagcttccg ctttcgtctc      420
cactgggtata tatttggtag gttcagcata tgccaagaaa actgtagagt ccgctgagca      480
agctgagaaa tcttctaaga ggaagaggaa gaatcagtac cgagggatta ggcagcgtcc      540
ttggggaaaa tgggctgcgg agatccgtga tccgagaaaa ggctcccagag aatggcttgg      600
aacattcgac actgctgagg aagcagcaag agcttatgat gctgcagcac gcagaatccg      660
tggcacgaaa gctaagtgta attttccgga ggagaagaac cctagcgtcg tatcccagaa      720
acgtcttagt gctaagacta ataactctca gaaatcagtg gctaaaccaa acaaaagcgt      780
aactttgggt cagcagccaa cacatctgag tcagcagtac tgcaacaact cttttgacaa      840
ctcttttggt gatatgagtt tcatggaaga gaagcctcag atgtacaaca atcagtttgg      900
gttaacaaac tcgttcgatg ctggaggtaa caatggatac cagtatttca gttccgatca      960
gggcagtaac tccttcgact gttctgagtt cgggtggagt gatcacggcc ctaaaacacc     1020
cgagatctct tcaatgcttg tcaataacaa cgaagcatca tttgttgaag aaaccaatgc     1080
agccaagaag ctcaaaccta actctgatga gtcagacgat ctgatggcat accttgacaa     1140
cgcttgtggt gacacccac tagaagtga agccatgctt ggcgcagatg ctggtgctgt     1200
gactcaggaa gaggaaaacc cagtggagct atggagctta gatgagatca atttcatgct     1260
ggaaggagac ttttgaagtg atcgatgggt ccttagtttg taaataaagc tgtgttggat     1320
tttgctgttg ggggatggt caagtcacac ctcaagctct atgcattggt atctcatgag     1380
cctctcttcc atagagagtt tctcttttaa ttttgctgaa ataaaaaagg tgtgatgaag     1440
taaatagagg tataataata tctatctatt aagtcttgtt ttgttcttcc atttttgtat     1500
ttcttttcta tttaaaagac agtttattag tcttctgagc tctctttttg atctttgtta     1560
tagcgtatca tcaccctcga aagtgaatg ttttgtacc ccaaacttgt ttagcattat     1620
aataaagtct ctttgg
```

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 379 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..379  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499136  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

```
Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Arg Ser
1          5          10          15
Leu Arg Val Thr Asn Glu Phe Ile Trp Pro Asp Leu Lys Asn Lys Val
20          25          30
Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu
35          40          45
Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
50          55          60
Phe Asp Cys Glu Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe
65          70          75          80
Val Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr
85          90          95
```

Gly Ile Tyr Leu Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser  
100 105 110  
Ala Glu Gln Ala Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr  
115 120 125  
Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg  
130 135 140  
Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala  
145 150 155 160  
Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Arg Arg Ile Arg Gly  
165 170 175  
Thr Lys Ala Lys Val Asn Phe Pro Glu Lys Asn Pro Ser Val Val  
180 185 190  
Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val  
195 200 205  
Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu  
210 215 220  
Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met  
225 230 235 240  
Ser Phe Met Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu  
245 250 255  
Thr Asn Ser Phe Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser  
260 265 270  
Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser  
275 280 285  
Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn  
290 295 300  
Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Lys Lys Leu Lys  
305 310 315 320  
Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala  
325 330 335  
Leu Trp Asp Thr Pro Leu Glu Val Lys Ala Met Leu Gly Ala Asp Ala  
340 345 350  
Gly Ala Val Thr Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu  
355 360 365  
Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe  
370 375

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..907
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

ctatctttgt cgccgccaaa cctctctcag attcttcttc ttctctgcag atcgattttt	60
ttttgaagct aaatctcaaa aatggagAAC gacgcaggtc aggtcacaga gctctacatt	120
tttgagattt agcttcaaaa acaaatccca aagcttcaga ggaagaagaa gaagagagt	180
agaaacaatg gcgtcgacga ctctctcaat cgcaacaaca atccgttcct cttctcctct	240
cacttccgct tccactcatc acttcctttc caaaccacc gcaatcgaat tcccatttcg	300
tctcagctct tcttctagcc accgtgcaat caacctccgt cctatctccg ccgtcgaagc	360
tccggagaaa atcgagaaga tcggatccga aatctcatcc ctaaccctcg aagaagctcg	420
tatcctcgtc gactatctcc aagacaaaatt cgggtgtctcc ccactctctt tagccccgc	480
agcagcggcg gttgctgctc cagccgacg tggcgcgggc gctgtagtgg aggagcaaac	540
agagtgcgat gtggttatca atgaagtcc cagcagttcc cgtattgcag tgattaaagc	600
tgtagggct ttaactagct tggcgttgaa ggaagctaag gagctaatac aaggattacc	660
aaagaagttt aaagaagata tcaactaaaga tgaagctgaa gaagctaaga agactcttga	720
agaagctggg gctaaagtct ccattgctta agtttcttca acaatcggaa aaaaaaaat	780

gtgatctttt cggaatttat gaggcttttt gttgttttagt atagtttggt tttgagttgt 840  
tgattcagct tttgagaaat tggtgtactt tgaatcaatt tggtttcgta ttacagtttt 900  
agtcttc

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser  
1 5 10 15  
Pro Leu Thr Ser Ala Ser Thr His His Phe Leu Ser Lys Pro Thr Ala  
20 25 30  
Ile Glu Phe Pro Phe Arg Leu Ser Ser Ser Ser His Arg Ala Ile  
35 40 45  
Asn Leu Arg Pro Ile Ser Ala Val Glu Ala Pro Glu Lys Ile Glu Lys  
50 55 60  
Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu Ala Arg Ile Leu  
65 70 75 80  
Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro Leu Ser Leu Ala  
85 90 95  
Pro Ala Ala Ala Val Ala Ala Pro Ala Asp Gly Gly Ala Ala Ala  
100 105 110  
Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile Asn Glu Val Pro  
115 120 125  
Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg Ala Leu Thr Ser  
130 135 140  
Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly Leu Pro Lys Lys  
145 150 155 160  
Phe Lys Glu Asp Ile Thr Lys Asp Glu Ala Glu Glu Ala Lys Lys Thr  
165 170 175  
Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala  
180 185

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..674
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

acataactcc aatgtcccag ttctgcaaac gcttagcctc aaaagggtctt aagctcactc 60  
tggtcctcgt ctccgacaaa cctctcctc catacaaaac agagcacgac tcaatcactg 120  
tcttccccat ctccaacggc ttccaagaac gcgaggaacc attacaagac ctcgatgatt 180  
acatggaaag agtagaacc agcatcaaaa acaccttacc gaagttgggt gaagacatga 240  
aactgtcggg aaatccacct agggctatcg tgtacgactc caccatgcca tggcttcttg 300  
atgtagctca tagttatgga ttgagcgggt cggtgtttt cacgcaacct tggcttgta 360  
cagctatatta ctaccatggt ttcaagggtt cggtctctgt accatctaca aagtacggtc 420  
actcgacatt agcatctttc ccttcgttcc cgatgctgac tgcaaatgat ttgccgtctt 480  
tcctctgcga atcgtcctca taccggaata tactgaggat tgtgggtggat cagctctcaa 540  
acattgatcg agtcgacata gtgtgtgcaa cactttcgat aaattggagg aaaagtgttg 600

aaatgggtca aagcttgtgg ccagctctgaa tatkgaccaa cggttccatc gatgtattag 660  
acaacgactg tctg

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Ile	Thr	Pro	Met	Ser	Gln	Phe	Cys	Lys	Arg	Leu	Ala	Ser	Lys	Gly	Leu
1				5				10						15	
Lys	Leu	Thr	Leu	Val	Leu	Val	Ser	Asp	Lys	Pro	Ser	Pro	Pro	Tyr	Lys
			20					25					30		
Thr	Glu	His	Asp	Ser	Ile	Thr	Val	Phe	Pro	Ile	Ser	Asn	Gly	Phe	Gln
		35					40					45			
Glu	Arg	Glu	Glu	Pro	Leu	Gln	Asp	Leu	Asp	Asp	Tyr	Met	Glu	Arg	Val
		50				55					60				
Glu	Thr	Ser	Ile	Lys	Asn	Thr	Leu	Pro	Lys	Leu	Val	Glu	Asp	Met	Lys
65					70					75				80	
Leu	Ser	Gly	Asn	Pro	Pro	Arg	Ala	Ile	Val	Tyr	Asp	Ser	Thr	Met	Pro
				85					90					95	
Trp	Leu	Leu	Asp	Val	Ala	His	Ser	Tyr	Gly	Leu	Ser	Gly	Ala	Val	Phe
			100					105					110		
Phe	Thr	Gln	Pro	Trp	Leu	Val	Thr	Ala	Ile	Tyr	Tyr	His	Val	Phe	Lys
		115					120					125			
Gly	Ser	Phe	Ser	Val	Pro	Ser	Thr	Lys	Tyr	Gly	His	Ser	Thr	Leu	Ala
		130				135					140				
Ser	Phe	Pro	Ser	Phe	Pro	Met	Leu	Thr	Ala	Asn	Asp	Leu	Pro	Ser	Phe
145					150					155				160	
Leu	Cys	Glu	Ser	Ser	Ser	Tyr	Pro	Asn	Ile	Leu	Arg	Ile	Val	Val	Asp
				165					170					175	
Gln	Leu	Ser	Asn	Ile	Asp	Arg	Val	Asp	Ile	Val	Cys	Ala	Thr	Leu	Ser
			180					185					190		
Ile	Asn	Trp	Arg	Lys	Ser	Val	Glu	Met	Gly	Gln	Ser	Leu	Trp	Pro	Val
		195					200						205		

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met	Ser	Gln	Phe	Cys	Lys	Arg	Leu	Ala	Ser	Lys	Gly	Leu	Lys	Leu	Thr
1				5				10						15	
Leu	Val	Leu	Val	Ser	Asp	Lys	Pro	Ser	Pro	Pro	Tyr	Lys	Thr	Glu	His
			20					25					30		
Asp	Ser	Ile	Thr	Val	Phe	Pro	Ile	Ser	Asn	Gly	Phe	Gln	Glu	Arg	Glu
		35				40					45				
Glu	Pro	Leu	Gln	Asp	Leu	Asp	Asp	Tyr	Met	Glu	Arg	Val	Glu	Thr	Ser

50	55	60
Ile Lys Asn Thr Leu	Pro Lys Leu Val Glu	Asp Met Lys Leu Ser Gly
65	70	75
Asn Pro Pro Arg Ala	Ile Val Tyr Asp Ser	Thr Met Pro Trp Leu Leu
85	90	95
Asp Val Ala His Ser	Tyr Gly Leu Ser Gly	Ala Val Phe Phe Thr Gln
100	105	110
Pro Trp Leu Val Thr	Ala Ile Tyr Tyr His	Val Phe Lys Gly Ser Phe
115	120	125
Ser Val Pro Ser Thr	Lys Tyr Gly His Ser	Thr Leu Ala Ser Phe Pro
130	135	140
Ser Phe Pro Met Leu	Thr Ala Asn Asp Leu	Pro Ser Phe Leu Cys Glu
145	150	155
Ser Ser Ser Tyr Pro	Asn Ile Leu Arg Ile	Val Val Asp Gln Leu Ser
165	170	175
Asn Ile Asp Arg Val	Asp Ile Val Cys Ala	Thr Leu Ser Ile Asn Trp
180	185	190
Arg Lys Ser Val Glu	Met Gly Gln Ser Leu	Trp Pro Val
195	200	205

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1499150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

Met Glu Arg Val Glu Thr Ser Ile Lys Asn Thr Leu Pro Lys Leu Val	
1	15
Glu Asp Met Lys Leu Ser Gly Asn Pro Pro Arg Ala Ile Val Tyr Asp	
20	30
Ser Thr Met Pro Trp Leu Leu Asp Val Ala His Ser Tyr Gly Leu Ser	
35	45
Gly Ala Val Phe Phe Thr Gln Pro Trp Leu Val Thr Ala Ile Tyr Tyr	
50	60
His Val Phe Lys Gly Ser Phe Ser Val Pro Ser Thr Lys Tyr Gly His	
65	80
Ser Thr Leu Ala Ser Phe Pro Ser Phe Pro Met Leu Thr Ala Asn Asp	
85	95
Leu Pro Ser Phe Leu Cys Glu Ser Ser Ser Tyr Pro Asn Ile Leu Arg	
100	110
Ile Val Val Asp Gln Leu Ser Asn Ile Asp Arg Val Asp Ile Val Cys	
115	125
Ala Thr Leu Ser Ile Asn Trp Arg Lys Ser Val Glu Met Gly Gln Ser	
130	140
Leu Trp Pro Val	
145	

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1689

(D) OTHER INFORMATION: / Ceres Seq. ID 1499159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

```
accgactctc tctctctctc tctccgtaac aaaaaaatca ccaatggcaa aacaatatct 60
ctttgtactc ctctcaatct cctatctctt atcactggag ctacacggcg ccaccgcagc 120
ctcacagacc ggagcttcca aaaaagccat aaacttcac caatcttctt aaaaaaccac 180
cacataccct gccttatgtg tccactcact ctccgtctac gcaaacgaca tccaaacaag 240
ccctaaacgt ttagctgaga ccgctatagc cgtgacacta agccgagccc aatccacgaa 300
gctcttcgtc tcgctcttaa cacgtatgaa gggctcttaag aagcgcgagg tcgaagccat 360
caaagattgc gtcgaggaga tgaacgatac cgttgaccgt ttgaccaa atctgttcaaga 420
actgaagttg tgtgggagtg tcaaacagaa gaaagagtcg agttctgaag agtcgggatc 480
ggaggaagag tgaacagaa atgagatttt acattgataa aaaaaacaaa aaatacaata 540
cttttgtcct aatcttgacg gaaacttttt tttttgctgc ggaacatttc ctttatttta 600
atataatggt atgtgaaaat gaattcatct aaagacaaac tgaaaaacat gaaacaagac 660
tctctttttg tagcagatag agagagacac agagagaaaa agagatggca aacgaaacgg 720
ctagtaaaagt agcgggttac ttatctaacc aagactcaag acaccaaaac agacatgttt 780
gcatctaaga tatgcttatt tgttgacaga ttaataatac tcagggtagt ggcactgggtg 840
gaacttgccc gttgcttctc gtgccagctc caatggctcg ggttggcgct tcaaattccgg 900
ggtttgggac aagcgtatca tcgccaccag ggagttgggt gtgaggtccg gcccttctgc 960
caccattata tgatgggatt cccccaccag taagtggagc tccggtgaca ggattgtaag 1020
ggtagaacgg cttcttgcac ttgggaggaa gcaagaacct tccaacaccg ggaatgagaa 1080
tagttggttt gggctcaatg gttacaagaa agtcagggtg tttgacatca gtggtcttag 1140
gggacttggg aacgtgacgt agtcactca cttgctctac agatccaagc actaggctta 1200
aaaccacgac aatgactgcg gaggtgataa gtgaagaagc cattaatttt attttatttt 1260
gttgtagagg agaaagctcg tgtgtttgtt tgaccaaatc tgttcaagaa ctgaagttgt 1320
gtgggagtg caaagatcaa gaccagtttg cgtaccacat tagtaatgct cagacttgga 1380
ctagtgcggc tttgactgac gagaacactt gctccgatgg gttctcgggt cgggttatgg 1440
atgggaggat caagaactcg gttcgggcta gaatcatgaa cgtgggacat gaaaccagca 1500
acgctttgtc cttgattaat gcctttgcta aaacttacta atttaaaact atattttgtc 1560
ctgtaaaata tatatataga taaatgtaat gtcttgctaa gagtttgatg tgatatattt 1620
ttttcgattt tggtagtttc tttttgtttt gtaacgtggg ttataatagt ataatgtgta 1680
ttttgagct
```

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1499160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```
Thr Asp Ser Leu Ser Leu Ser Leu Arg Asn Lys Lys Ile Thr Asn Gly
1          5          10          15
Lys Thr Ile Ser Leu Cys Thr Pro Leu Asn Leu Leu Ser Leu Ile Thr
          20          25          30
Gly Ala His Gly Gly His Arg Ser Leu Thr Asp Arg Ser Phe Gln Lys
          35          40          45
Ser His Lys Leu His Pro Ile Phe Leu Lys Asn His His Ile Pro Cys
          50          55          60
Leu Met Cys Pro Leu Thr Leu Arg Leu Arg Lys Arg His Pro Asn Lys
65          70          75          80
Pro
```

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..72  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499161  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:  
Met Phe Ala Ser Lys Ile Cys Leu Phe Val Asp Arg Leu Ile Ile Leu  
1                    5                    10                    15  
Arg Val Val Ala Leu Val Glu Leu Gly Arg Cys Phe Leu Cys Gln Leu  
                    20                    25                    30  
Gln Trp Ser Gly Leu Ala Leu Gln Ile Arg Gly Leu Gly Gln Ala Tyr  
                    35                    40                    45  
His Arg His Gln Gly Val Gly Cys Glu Val Arg Pro Leu Val His His  
50                    55                    60  
Tyr Met Met Gly Phe Pro His Gln  
65                    70

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

Met Thr Ala Glu Val Ile Ser Glu Glu Ala Ile Asn Phe Ile Leu Phe  
1                    5                    10                    15  
Cys Cys Arg Gly Glu Ser Ser Cys Val Cys Leu Thr Lys Ser Val Gln  
                    20                    25                    30  
Glu Leu Lys Leu Cys Gly Ser Ala Lys Asp Gln Asp Gln Phe Ala Tyr  
                    35                    40                    45  
His Ile Ser Asn Ala Gln Thr Trp Thr Ser Ala Ala Leu Thr Asp Glu  
50                    55                    60  
Asn Thr Cys Ser Asp Gly Phe Ser Gly Arg Val Met Asp Gly Arg Ile  
65                    70                    75                    80  
Lys Asn Ser Val Arg Ala Arg Ile Met Asn Val Gly His Glu Thr Ser  
                    85                    90                    95  
Asn Ala Leu Ser Leu Ile Asn Ala Phe Ala Lys Thr Tyr  
100                    105

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

gattttcact ttcaaaattc gttccgcttt ttcttttttc ggagaaagat tcaatctttc	60
tgaatcatgt actgaaatat catcattcaa acgaacagtg ttctccattt tgtcgggaat	120
cagagtttct gcttctctgt aaaaccaaag ctttctcttt tataattttc taatggcgctc	180
aagagaagta tcaacgatga taagaaaagg gtttatctct gatcattctc tctctttctc	240
tcctttaaga accacgtctg tctccaaacc cttgtccccc atagcctctc ctcttctcc	300
gtacgattcc actagcctct ggcaagaagc tgaatttggt gggcatagat gggtagagag	360
tgaccatgga tgtgcacaag aggcttttga agagagaatg gagtctctca ttctaaaaat	420



ggtggagata agtgagtgcg atgtgtacgt agagactgtg gtgttgatgt attgagatga 480  
tcttaacaac aagttagtgt gtgaaactgt catcaaatc ttggctttcc ttaaggtttc 540  
ttcagctata atgcttgacg agggaataaa gtattaccta ctatggccgg gtcagaagga 600  
gctagcaatc cccattccaa gattccagct atgtacagac acaaaatatg caagatcact 660  
gcaagaaatc tatctttttg gtaaagggaag gatcttgggtg aatagggaga ctcggttttc 720  
ggtgaattga tacagtgact actctacttt gcaactgcaa actaataatg aaacagagag 780  
aactcaacat ggtcctattc acttccgtgc tccttccaaa atcttctggc gtaccgttcg 840  
cggtatgatt ccacacaaga cgaagcgtgg agctgctgca ctacgacgtt tgaaggata 900  
tgaagggtgtt cctactccat atgacaagat caagaggatg gtcacccctg atgctctcaa 960  
ggtgttgagg cttcaagctg gtcacaaata ctgtctgttg ggccgtcttt cttctgaagt 1020  
tgggtggaac cattacgaca ccatcaagga gctggagaca aagaggaagg agagagccca 1080  
cgtggtttac gagcgaaaga agcaacttaa caaacttaga gttaaggccg agaaggctcg 1140  
tgaagagaag ctccggagcac agctcgatat tcttgcgcca gttaagtact gagcttgta 1200  
gtagtagttt tttttttttt ggtaaggagc ttgtcagtag tagtttgtct ttgcatgttt 1260  
tgagccaacc caataccttt ttacttttta tcttttactt aggtcttgta tcgaaatttg 1320  
tactcctaac atttttattct tgagttttat ttattatatt gcgtggc

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1499164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

Met Ala Ser Arg Glu Val Ser Thr Met Ile Arg Lys Gly Phe Ile Ser  
1 5 10 15  
Asp His Ser Leu Ser Phe Ser Pro Leu Arg Thr Thr Ser Val Ser Lys  
20 25 30  
Pro Leu Ser Pro Ile Ala Ser Pro Pro Ser Pro Tyr Asp Ser Thr Ser  
35 40 45  
Leu Trp Gln Glu Ala Glu Phe Gly Gly His Arg Trp Val Gln Ser Asp  
50 55 60  
His Gly Cys Ala Gln Glu Ala Phe Glu Glu Arg Met Glu Ser Leu Ile  
65 70 75 80  
Leu Lys Met Val Glu Ile Ser Glu Cys Asp Val Tyr Val Glu Thr Val  
85 90 95  
Val Leu Met Tyr  
100

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1499165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met Ile Arg Lys Gly Phe Ile Ser Asp His Ser Leu Ser Phe Ser Pro  
1 5 10 15  
Leu Arg Thr Thr Ser Val Ser Lys Pro Leu Ser Pro Ile Ala Ser Pro  
20 25 30  
Pro Ser Pro Tyr Asp Ser Thr Ser Leu Trp Gln Glu Ala Glu Phe Gly  
35 40 45  
Gly His Arg Trp Val Gln Ser Asp His Gly Cys Ala Gln Glu Ala Phe

50 55 60  
Glu Glu Arg Met Glu Ser Leu Ile Leu Lys Met Val Glu Ile Ser Glu  
65 70 75 80  
Cys Asp Val Tyr Val Glu Thr Val Val Leu Met Tyr  
85 90

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..115  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

Met Ile Pro His Lys Thr Lys Arg Gly Ala Ala Ala Leu Ala Arg Leu  
1 5 10 15  
Lys Val Tyr Glu Gly Val Pro Thr Pro Tyr Asp Lys Ile Lys Arg Met  
20 25 30  
Val Ile Pro Asp Ala Leu Lys Val Leu Arg Leu Gln Ala Gly His Lys  
35 40 45  
Tyr Cys Leu Leu Gly Arg Leu Ser Ser Glu Val Gly Trp Asn His Tyr  
50 55 60  
Asp Thr Ile Lys Glu Leu Glu Thr Lys Arg Lys Glu Arg Ala His Val  
65 70 75 80  
Val Tyr Glu Arg Lys Lys Gln Leu Asn Lys Leu Arg Val Lys Ala Glu  
85 90 95  
Lys Val Ala Glu Glu Lys Leu Gly Ala Gln Leu Asp Ile Leu Ala Pro  
100 105 110  
Val Lys Tyr  
115

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1368  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

aactgataaa gtgataacgg agttggttgg aacgtgaaac gcttataaaa ataaaccggt 60  
ttaatttcac cggtttacct tccgccgtag atatcagccg caatgtacat tctcgacacc 120  
ggagctcgat tctccgccgt cagattctca ccggtattca atcctcctcc aacatctctc 180  
cgtagacgat acttcacgtg aagagctaat cttccattcc caaagcatca agctaagtat 240  
cataaagagc ttgaggtcgc cattgatgct gttgatcgag cttgtcgtct ctgtgttgat 300  
gtcaaaagat ctcttttttc ttctaaagag aagattgttg agaagaatga tcaaaactcca 360  
gttacaattg cagatttttg agttcaagct ttagtcagct tggagctttc gaaattgttt 420  
ccttcaatac cattagtggc tgaggaagac tctcattttg tgcgtgctaa taaccttgta 480  
agctctgtgg taagtgaagt caaatcaaaa gcaagcattg gagacaatca cttgtctgat 540  
gctgatgtac ttgaagcaat tgatagaggt ggcaagatg cttacacggt ttgcaacaaa 600  
ccagctactt attgggtttt ggatccaatt gatggcacca ggggatttct taaaggagat 660  
gaggctttat atgtggtagg attggccctt gttgtagata atgaaattgt gctaggagtc 720  
atgggttgtc caaactggcc aggagattct tcagatggat ctactggaac cctaattgctc 780  
tcgcataatg gctgtggaac gtggaccaag aagttacaaa atgtctctgg caatgtagcc 840  
ggtgattgga taagggtgtt cgttgatgct tgtgttttaa tgaacaaaagc aagattttgt 900  
atacaagaaa gccaaacctg ggaatcactt cctctctctg gtttcttcga cgcaagtact 960

```
gtttcagagg acttaaaaca taaagagatt cttcttttgc ccacatgttg tggaagtttg 1020
tgcaagtatc tgatggtagc ttctggcaga gcatcagttt ttcttctcog agccaaaact 1080
cagagaacaa taaagtcgtg ggatcatgct gttgggatca tatgtgtaca tgaagctgga 1140
ggaaaggtaa cagattggga aggagatgaa ataaatttgg aggaagatca atcagaaagg 1200
aggctcattt ttccggcggg cggtgttgta gtaagcaacg gaagtttaca taatcagatt 1260
cttgagatga tctctttctgc ttcaccaact ctttgattta tgacactact actctctata 1320
cacttgtaaa tgtttaccgt tactatttat ttatcataat ccttttct
```

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1499186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

```
Met Tyr Ile Leu Asp Thr Gly Ala Arg Phe Ser Ala Val Arg Phe Ser
1      5      10      15
Pro Val Phe Asn Pro Pro Pro Thr Ser Leu Arg Arg Arg Tyr Phe Ile
20      25      30
Val Arg Ala Asn Leu Pro Phe Pro Lys His Gln Ala Lys Tyr His Lys
35      40      45
Glu Leu Glu Val Ala Ile Asp Ala Val Asp Arg Ala Cys Arg Leu Cys
50      55      60
Val Asp Val Lys Arg Ser Leu Phe Ser Ser Lys Glu Lys Ile Val Glu
65      70      75      80
Lys Asn Asp Gln Thr Pro Val Thr Ile Ala Asp Phe Gly Val Gln Ala
85      90      95
Leu Val Ser Leu Glu Leu Ser Lys Leu Phe Pro Ser Ile Pro Leu Val
100     105     110
Ala Glu Glu Asp Ser His Phe Val Arg Ala Asn Asn Leu Val Ser Ser
115     120     125
Val Val Ser Glu Val Lys Ser Lys Ala Ser Ile Gly Asp Asn His Leu
130     135     140
Ser Asp Ala Asp Val Leu Glu Ala Ile Asp Arg Gly Gly Lys Asp Ala
145     150     155     160
Tyr Thr Phe Cys Asn Lys Pro Ala Thr Tyr Trp Val Leu Asp Pro Ile
165     170     175
Asp Gly Thr Arg Gly Phe Leu Lys Gly Asp Glu Ala Leu Tyr Val Val
180     185     190
Gly Leu Ala Leu Val Val Asp Asn Glu Ile Val Leu Gly Val Met Gly
195     200     205
Cys Pro Asn Trp Pro Gly Asp Ser Ser Asp Gly Ser Thr Gly Thr Leu
210     215     220
Met Leu Ser His Ile Gly Cys Gly Thr Trp Thr Lys Lys Leu Gln Asn
225     230     235     240
Val Ser Gly Asn Val Ala Gly Asp Trp Ile Arg Cys Phe Val Asp Ala
245     250     255
Cys Val Leu Met Asn Lys Ala Arg Phe Cys Ile Gln Glu Ser Gln Thr
260     265     270
Trp Glu Ser Leu Pro Leu Ser Gly Phe Phe Asp Ala Ser Thr Val Ser
275     280     285
Glu Asp Leu Lys His Lys Glu Ile Leu Leu Leu Pro Thr Cys Cys Gly
290     295     300
Ser Leu Cys Lys Tyr Leu Met Val Ala Ser Gly Arg Ala Ser Val Phe
305     310     315     320
Leu Leu Arg Ala Lys Thr Gln Arg Thr Ile Lys Ser Trp Asp His Ala
325     330     335
```

Val Gly Ile Ile Cys Val His Glu Ala Gly Gly Lys Val Thr Asp Trp  
340 345 350  
Glu Gly Asp Glu Ile Asn Leu Glu Glu Asp Gln Ser Glu Arg Arg Leu  
355 360 365  
Ile Phe Pro Ala Gly Gly Val Val Val Ser Asn Gly Ser Leu His Asn  
370 375 380  
Gln Ile Leu Glu Met Ile Ser Ser Ala Ser Pro Thr Leu  
385 390 395

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1063
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

ctctttcctt ttctcacgcc gagatttctg cgactgctct agtcttacga ccttataaga	60
aacgacgcta ttttcactct gcttgagctc ttcacgtgtg cacacagcac gatcttgac	120
gtcgttttta ggcgaaaaca aaggaaaaag actgacgttt atacatacta aataccggtt	180
tggagttttg ccttttgac tcagaaaact caaaagagag agagagagag agacatttct	240
gtatcttata gggttttgtg ttgtcagaaa gaagctcaag gacaaaaaaa aaagcaatta	300
tttttagggg tcaaaagaag caaaatttgg aactttcaga agttgtgggt ggtggcttct	360
tgaacaataa agctttttct tagactcttc ttccaatttg tgactctacc tatctctctc	420
tccaggtatg gaattctctg gagacgctgg aatgatgatg gagaacaagc ggaatgtctg	480
ctctctcgga gaaagcgaca tcaaacgcca caagtctgat ctctctttca attccaagga	540
gaggaaggac aaggttggag aacgtatttc agctcttcaa caaatagttt ccccttatgg	600
aaagaccgac actgcatcag ttcttctaga cgcgatgcat tacatagagt ttcttcacga	660
acaagtgaag gtgctaagtg ctccgtatct gcaaacgata cctgatgcta cgcaggagga	720
gctggagcag tacagcctga gaaacagagg attatgtctt gttccaatgg agaatacagt	780
tggagttgct caaagcaacg gcgctgatat atgggcgccc gtgaagactc ctctatcacc	840
agctttcagt gtcacatctc aatcacccct tagatgacca attcgactaa tcacctacta	900
cgatctttgt gtttaagccta aaaaagaatg accaattggt atttttctga tgatgcctct	960
gtaacatata tagacagaga gcacatgatg ttggtttaga actgctcatg gttggcaatg	1020
attgttatta ttatttgact gcttaatgca tccccttact ttg	

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

Met Glu Phe Ser Gly Asp Ala Gly Met Met Glu Asn Lys Arg Asn	
1 5 10 15	
Val Cys Ser Leu Gly Glu Ser Ser Ile Lys Arg His Lys Ser Asp Leu	
20 25 30	
Ser Phe Asn Ser Lys Glu Arg Lys Asp Lys Val Gly Glu Arg Ile Ser	
35 40 45	
Ala Leu Gln Gln Ile Val Ser Pro Tyr Gly Lys Thr Asp Thr Ala Ser	
50 55 60	
Val Leu Leu Asp Ala Met His Tyr Ile Glu Phe Leu His Glu Gln Val	
65 70 75 80	
Lys Val Leu Ser Ala Pro Tyr Leu Gln Thr Ile Pro Asp Ala Thr Gln	

			85					90					95		
Glu	Glu	Leu	Glu	Gln	Tyr	Ser	Leu	Arg	Asn	Arg	Gly	Leu	Cys	Leu	Val
			100					105					110		
Pro	Met	Glu	Asn	Thr	Val	Gly	Val	Ala	Gln	Ser	Asn	Gly	Ala	Asp	Ile
			115					120					125		
Trp	Ala	Pro	Val	Lys	Thr	Pro	Leu	Ser	Pro	Ala	Phe	Ser	Val	Thr	Ser
			130					135					140		
Gln	Ser	Pro	Phe	Arg											
145															

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1499192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

Met	Met	Met	Glu	Asn	Lys	Arg	Asn	Val	Cys	Ser	Leu	Gly	Glu	Ser	Ser
1				5				10					15		
Ile	Lys	Arg	His	Lys	Ser	Asp	Leu	Ser	Phe	Asn	Ser	Lys	Glu	Arg	Lys
			20					25					30		
Asp	Lys	Val	Gly	Glu	Arg	Ile	Ser	Ala	Leu	Gln	Gln	Ile	Val	Ser	Pro
			35					40					45		
Tyr	Gly	Lys	Thr	Asp	Thr	Ala	Ser	Val	Leu	Leu	Asp	Ala	Met	His	Tyr
			50					55				60			
Ile	Glu	Phe	Leu	His	Glu	Gln	Val	Lys	Val	Leu	Ser	Ala	Pro	Tyr	Leu
65				70				75					80		
Gln	Thr	Ile	Pro	Asp	Ala	Thr	Gln	Glu	Glu	Leu	Glu	Gln	Tyr	Ser	Leu
				85				90					95		
Arg	Asn	Arg	Gly	Leu	Cys	Leu	Val	Pro	Met	Glu	Asn	Thr	Val	Gly	Val
			100					105					110		
Ala	Gln	Ser	Asn	Gly	Ala	Asp	Ile	Trp	Ala	Pro	Val	Lys	Thr	Pro	Leu
			115					120					125		
Ser	Pro	Ala	Phe	Ser	Val	Thr	Ser	Gln	Ser	Pro	Phe	Arg			
			130					135				140			

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1499193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

Met	Met	Glu	Asn	Lys	Arg	Asn	Val	Cys	Ser	Leu	Gly	Glu	Ser	Ser	Ile
1				5				10					15		
Lys	Arg	His	Lys	Ser	Asp	Leu	Ser	Phe	Asn	Ser	Lys	Glu	Arg	Lys	Asp
			20					25					30		
Lys	Val	Gly	Glu	Arg	Ile	Ser	Ala	Leu	Gln	Gln	Ile	Val	Ser	Pro	Tyr
			35					40					45		
Gly	Lys	Thr	Asp	Thr	Ala	Ser	Val	Leu	Leu	Asp	Ala	Met	His	Tyr	Ile
			50					55				60			
Glu	Phe	Leu	His	Glu	Gln	Val	Lys	Val	Leu	Ser	Ala	Pro	Tyr	Leu	Gln
65				70				75					80		

Thr Ile Pro Asp Ala Thr Gln Glu Glu Leu Glu Gln Tyr Ser Leu Arg  
                  85                  90                  95  
Asn Arg Gly Leu Cys Leu Val Pro Met Glu Asn Thr Val Gly Val Ala  
          100                  105                  110  
Gln Ser Asn Gly Ala Asp Ile Trp Ala Pro Val Lys Thr Pro Leu Ser  
          115                  120                  125  
Pro Ala Phe Ser Val Thr Ser Gln Ser Pro Phe Arg  
          130                  135                  140

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

gtcttttgggt	gggtcttctgt	caaagctctc	tcctttacgg	tccttttctc	cagcgcatga	60
aataataaag	gacacctgta	tttattaaaa	tcactacatt	ttccgtaaca	aaaaaaatca	120
aactttgttt	tctcaatgga	cgggtcgggga	gaatcacgac	tcgggtggtga	tgggtggtggt	180
gatggttctg	ttggagttca	gatccgacaa	acacggatgc	taccggattt	tctccagagc	240
gtgaatctca	agtatgtgaa	attaggttac	aattacttaa	tctcaaactct	cttgactctc	300
tgtttattcc	ctctcgccgt	tgttatctcc	gtcgaagcct	ctcagatgaa	cccagatgat	360
ctcaaacagc	tctggatcca	tctacaatac	aatctggtta	gtatcatcat	ctgttcagcg	420
attctagtct	tcggggttaac	ggtttatggt	acgacccgac	ctagaccctg	ttacttggtt	480
gatttctctt	gttatctccc	acctgatcat	ctcaaagctc	cttacgctcg	gttcattgaa	540
cattctagac	tcaccggaga	tttcgatgac	tctgctctcg	agtttcaacg	caagatcctt	600
gagcgttctg	gttttagggga	agacacttgt	ccctgaagct	atgcattatg	ttccaccgag	660
aatttcaatg	gctgctgcta	gagaagaagc	tgaacaagtc	atgtttggtg	ctttagataa	720
ccttttcgct	aacactaatg	tgaaaccaaa	ggatattgga	atccttggtg	tgaattgtag	780
tctctttaat	ccaactcctt	cgttatctgc	aatgattgtg	aacaagtata	agcttagagg	840
taacattaga	agctacaatc	taggcgggtat	gggttgcagc	gcgggagtta	tcgctgtgga	900
tcttgctaaa	gacatgttgt	tggtacatag	gaacacttat	gcgggtgttg	tttctactga	960
gaacattact	cagaattggg	attttggtaa	caagaaatcg	atgttgatac	cgaactgctt	1020
gtttcgagtt	ggtggctctg	cgggtttgct	atcgaacaag	tcgagggaca	agagacggtc	1080
taagtacagg	cttgtacatg	tagtcaggac	tcaccgtgga	gcagatgata	aagctttccg	1140
ttgtgtttat	caagagcagg	atgatacagg	gagaaccggg	gtttcgttgt	cgaaagatct	1200
aatggcgatt	gcaggggaaa	ctctcaaaac	caatatcact	acattgggtc	ctcttggtct	1260
accgataagt	gagcagattc	totttctttat	gactctagtt	gtgaagaagc	tctttaacgg	1320
taaagtgaag	ccgtatatcc	cggatttcaa	acttgctttc	gagcatttct	gtatccatgc	1380
tggtggaaga	gctgtgatcg	atgagttaga	gaagaatctg	cagctttcac	cagttcatgt	1440
cgaggcttcg	aggatgactc	ttcatcgatt	tggtaacaca	tcttcgagct	ccatttggtt	1500
tgaattggct	tacattgaag	cgaagggaag	gatgcgaaga	ggtaatcgtg	tttggcaaat	1560
cgcgttcgga	agtggattta	aatgtaatag	cgcgatttgg	gaagcattaa	ggcatgtgaa	1620
accttcgaac	aacagtcctt	gtgaagattg	tattgacaag	tatccggtaa	ctttaagtta	1680
ttagcttcgt	ttgaggaaact	gttattgtgt	aacttcgaga	ctaataccatg	gttggttttt	1740
ttcttagaga	agaaacctt	agatttgatc	tctgacaatg	tcaatgtgtt	tgttggtttat	1800
gtgttttggg	gagtttgtg					

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1499195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

```
Met His Tyr Val Pro Pro Arg Ile Ser Met Ala Ala Ala Arg Glu Glu
1          5          10          15
Ala Glu Gln Val Met Phe Gly Ala Leu Asp Asn Leu Phe Ala Asn Thr
20          25          30
Asn Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu
35          40          45
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys
50          55          60
Leu Arg Gly Asn Ile Arg Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser
65          70          75          80
Ala Gly Val Ile Ala Val Asp Leu Ala Lys Asp Met Leu Leu Val His
85          90          95
Arg Asn Thr Tyr Ala Val Val Val Ser Thr Glu Asn Ile Thr Gln Asn
100          105          110
Trp Tyr Phe Gly Asn Lys Lys Ser Met Leu Ile Pro Asn Cys Leu Phe
115          120          125
Arg Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Ser Arg Asp Lys
130          135          140
Arg Arg Ser Lys Tyr Arg Leu Val His Val Val Arg Thr His Arg Gly
145          150          155          160
Ala Asp Asp Lys Ala Phe Arg Cys Val Tyr Gln Glu Gln Asp Asp Thr
165          170          175
Gly Arg Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ala Ile Ala Gly
180          185          190
Glu Thr Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro
195          200          205
Ile Ser Glu Gln Ile Leu Phe Met Thr Leu Val Val Lys Lys Leu
210          215          220
Phe Asn Gly Lys Val Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe
225          230          235          240
Glu His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu Leu
245          250          255
Glu Lys Asn Leu Gln Leu Ser Pro Val His Val Glu Ala Ser Arg Met
260          265          270
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
275          280          285
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Arg Arg Gly Asn Arg Val
290          295          300
Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Ile Trp
305          310          315          320
Glu Ala Leu Arg His Val Lys Pro Ser Asn Asn Ser Pro Cys Glu Asp
325          330          335
Cys Ile Asp Lys Tyr Pro Val Thr Leu Ser Tyr
340          345
```

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1499196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

```
Met Ala Ala Ala Arg Glu Glu Ala Glu Val Met Phe Gly Ala Leu
1          5          10          15
Asp Asn Leu Phe Ala Asn Thr Asn Val Lys Pro Lys Asp Ile Gly Ile
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..327  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

Met	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Ala	Asn	Thr	Asn	Val	Lys	Pro
1				5					10					15	
Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr
			20					25					30		
Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	Asn
			35				40					45			
Ile	Arg	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Val	Ile
	50					55					60				



Ala Val Asp Leu Ala Lys Asp Met Leu Leu Val His Arg Asn Thr Tyr  
65 70 75 80  
Ala Val Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr Phe Gly  
85 90 95  
Asn Lys Lys Ser Met Leu Ile Pro Asn Cys Leu Phe Arg Val Gly Gly  
100 105 110  
Ser Ala Val Leu Leu Ser Asn Lys Ser Arg Asp Lys Arg Arg Ser Lys  
115 120 125  
Tyr Arg Leu Val His Val Val Arg Thr His Arg Gly Ala Asp Asp Lys  
130 135 140  
Ala Phe Arg Cys Val Tyr Gln Glu Gln Asp Asp Thr Gly Arg Thr Gly  
145 150 155 160  
Val Ser Leu Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Thr Leu Lys  
165 170 175  
Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser Glu Gln  
180 185 190  
Ile Leu Phe Phe Met Thr Leu Val Val Lys Lys Leu Phe Asn Gly Lys  
195 200 205  
Val Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys  
210 215 220  
Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu Leu Glu Lys Asn Leu  
225 230 235 240  
Gln Leu Ser Pro Val His Val Glu Ala Ser Arg Met Thr Leu His Arg  
245 250 255  
Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile  
260 265 270  
Glu Ala Lys Gly Arg Met Arg Arg Gly Asn Arg Val Trp Gln Ile Ala  
275 280 285  
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Ile Trp Glu Ala Leu Arg  
290 295 300  
His Val Lys Pro Ser Asn Asn Ser Pro Cys Glu Asp Cys Ile Asp Lys  
305 310 315 320  
Tyr Pro Val Thr Leu Ser Tyr  
325

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

acgtctgacg gaagtcgggt cacttcacc tgtgccgtgg ggatgttctg tcgtcacagt	60
cggtcaagag atgtatgtaa ttggtggact cctagacata agacgtttac aggtaatgac	120
tctcatcgat tgcagaactc acaaatttcg ctgcgttcgc agtatgaaaa gaggtcggtg	180
caaagcagcc gccggagttg tcgacggaaa gatttacgta atcggaggtt tcaggatgag	240
aaaaccggat gctgaatgga ttgaagtgtt tgatctaaag acacagattt gggaaatctt	300
gcctgggtccg taccctaaaa ctagtctcgt ttgctgagtt gagcgttatg tggatgatga	360
agagaagtta tacatgttgg gttctaaatt ttgtttggtt tacgaaccaa aaagaaacgg	420
tgaatgggac gcatccgtcg gagcaacccc attaaaagat ttgtgggaca agacttggtg	480
tgtggtagat gatagtgtgt atacgactga tcctcggcgt actcttgga atccaatagt	540
cgtgtatcat ccaaaggaca agacttgag acctgtgaaa ggtgaatcct tggggagttt	600
gcctagttat ttcttttcta agtctgaaaa tggcgaattt tgggtgaaaag ttggtgattt	660
tgggcagaaa caagagctat gttactggtg attgcattgg agaaaaagtt atttgggtgcg	720
taatgatcga gttggaaaaa cgtgaaggag gtgagatttg ggggaagggt gaatcactcg	780
actgtgtgtt tggatacata gacattgtgt cggttgggct ttgtcgatct ctgaccattt	840
gatgatacat gggatggtat cttgcaggta cgttgatgtg aatgagtatg acttttttgt	900

tggtcatgcc ttttcttttag cctcaagact tacttgtctt tttcatgatc tttattactc 960  
accttaacct ttgtgc

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Arg Leu Thr Glu Val Gly Ser Leu Pro Pro Val Pro Trp Gly Cys Ser  
1 5 10 15  
Val Val Thr Val Gly Gln Glu Met Tyr Val Ile Gly Gly Leu Leu Asp  
20 25 30  
Ile Arg Arg Leu Gln Val Met Thr Leu Ile Asp Cys Arg Thr His Lys  
35 40 45  
Phe Arg Ser Leu Pro Ser Met Lys Arg Gly Arg Cys Lys Ala Ala Ala  
50 55 60  
Gly Val Val Asp Gly Lys Ile Tyr Val Ile Gly Gly Phe Arg Met Arg  
65 70 75 80  
Lys Pro Asp Ala Glu Trp Ile Glu Val Phe Asp Leu Lys Thr Gln Ile  
85 90 95  
Trp Glu Ser Leu Pro Gly Pro Tyr Pro Lys Thr Ser Ser Cys Cys Glu  
100 105 110  
Leu Asp Ala Tyr Val Val Met Glu Lys Leu Tyr Met Leu Gly Ser  
115 120 125  
Lys Phe Cys Leu Val Tyr Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala  
130 135 140  
Ser Val Gly Ala Thr Pro Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys  
145 150 155 160  
Val Val Asp Asp Met Leu Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly  
165 170 175  
His Pro Ile Val Val Tyr His Pro Lys Asp Lys Thr Trp Arg Pro Val  
180 185 190  
Lys Gly Glu Ser Leu Gly Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser  
195 200 205  
Glu Asn Gly Glu Phe Trp Trp Lys Val Gly Asp Phe Gly Gln Lys Gln  
210 215 220  
Glu Leu Cys Tyr Trp  
225

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met Tyr Val Ile Gly Gly Leu Leu Asp Ile Arg Arg Leu Gln Val Met  
1 5 10 15  
Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser Met  
20 25 30  
Lys Arg Gly Arg Cys Lys Ala Ala Gly Val Val Asp Gly Lys Ile

(2) INFORMATION FOR SEQ ID NO:915:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1499201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1255 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1255  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

atcatcgaaa	atggcggaaa	gaggaggaga	aagcggcgca	gggcggtgac	cgtgggtgact	60
tcggacgtgg	attcggcggt	ggacgtggag	gtggccgtgg	ccgtgatcgt	gggtccaagag	120
gccgtggacg	acgtggaggc	cgtgcttcgg	aagaaacgaa	atgggttcca	gtgaccaaac	180
taggtcgtct	agtggctgac	aataaaataa	cgaagctaga	gcagatctat	ctccattctc	240
tcccagtaaa	ggagtaccaa	atcatagatc	atctggttgg	acctacgttg	aaagacgagg	300
ttatgaagat	catgcctgtt	cagaaacaaa	ccagagctgg	tcaaagaact	agattcaagg	360
cctttgttgt	tgttggtgat	ggtaatggtc	atggttggtt	gggtgtcaag	cgttctaagg	420
aagttgcaac	tgccattaga	ggagctatta	ttcttgctaa	gctttctgtt	gttcccggtga	480
ggagaggtta	ttgggggaat	aagattggga	agccacacac	tgtgccttgt	aaggttactg	540
gtaaatgtgg	ttctgttact	gtgagaatgg	ttcctgctcc	gagaggttct	ggtattgttg	600
ctgctagggt	tcctaagaag	gttcttcagt	tcgctggtat	tgatgatgtt	ttcacttctt	660
ctagaggatc	taccaaaca	ctcgaaaact	ttgttaaggc	gacattcgat	tgcttacaga	720
agacatatgg	gttcctttaca	ccagagttct	ggaaagagac	tagattctcc	agatcgccct	780
accaagagca	cactgatttc	ctgtcgacta	aggctcttca	ggccgccaaa	gttgtcaccg	840
agggtgaaga	acaagcttaa	gaccttcatg	agatgagctt	ggttttatag	gttctgggtg	900
tggcaaatat	ctttatcttt	tctggtcatg	tttcttggtt	gtcttatcag	tttttgatat	960
tggagattta	attacaagga	taatcatatt	tagttatgtt	tgggttttag	tacgaatttt	1020
ataatgagtg	tgccataatt	tacctaaaaa	agaaaaaaa	agaaaaaaag	agtgttgat	1080
gtacgtgtgt	ttgacttgga	taattagtga	cattttaagc	aaatgtgtat	ttggaaaagt	1140
gatgtcaatg	aaatatgaat	atgggtcgaa	taaagaagcg	aagatctgta	gactgttgct	1200
tctctgcac	tggtgttgta	ttcccgatca	tattgttgta	tgtttataat	ttatt	

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 285 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..285  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

His	Arg	Lys	Trp	Arg	Lys	Glu	Glu	Glu	Lys	Ala	Ala	Gln	Gly	Gly	Asp	
1			5						10						15	
Arg	Gly	Asp	Phe	Gly	Arg	Gly	Phe	Gly	Gly	Gly	Arg	Gly	Gly	Gly	Arg	
			20					25					30			
Gly	Arg	Asp	Arg	Gly	Pro	Arg	Gly	Arg	Gly	Arg	Arg	Gly	Gly	Arg	Ala	
			35				40					45				
Ser	Glu	Glu	Thr	Lys	Trp	Val	Pro	Val	Thr	Lys	Leu	Gly	Arg	Leu	Val	
			50			55					60					
Ala	Asp	Asn	Lys	Ile	Thr	Lys	Leu	Glu	Gln	Ile	Tyr	Leu	His	Ser	Leu	
65				70					75					80		
Pro	Val	Lys	Glu	Tyr	Gln	Ile	Ile	Asp	His	Leu	Val	Gly	Pro	Thr	Leu	
			85					90						95		
Lys	Asp	Glu	Val	Met	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	
			100				105						110			
Gly	Gln	Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Val	Val	Gly	Asp	Gly	Asn	
			115				120						125			
Gly	His	Val	Gly	Leu	Gly	Val	Lys	Arg	Ser	Lys	Glu	Val	Ala	Thr	Ala	
			130			135					140					
Ile	Arg	Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Val	Val	Pro	Val	Arg	
145				150					155						160	

Arg Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys  
165 170 175  
Lys Val Thr Gly Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala  
180 185 190  
Pro Arg Gly Ser Gly Ile Val Ala Ala Arg Val Pro Lys Lys Val Leu  
195 200 205  
Gln Phe Ala Gly Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr  
210 215 220  
Lys Thr Leu Gly Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys  
225 230 235 240  
Thr Tyr Gly Phe Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser  
245 250 255  
Arg Ser Pro Tyr Gln Glu His Thr Asp Phe Leu Ser Thr Lys Ala Leu  
260 265 270  
Gln Ala Ala Lys Val Val Thr Glu Gly Glu Glu Gln Ala  
275 280 285

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1499208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

Met Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr  
1 5 10 15  
Arg Phe Lys Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly  
20 25 30  
Leu Gly Val Lys Arg Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala  
35 40 45  
Ile Ile Leu Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp  
50 55 60  
Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly  
65 70 75 80  
Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser  
85 90 95  
Gly Ile Val Ala Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly  
100 105 110  
Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly  
115 120 125  
Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe  
130 135 140  
Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr  
145 150 155 160  
Gln Glu His Thr Asp Phe Leu Ser Thr Lys Ala Leu Gln Ala Ala Lys  
165 170 175  
Val Val Thr Glu Gly Glu Glu Gln Ala  
180 185

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1499209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys  
1 5 10 15  
Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly Leu Gly Val  
20 25 30  
Lys Arg Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu  
35 40 45  
Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys  
50 55 60  
Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Lys Cys Gly  
65 70 75 80  
Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser Gly Ile Val  
85 90 95  
Ala Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly Ile Asp Asp  
100 105 110  
Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly Asn Phe Val  
115 120 125  
Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe Leu Thr Pro  
130 135 140  
Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr Gln Glu His  
145 150 155 160  
Thr Asp Phe Leu Ser Thr Lys Ala Leu Gln Ala Ala Lys Val Val Thr  
165 170 175  
Glu Gly Glu Glu Gln Ala  
180

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1170

(D) OTHER INFORMATION: / Ceres Seq. ID 1499210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

aagtgttagc tgcgtccgct gttgtttctc ctccatttct ctatctttct ctctcgctgc 60  
ttctcgaatc ttctgtatca tcttcttctt cttcaagtga aaaatggccg atggtgagga 120  
tattcagcca cttgtctgtg acaatggaac tggaaatggtg aaggctggtt ttgctggtga 180  
tgatgccccg agagcagtggt tcccaagtat tgttggtcgt acaaccggta ttgtgctcga 240  
ttctggtgat ggtgtgtctc acactgtgcc aatctacgar gggatgctc ttcctcatgc 300  
tatccttcgt cttgatcttg cgggtcggga tctcacagac tcatcatga agattctcac 360  
tgagagaggt tacatgttca ccactaccgc agaacgggaa attgtccgtg acataaagga 420  
gaaacttgck tatgtcgctc ttgactacga gcaagagcta gagacagcca agagcagttc 480  
ttcagtgag aargaactac gagcttctct atggacaagt cataaccatc ggagctgaga 540  
gatyccgttg tcttgaggtt ctgttccagc catcgctcat cggaatggaa gctcctggaa 600  
tccatgaaac aacttacaac tccatcatga aatgtgatgt cgatatcagg aaggttctct 660  
atggaaacat cgttctcaggt ggtggttcca ccatgttccc aggaattgct gaccgtatga 720  
gcaaagagat caccgctctt gcacctagca gcatgaagat caaggtggtt gcaccgccag 780  
agagaaaata cagtgtcttg atcggagat caatccttgc atccctcagc accttccaac 840  
agatgtggat ttcaaagagt gactacgat agtcagggtc atcgattgtt cacaggaaat 900  
gtttctaagt gtgtcttgtc ttatctggtt cgtggtggtg agtttggttac aaaaaaatct 960  
attttcccta gttgagatgg gaattgaact atctgttgtt atgtggattt tattttcttt 1020  
tttctcttta gaaccttatg gttgtgtcaa gaagtcttgt gtactttagt tttatatctc 1080  
tgttttatct cttctatattt ctttaggatg cttgtgatga tgctgttttt ttttgcctct 1140  
aagcaaaaaa atatcatatt atatttgccc

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499211  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:  
Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val Cys Asp Asn Gly Thr  
1 5 10 15  
Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val  
20 25 30  
Phe Pro Ser Ile Val Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly  
35 40 45  
Asp Gly Val Ser His Thr Val Pro Ile Tyr Xaa Gly Tyr Ala Leu Pro  
50 55 60  
His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ser  
65 70 75 80  
Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Met Phe Thr Thr Thr Ala  
85 90 95  
Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Val Ala  
100 105 110  
Leu Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Ser Ser Ser Ser Val  
115 120 125  
Glu Xaa Glu Leu Arg Ala Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1499212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe  
1 5 10 15  
Pro Ser Ile Val Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp  
20 25 30  
Gly Val Ser His Thr Val Pro Ile Tyr Xaa Gly Tyr Ala Leu Pro His  
35 40 45  
Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ser Leu  
50 55 60  
Met Lys Ile Leu Thr Glu Arg Gly Tyr Met Phe Thr Thr Thr Ala Glu  
65 70 75 80  
Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Val Ala Leu  
85 90 95  
Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Ser Ser Ser Ser Val Glu  
100 105 110  
Xaa Glu Leu Arg Ala Ser  
115

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..107  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499213  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:  
Met Glu Ala Pro Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys  
1                    5                    10                    15  
Cys Asp Val Asp Ile Arg Lys Xaa Leu Tyr Gly Asn Ile Val Leu Ser  
                    20                    25                    30  
Gly Gly Ser Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu  
                    35                    40                    45  
Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro  
                    50                    55                    60  
Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser  
65                    70                    75                    80  
Leu Ser Thr Phe Gln Met Trp Ile Ser Lys Ser Glu Tyr Asp Glu  
                    85                    90                    95  
Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe  
                    100                    105

(2) INFORMATION FOR SEQ ID NO:924:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1107 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..1107  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

```
aaatttcggt gtmcagagaa gaagcaaaag agagaaacat ccgacccgga atctgacctg      60
aaaacccgga agaatcgaaa aatgggggaaa gatggtctga gcgacgatca ggtctcgctg      120
atgaaggaag ctttcgatgct cttcgacacc gatggcgacg gcaaaatcgc accgtcagag      180
ctcgggatcc tcatgcatc tctcgcgga aaccgcgacc aagcccagct gaaatccata      240
atcgcatccg agaatctctc ttccacgttt gatttcaaca gattcctcga tctcatggcg      300
aaacatctga agacggaacc ttctgatcgc cagctccgtg acgcattcaa agtgctcgat      360
aaggaaggta ccgggttcgt tgctgtggcg gatctgaggc atattctgac cagtatcgga      420
gagaagctgg agcctaata gttcgatgag tggatcaagg aggtggatgt tggatccgat      480
ggaaagatcc ggtacttctg aatgtatgtc cgcaattgcc ggctcctacg gctacatagc      540
tccagagtac gcgtatacat tgaaggtaga tgagaagagc gatgtgtata gtttcggtgt      600
tggtcttcta gaactcatca ccgggaaaaa acccgctcga gaatttggcg acggcggttg      660
tattgttcaa tgggtgagaa gcatgacgga ttcaaataaa gattgtgtgc tcaaagtaat      720
cgatcttaga ctctcttcag ttccagttca cgaggtaaca cacgtcttct acgttgcggt      780
gctctgtgtt gaagaacaag cggtggagag gccgacgatg cgtgaagtcg ttcagattct      840
cactgagatc ccaaaaattc ctcttctgaa gcagcaagcg gcggaatcag acgtgactga      900
gaaagctccg gcgattaatg aatcgtcgcc ggattcagga agtccaccgg atcttttaag      960
taattagact ttccggcgat tgggtttggt cattgagggg caaatttgtc tttctaattt     1020
tcttgtcacc gacgtctcgg tagtggagtt aattacttaa ttagcccgtt gttgtctggt     1080
tccggttaag gcaacaatta gtggttt
```

(2) INFORMATION FOR SEQ ID NO:925:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 166 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide



(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1499215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

Lys	Phe	Arg	Cys	Xaa	Glu	Lys	Lys	Gln	Lys	Arg	Glu	Thr	Ser	Asp	Pro
1			5						10					15	
Glu	Ser	Asp	Leu	Lys	Thr	Arg	Lys	Asn	Arg	Lys	Met	Gly	Lys	Asp	Gly
			20					25					30		
Leu	Ser	Asp	Asp	Gln	Val	Ser	Ser	Met	Lys	Glu	Ala	Phe	Met	Leu	Phe
			35				40					45			
Asp	Thr	Asp	Gly	Asp	Gly	Lys	Ile	Ala	Pro	Ser	Glu	Leu	Gly	Ile	Leu
	50					55					60				
Met	Arg	Ser	Leu	Gly	Gly	Asn	Pro	Thr	Gln	Ala	Gln	Leu	Lys	Ser	Ile
65					70					75					80
Ile	Ala	Ser	Glu	Asn	Leu	Ser	Ser	Pro	Phe	Asp	Phe	Asn	Arg	Phe	Leu
				85					90					95	
Asp	Leu	Met	Ala	Lys	His	Leu	Lys	Thr	Glu	Pro	Phe	Asp	Arg	Gln	Leu
			100					105					110		
Arg	Asp	Ala	Phe	Lys	Val	Leu	Asp	Lys	Glu	Gly	Thr	Gly	Phe	Val	Ala
		115					120					125			
Val	Ala	Asp	Leu	Arg	His	Ile	Leu	Thr	Ser	Ile	Gly	Glu	Lys	Leu	Glu
		130				135					140				
Pro	Asn	Glu	Phe	Asp	Glu	Trp	Ile	Lys	Glu	Val	Asp	Val	Gly	Ser	Asp
145					150					155					160
Gly	Lys	Ile	Arg	Tyr	Phe										
					165										

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1499216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met	Ser	Ser	Met	Ser	Gly	Ser	Arg	Arg	Trp	Met	Leu	Asp	Pro	Met	Glu
1			5						10					15	
Arg	Ser	Gly	Thr	Ser	Glu	Cys	Met	Ser	Ala	Ile	Ala	Gly	Ser	Tyr	Gly
			20					25					30		
Tyr	Ile	Ala	Pro	Glu	Tyr	Ala	Tyr	Thr	Leu	Lys	Val	Asp	Glu	Lys	Ser
		35				40						45			
Asp	Val	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu	Leu	Ile	Thr	Gly	Lys
	50					55					60				
Lys	Pro	Val	Gly	Glu	Phe	Gly	Asp	Gly	Val	Asp	Ile	Val	Gln	Trp	Val
65				70						75					80
Arg	Ser	Met	Thr	Asp	Ser	Asn	Lys	Asp	Cys	Val	Leu	Lys	Val	Ile	Asp
				85					90					95	
Leu	Arg	Leu	Ser	Ser	Val	Pro	Val	His	Glu	Val	Thr	His	Val	Phe	Tyr
			100					105					110		
Val	Ala	Leu	Leu	Cys	Val	Glu	Glu	Gln	Ala	Val	Glu	Arg	Pro	Thr	Met
		115					120					125			
Arg	Glu	Val	Val	Gln	Ile	Leu	Thr	Glu	Ile	Pro	Lys	Ile	Pro	Leu	Ser
		130				135					140				
Lys	Gln	Gln	Ala	Ala	Glu	Ser	Asp	Val	Thr	Glu	Lys	Ala	Pro	Ala	Ile
145					150					155					160
Asn	Glu	Ser	Ser	Pro	Asp	Ser	Gly	Ser	Pro	Pro	Asp	Leu	Leu	Ser	Asn
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Ser Gly Ser Arg Trp Met Leu Asp Pro Met Glu Arg Ser Gly  
1 5 10 15  
Thr Ser Glu Cys Met Ser Ala Ile Ala Gly Ser Tyr Gly Tyr Ile Ala  
20 25 30  
Pro Glu Tyr Ala Tyr Thr Leu Lys Val Asp Glu Lys Ser Asp Val Tyr  
35 40 45  
Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Lys Lys Pro Val  
50 55 60  
Gly Glu Phe Gly Asp Gly Val Asp Ile Val Gln Trp Val Arg Ser Met  
65 70 75 80  
Thr Asp Ser Asn Lys Asp Cys Val Leu Lys Val Ile Asp Leu Arg Leu  
85 90 95  
Ser Ser Val Pro Val His Glu Val Thr His Val Phe Tyr Val Ala Leu  
100 105 110  
Leu Cys Val Glu Glu Gln Ala Val Glu Arg Pro Thr Met Arg Glu Val  
115 120 125  
Val Gln Ile Leu Thr Glu Ile Pro Lys Ile Pro Leu Ser Lys Gln Gln  
130 135 140  
Ala Ala Glu Ser Asp Val Thr Glu Lys Ala Pro Ala Ile Asn Glu Ser  
145 150 155 160  
Ser Pro Asp Ser Gly Ser Pro Pro Asp Leu Leu Ser Asn  
165 170

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1663
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

aagcaaaaat gctacaaatt aaaaagtgtc tccaacatgt gcatattcac acacaagttg 60  
gtgtcaacgc tcagacaaga aaggcgtgtg ttcattgttg aatcttccca tttcctcatc 120  
caaattccga cataactatc ctagccgcca tttgttctcc acattacaaa accctcagca 180  
gcttcaaaaac tcttcgatac tctccctcac gctcgcaatt ctctcgtctc cattttaata 240  
gtttttcttc tcggaatcac aaatcttcgg ctctctgttc cttggcgtgt gtgtgtgttg 300  
ttgaatggct cttgttcagc ggattccaat ttcctccccc agtattcgga attggcaaca 360  
agcgaggacc aatttgactc ctatttggtg ttacattac aatactgcat cttcttcttc 420  
ttcacccttt acagagaagc actctgtgga gagataccaa agggatcaat ggctgtacaa 480  
agcggttgaa ccaacgccac catcgactcc atctccatcg ccatttgaag atgaagtctt 540  
tgtaggggaa aacgacattg catcgagct gcctgagctg aagaagcttt tggcagtgct 600  
gaaagagaag agagttaaag gatgcaaagg tggtagattg ggaccaggag atgtgtatct 660  
tgtaggggaca gggccaggag atcctgagct tttgactctt aaagctgtca gagttattca 720  
aagtgccgat cttttgcttt acgacagget tgtctccaat gatgtcttgg agttggttgc 780  
tcctgatgct agacttcttt atgtcggcaa aactgctggg tatcatagca gaactcagga 840  
agagattcat gaactactcc taaattttgc tgaagctggg gccactgttg tcaggcttaa 900

aggtggagat cctctggtct ttggacgggg cggcgaagaa atggactttc tgcaacagca 960  
agggattcga gttcaagtta taccagggat aactgcggcg tcgggggatag cagcagagtt 1020  
ggggattcca ctaacacatc gaggtgttgc aactagtgtg aggtttctca ctggtcattc 1080  
aaggaaagga gggacagacc ctctgtttgt tcgagagaat gcagctgacc cggatacaac 1140  
acttgtcgtt tatatgggtt tgggaacttt accttctctt gcacaaaaac taatggacca 1200  
tgggtctccct tctgatacac cagctgttgc ggttgaacgt ggaaccactc ctctacagcg 1260  
tacagttttt gctgagctta aagattttgc aactgagatt cagtcagctg gattggtgtc 1320  
accaacactc atcatcatag ggaaagtcgt tgagctctca cctttatggc cacattgcac 1380  
gaaagaatcc tctgccttg tagagaccgg gtagatatct cactcttatt ttacgggcgt 1440  
gtggcttcca tcgacattac ggtgaagttt taggagctat ggagctatga aggttgagac 1500  
ttgagagatg taataaaca aaaggaaagc tgatagtttc ttatgacgtg tccttcaatt 1560  
gttttgggac aatggtaatg gcaatgttaa tgaataaac aagttatcaa tcagtgccac 1620  
tgtgactaat tttccacca caagatgatg tctttaaaac ttt

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..369
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

Met	Ala	Leu	Val	Gln	Arg	Ile	Pro	Ile	Ser	Ser	Ser	Ser	Ile	Arg	Asn
1				5				10					15		
Trp	Gln	Gln	Ala	Arg	Thr	Asn	Leu	Thr	Pro	Ile	Cys	Cys	Leu	His	Tyr
			20					25					30		
Asn	Thr	Ala	Ser	Ser	Ser	Ser	Ser	Pro	Phe	Thr	Glu	Lys	His	Ser	Val
		35					40					45			
Glu	Arg	Tyr	Gln	Arg	Asp	Gln	Trp	Leu	Tyr	Lys	Ala	Val	Glu	Pro	Thr
	50					55				60					
Pro	Pro	Ser	Thr	Pro	Ser	Pro	Ser	Pro	Phe	Glu	Asp	Glu	Val	Phe	Val
65				70					75					80	
Arg	Glu	Asn	Asp	Ile	Ala	Ser	Gln	Leu	Pro	Glu	Leu	Lys	Lys	Leu	Leu
		85						90						95	
Ala	Val	Leu	Lys	Glu	Lys	Arg	Val	Lys	Gly	Cys	Lys	Gly	Gly	Asp	Cys
		100						105					110		
Gly	Pro	Gly	Asp	Val	Tyr	Leu	Val	Gly	Thr	Gly	Pro	Gly	Asp	Pro	Glu
	115					120						125			
Leu	Leu	Thr	Leu	Lys	Ala	Val	Arg	Val	Ile	Gln	Ser	Ala	Asp	Leu	Leu
	130					135					140				
Leu	Tyr	Asp	Arg	Leu	Val	Ser	Asn	Asp	Val	Leu	Glu	Leu	Val	Ala	Pro
145				150					155						160
Asp	Ala	Arg	Leu	Leu	Tyr	Val	Gly	Lys	Thr	Ala	Gly	Tyr	His	Ser	Arg
		165						170					175		
Thr	Gln	Glu	Glu	Ile	His	Glu	Leu	Leu	Leu	Asn	Phe	Ala	Glu	Ala	Gly
	180							185					190		
Ala	Thr	Val	Val	Arg	Leu	Lys	Gly	Gly	Asp	Pro	Leu	Val	Phe	Gly	Arg
	195					200					205				
Gly	Gly	Glu	Glu	Met	Asp	Phe	Leu	Gln	Gln	Gln	Gly	Ile	Arg	Val	Gln
	210					215					220				
Val	Ile	Pro	Gly	Ile	Thr	Ala	Ala	Ser	Gly	Ile	Ala	Ala	Glu	Leu	Gly
225				230					235						240
Ile	Pro	Leu	Thr	His	Arg	Gly	Val	Ala	Thr	Ser	Val	Arg	Phe	Leu	Thr
		245						250					255		
Gly	His	Ser	Arg	Lys	Gly	Gly	Thr	Asp	Pro	Leu	Phe	Val	Ala	Glu	Asn
	260							265					270		
Ala	Ala	Asp	Pro	Asp	Thr	Thr	Leu	Val	Val	Tyr	Met	Gly	Leu	Gly	Thr
	275					280						285			

Leu Pro Ser Leu Ala Gln Lys Leu Met Asp His Gly Leu Pro Ser Asp  
290 295 300  
Thr Pro Ala Val Ala Val Glu Arg Gly Thr Thr Pro Leu Gln Arg Thr  
305 310 315 320  
Val Phe Ala Glu Leu Lys Asp Phe Ala Thr Glu Ile Gln Ser Ala Gly  
325 330 335  
Leu Val Ser Pro Thr Leu Ile Ile Ile Gly Lys Val Val Glu Leu Ser  
340 345 350  
Pro Leu Trp Pro His Cys Thr Lys Glu Ser Ser Cys Leu Val Glu Thr  
355 360 365  
Arg

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

aaaacacgag ttctaattgtt gctgttgatt taagtaaact tcagaaactt agaagtaaag 60  
gagtcagagg tagaggaggt gtaaggaaaa ctgacagtat aggtaataag agttccaagg 120  
tagcggaacc agccaaaaag gcgacaaaga aaaacagggt ttgggatgat gcggctccca 180  
aacaatcgaa attggacttc acggattcca tcgatgaaaa tgggaacaat gatcatgtag 240  
atattgtggc tgctgaccaa ggagaaagta tgatggacaa ggaagaggtt ttcagcagtg 300  
atagtgaag tgaagatgat gacgaaccag gaagtgatga gaagcctgct caggctaaga 360  
aaaagggatg gttttcttct gttttccaga gtattactgg gaaagcgaat cttgaaagga 420  
cagaccttgg accggcggtt aaagctctga aggaacggct catgaccaag aatgtggcag 480  
aagagattgc tgagaagctt tgcgaatcag tggaaagctag tcttgaagga aagaaattgt 540  
catctttcac caggatctct tcaaccgttc aggcagcgat ggaggatgct ctggttcgta 600  
tattgactcc aagacgctcc attgatatat taagagatgt tcatgctgcc aaagaacaga 660  
ggaaacctta tgtggttgtg tttgttgag tcaatggagt tgggaaatcc accaatctcg 720  
ctaaagtggc gtattggctt cagcagcata aggtcagtg aatgatggct gcttgtgaca 780  
ctttccgttc tggagctgtt gagcagttac ggactcatgc tcgtaggtta cagataccga 840  
tatttgaaaa gggttatgaa aaggatccag cagtagttgc taaagaagcc atacaagaag 900  
caactcgaaa tggatccgat gtcgttcttg ttgacacagc tggtcggatg caggataatg 960  
aacctttgat gagagcactc tcaaagctca tcaaccttaa tcagccggac ttggtcttgt 1020  
ttgttggtga agctcttgtt ggaaacgatg cagtagacca gctctcgaag ttcaatcaga 1080  
aactttcgga tctctcgact tctgggaacc caagactgat cgatggaatc ttactgacaa 1140  
agtttgatac cattgacgac aaggtcggag cagcgttgct tatggtttac atatcgggat 1200  
caccggttat gttcgtgggt tgtggccagt cttacactga cctgaagaag cttaatgtca 1260  
aagccatagt caagacactt ctcaagtgat ctctctttca tcatcatcat catcatcatc 1320  
actatcatca ttaccatcta ctatcaacaa tcaatgtctt atccatcatg ctgttgtttt 1380  
tggtttttta tttgaagacg gtttctcttt ggaagtgttg tgttttcttt aaaactcaaa 1440  
agactggagt cgcaaaaaat accatcccat gactttatat gatgcaacgt aacttttgtt 1500  
ttaaattaaa gattaataat catgtc

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

Asn	Thr	Ser	Ser	Val	Ala	Val	Asp	Leu	Ser	Lys	Leu	Gln	Lys	Leu
1			5				10					15		
Arg	Ser	Lys	Gly	Val	Arg	Gly	Arg	Gly	Gly	Val	Arg	Lys	Thr	Asp
			20				25					30		
Ile	Gly	Asn	Lys	Ser	Ser	Lys	Val	Ala	Glu	Pro	Ala	Lys	Lys	Ala
			35				40					45		
Lys	Lys	Asn	Arg	Val	Trp	Asp	Asp	Ala	Ala	Pro	Lys	Gln	Ser	Lys
			50			55				60				Leu
Asp	Phe	Thr	Asp	Ser	Ile	Asp	Glu	Asn	Gly	Asn	Asp	His	Val	Asp
65					70					75				80
Ile	Val	Ala	Ala	Asp	Gln	Gly	Glu	Ser	Met	Met	Asp	Lys	Glu	Glu
				85					90				95	Val
Phe	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Asp	Asp	Asp	Glu	Pro	Gly	Ser
			100					105					110	Asp
Glu	Lys	Pro	Ala	Gln	Ala	Lys	Lys	Lys	Gly	Trp	Phe	Ser	Ser	Val
			115				120					125		Phe
Gln	Ser	Ile	Thr	Gly	Lys	Ala	Asn	Leu	Glu	Arg	Thr	Asp	Leu	Gly
			130			135					140			Pro
Ala	Leu	Lys	Ala	Leu	Lys	Glu	Arg	Leu	Met	Thr	Lys	Asn	Val	Ala
145					150					155				Glu
Glu	Ile	Ala	Glu	Lys	Leu	Cys	Glu	Ser	Val	Glu	Ala	Ser	Leu	Glu
				165					170				175	Gly
Lys	Lys	Leu	Ser	Ser	Phe	Thr	Arg	Ile	Ser	Ser	Thr	Val	Gln	Ala
			180					185					190	Ala
Met	Glu	Asp	Ala	Leu	Val	Arg	Ile	Leu	Thr	Pro	Arg	Arg	Ser	Ile
		195				200					205			Asp
Ile	Leu	Arg	Asp	Val	His	Ala	Ala	Lys	Glu	Gln	Arg	Lys	Pro	Tyr
					215					220				Val
Val	Val	Phe	Val	Gly	Val	Asn	Gly	Val	Gly	Lys	Ser	Thr	Asn	Leu
225					230					235				Ala
Lys	Val	Ala	Tyr	Trp	Leu	Gln	Gln	His	Lys	Val	Ser	Val	Met	Met
				245					250				255	Ala
Ala	Cys	Asp	Thr	Phe	Arg	Ser	Gly	Ala	Val	Glu	Gln	Leu	Arg	Thr
			260					265					270	His
Ala	Arg	Arg	Leu	Gln	Ile	Pro	Ile	Phe	Glu	Lys	Gly	Tyr	Glu	Lys
			275				280					285		Asp
Pro	Ala	Val	Val	Ala	Lys	Glu	Ala	Ile	Gln	Glu	Ala	Thr	Arg	Asn
			290			295					300			Gly
Ser	Asp	Val	Val	Leu	Val	Asp	Thr	Ala	Gly	Arg	Met	Gln	Asp	Asn
305					310					315				Glu
Pro	Leu	Met	Arg	Ala	Leu	Ser	Lys	Leu	Ile	Asn	Leu	Asn	Gln	Pro
				325					330				335	Asp
Leu	Val	Leu	Phe	Val	Gly	Glu	Ala	Leu	Val	Gly	Asn	Asp	Ala	Val
			340					345					350	Asp
Gln	Leu	Ser	Lys	Phe	Asn	Gln	Lys	Leu	Ser	Asp	Leu	Ser	Thr	Ser
			355				360					365		Gly
Asn	Pro	Arg	Leu	Ile	Asp	Gly	Ile	Leu	Leu	Thr	Lys	Phe	Asp	Thr
			370			375					380			Ile
Asp	Asp	Lys	Val	Gly	Ala	Ala	Leu	Ser	Met	Val	Tyr	Ile	Ser	Gly
385					390					395				Ser
Pro	Val	Met	Phe	Val	Gly	Cys	Gly	Gln	Ser	Tyr	Thr	Asp	Leu	Lys
				405					410					Lys
Leu	Asn	Val	Lys	Ala	Ile	Val	Lys	Thr	Leu	Leu	Lys			
				420				425						

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..339
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

Met	Met	Asp	Lys	Glu	Glu	Val	Phe	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Asp
1			5						10					15	
Asp	Asp	Glu	Pro	Gly	Ser	Asp	Glu	Lys	Pro	Ala	Gln	Ala	Lys	Lys	Lys
		20						25					30		
Gly	Trp	Phe	Ser	Ser	Val	Phe	Gln	Ser	Ile	Thr	Gly	Lys	Ala	Asn	Leu
	35					40					45				
Glu	Arg	Thr	Asp	Leu	Gly	Pro	Ala	Leu	Lys	Ala	Leu	Lys	Glu	Arg	Leu
	50				55					60					
Met	Thr	Lys	Asn	Val	Ala	Glu	Glu	Ile	Ala	Glu	Lys	Leu	Cys	Glu	Ser
65				70					75					80	
Val	Glu	Ala	Ser	Leu	Glu	Gly	Lys	Lys	Leu	Ser	Ser	Phe	Thr	Arg	Ile
			85					90					95		
Ser	Ser	Thr	Val	Gln	Ala	Ala	Met	Glu	Asp	Ala	Leu	Val	Arg	Ile	Leu
		100						105					110		
Thr	Pro	Arg	Arg	Ser	Ile	Asp	Ile	Leu	Arg	Asp	Val	His	Ala	Ala	Lys
	115					120						125			
Glu	Gln	Arg	Lys	Pro	Tyr	Val	Val	Val	Phe	Val	Gly	Val	Asn	Gly	Val
	130					135					140				
Gly	Lys	Ser	Thr	Asn	Leu	Ala	Lys	Val	Ala	Tyr	Trp	Leu	Gln	Gln	His
145				150					155					160	
Lys	Val	Ser	Val	Met	Met	Ala	Ala	Cys	Asp	Thr	Phe	Arg	Ser	Gly	Ala
			165					170					175		
Val	Glu	Gln	Leu	Arg	Thr	His	Ala	Arg	Arg	Leu	Gln	Ile	Pro	Ile	Phe
		180						185				190			
Glu	Lys	Gly	Tyr	Glu	Lys	Asp	Pro	Ala	Val	Val	Ala	Lys	Glu	Ala	Ile
	195					200					205				
Gln	Glu	Ala	Thr	Arg	Asn	Gly	Ser	Asp	Val	Val	Leu	Val	Asp	Thr	Ala
	210				215						220				
Gly	Arg	Met	Gln	Asp	Asn	Glu	Pro	Leu	Met	Arg	Ala	Leu	Ser	Lys	Leu
225				230					235					240	
Ile	Asn	Leu	Asn	Gln	Pro	Asp	Leu	Val	Leu	Phe	Val	Gly	Glu	Ala	Leu
			245					250					255		
Val	Gly	Asn	Asp	Ala	Val	Asp	Gln	Leu	Ser	Lys	Phe	Asn	Gln	Lys	Leu
		260						265					270		
Ser	Asp	Leu	Ser	Thr	Ser	Gly	Asn	Pro	Arg	Leu	Ile	Asp	Gly	Ile	Leu
	275					280						285			
Leu	Thr	Lys	Phe	Asp	Thr	Ile	Asp	Asp	Lys	Val	Gly	Ala	Ala	Leu	Ser
	290				295						300				
Met	Val	Tyr	Ile	Ser	Gly	Ser	Pro	Val	Met	Phe	Val	Gly	Cys	Gly	Gln
305				310					315					320	
Ser	Tyr	Thr	Asp	Leu	Lys	Lys	Leu	Asn	Val	Lys	Ala	Ile	Val	Lys	Thr
			325					330					335		

Leu Leu Lys

- (2) INFORMATION FOR SEQ ID NO:933:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..338
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1499223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

Met Asp Lys Glu Glu Val Phe Ser Ser Asp Ser Glu Ser Glu Asp Asp  
1 5 10 15  
Asp Glu Pro Gly Ser Asp Glu Lys Pro Ala Gln Ala Lys Lys Lys Gly  
20 25 30  
Trp Phe Ser Ser Val Phe Gln Ser Ile Thr Gly Lys Ala Asn Leu Glu  
35 40 45  
Arg Thr Asp Leu Gly Pro Ala Leu Lys Ala Leu Lys Glu Arg Leu Met  
50 55 60  
Thr Lys Asn Val Ala Glu Glu Ile Ala Glu Lys Leu Cys Glu Ser Val  
65 70 75 80  
Glu Ala Ser Leu Glu Gly Lys Lys Leu Ser Ser Phe Thr Arg Ile Ser  
85 90 95  
Ser Thr Val Gln Ala Ala Met Glu Asp Ala Leu Val Arg Ile Leu Thr  
100 105 110  
Pro Arg Arg Ser Ile Asp Ile Leu Arg Asp Val His Ala Ala Lys Glu  
115 120 125  
Gln Arg Lys Pro Tyr Val Val Val Phe Val Gly Val Asn Gly Val Gly  
130 135 140  
Lys Ser Thr Asn Leu Ala Lys Val Ala Tyr Trp Leu Gln Gln His Lys  
145 150 155 160  
Val Ser Val Met Met Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val  
165 170 175  
Glu Gln Leu Arg Thr His Ala Arg Arg Leu Gln Ile Pro Ile Phe Glu  
180 185 190  
Lys Gly Tyr Glu Lys Asp Pro Ala Val Val Ala Lys Glu Ala Ile Gln  
195 200 205  
Glu Ala Thr Arg Asn Gly Ser Asp Val Val Leu Val Asp Thr Ala Gly  
210 215 220  
Arg Met Gln Asp Asn Glu Pro Leu Met Arg Ala Leu Ser Lys Leu Ile  
225 230 235 240  
Asn Leu Asn Gln Pro Asp Leu Val Leu Phe Val Gly Glu Ala Leu Val  
245 250 255  
Gly Asn Asp Ala Val Asp Gln Leu Ser Lys Phe Asn Gln Lys Leu Ser  
260 265 270  
Asp Leu Ser Thr Ser Gly Asn Pro Arg Leu Ile Asp Gly Ile Leu Leu  
275 280 285  
Thr Lys Phe Asp Thr Ile Asp Asp Lys Val Gly Ala Ala Leu Ser Met  
290 295 300  
Val Tyr Ile Ser Gly Ser Pro Val Met Phe Val Gly Cys Gly Gln Ser  
305 310 315 320  
Tyr Thr Asp Leu Lys Lys Leu Asn Val Lys Ala Ile Val Lys Thr Leu  
325 330 335  
Leu Lys

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..521
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

atttgtgatga atcatcatga gcagtgactt catacttgat attacgggtg agaggccact	60
ataaaaaagca ggcgcgctcct cgaagaagaa gaagaagaag taacaaattg gtggaaatca	120
gaagttgaat cggagaataa caacgatgac gacgaacaag caggtcatat tcaaagacca	180
cgtgagvgwr ttccctaagg aatccgattt caatttcacc accaccaccg tcgaacttag	240

ggttccggaa ggttctaaat cggttcttgt gaagaatctc tacctgtcat gcgatacctta 300  
tatgcgggtct cgcattggga aacctgatcc ctctcttgct cttgctcaag cttacgctcc 360  
cggcaagcca atctatgggt atggagtgtc tagagtata gaatctgggc atccagatta 420  
caagaaaggt gatttactct ggggaatagt tggatktgag gagtatagt ttattacacc 480  
aatggctcac atgcatttca agatccaaca tacagatgtt c

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

Met Thr Thr Asn Lys Gln Val Ile Phe Lys Asp His Val Xaa Xaa Phe  
1 5 10 15  
Pro Lys Glu Ser Asp Phe Asn Phe Thr Thr Thr Val Glu Leu Arg  
20 25 30  
Val Pro Glu Gly Ser Lys Ser Val Leu Val Lys Asn Leu Tyr Leu Ser  
35 40 45  
Cys Asp Pro Tyr Met Arg Ser Arg Met Gly Lys Pro Asp Pro Ser Ser  
50 55 60  
Ala Leu Ala Gln Ala Tyr Ala Pro Gly Lys Pro Ile Tyr Gly Tyr Gly  
65 70 75 80  
Val Ser Arg Val Ile Glu Ser Gly His Pro Asp Tyr Lys Lys Gly Asp  
85 90 95  
Leu Leu Trp Gly Ile Val Gly Xaa Glu Glu Tyr Ser Val Ile Thr Pro  
100 105 110  
Met Ala His Met His Phe Lys Ile Gln His Thr Asp Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

Met Arg Ser Arg Met Gly Lys Pro Asp Pro Ser Ser Ala Leu Ala Gln  
1 5 10 15  
Ala Tyr Ala Pro Gly Lys Pro Ile Tyr Gly Tyr Gly Val Ser Arg Val  
20 25 30  
Ile Glu Ser Gly His Pro Asp Tyr Lys Lys Gly Asp Leu Leu Trp Gly  
35 40 45  
Ile Val Gly Xaa Glu Glu Tyr Ser Val Ile Thr Pro Met Ala His Met  
50 55 60  
His Phe Lys Ile Gln His Thr Asp Val  
65 70

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..69  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:  
Met Gly Lys Pro Asp Pro Ser Ser Ala Leu Ala Gln Ala Tyr Ala Pro  
1                  5                  10                  15  
Gly Lys Pro Ile Tyr Gly Tyr Gly Val Ser Arg Val Ile Glu Ser Gly  
                  20                  25                  30  
His Pro Asp Tyr Lys Lys Gly Asp Leu Leu Trp Gly Ile Val Gly Xaa  
                  35                  40                  45  
Glu Glu Tyr Ser Val Ile Thr Pro Met Ala His Met His Phe Lys Ile  
50                  55                  60  
Gln His Thr Asp Val  
65

(2) INFORMATION FOR SEQ ID NO:938:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1721 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..1721  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

aaaaaattca gccatgcgct cgaagaaaaa acctcccaaa tctgagaaat cggaaaagat 60  
gaccacacacc gaaaccctaa atctgctcga tgaaatcgag tctcttgtct ccgatcagct 120  
tcaagtggta tcttacaaat ggctgagtcg aaattttctcg ctttcatcaa atactgccaa 180  
gaggttgtctc aaggatttta tagagaaaca tgggaagggt ttggaagttg tatatattgt 240  
gtccggattg ctaaagaacg gacctccga ttaccacgca aggcttgctt ctagtaccga 300  
acttccagaa gtagagaaag agttcaatgg aaaatattca gtacatatct acagtgttca 360  
agctagtatt ccaatggatc cagcagccat atggaacact gagtttgtac aagcagaaga 420  
actcttcagg cagccttctg ccactgataa ttgtttgaaa ggcaacagtt tttgtggcgt 480  
ctccaattct tgtgtgaagc gcaatataga gggagccact gaaaatgtta ccgcccgcgcg 540  
aactgaaagt gtgagaacta caggacaatc taaaagtagt tcaaattttc aaaatagtac 600  
agtgcgctca aaccagggaa agaatttcca gcaactcaagc tctaattgtg gccatcaggc 660  
taagagtga tctattgctg ctccagctaa aaatcgggtc gcgaaatcct ctttggataa 720  
agaaaaagct tttcatgtgc ccgctaataa aaagaatgga cagggcgaga agagcgtgac 780  
tggaactggg ggtttgttga aaaatatgtg gggccgtgtg cctgtgaaaa cagaagatga 840  
ttctccaaca gtagatgtga aaaatcatat tactaatcat tcggaacccc aaaaaccttc 900  
tcatgatgct gacaagaagg gaggcagcga tgatgagact cgagacgcca atttcatgag 960  
agcgcctaaa gataacagaa aaagaaagggt gatatttgat ttttcagatg acgagtatga 1020  
agatgtaatc agcttagcat ctcatagtag tccaaagggt aattcacgctc cagatgtcga 1080  
actcagttcg gaagattcag gtccagagaa gcctgaacgca gatgtttctc cagagataaa 1140  
atctgaggaa ccagaggcca gcaaagaaga caggcaaaac actgcttctg ttgatgcttc 1200  
tacgactttg tcaacggaga agatccaggc cattggttct gaagctgaag tgaatccctc 1260  
aaagagaaga actactgcag ttcctagttc gccgaaaagg aaaaagggtg tgaagtacag 1320  
gattgatgat cgtgggagag aagtaactga ggtagtgtgg gaggagacag aaacgaacgc 1380  
aaagaagaaa gaggacacta atacaagtaa gaagttagat gatggcaaaa ccgcaaatgc 1440  
tgtaacacag gcggttgac agaagaagag tccggccatt ggaaacacag cagcgacaaa 1500  
cgcaggagga aaagcgggaa gcaagaagg aggaaacgctc aaagatccaa agcaagggaa 1560  
tataatgtcc ttcttcaaga aagtttaaaa aggcttcttt tttgtattta ttgtttgcta 1620  
agtttgagtt gaggatatta taggaaaatc agaacttgga ttcatctgac tgtatgttct 1680  
gatccattgt gtctaagaaa aaaacttttg agccgtttct c

(2) INFORMATION FOR SEQ ID NO:939:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 528 amino acids  
    (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..528  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499229  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

Lys	Asn	Ser	Ala	Ile	Ala	Ser	Lys	Lys	Lys	Pro	Pro	Lys	Ser	Glu	Lys
1				5				10						15	
Ser	Glu	Lys	Met	Thr	His	Thr	Glu	Thr	Leu	Asn	Leu	Leu	Asp	Glu	Ile
			20					25					30		
Glu	Ser	Leu	Val	Ser	Asp	Gln	Leu	Gln	Val	Val	Ser	Tyr	Lys	Trp	Leu
		35				40					45				
Ser	Arg	Asn	Phe	Ser	Leu	Ser	Ser	Asn	Thr	Ala	Lys	Arg	Leu	Leu	Lys
	50					55					60				
Asp	Phe	Ile	Glu	Lys	His	Gly	Lys	Gly	Leu	Glu	Val	Val	Tyr	Ile	Val
65					70					75				80	
Ser	Gly	Leu	Leu	Lys	Asn	Gly	Pro	Ser	Asp	Tyr	His	Ala	Arg	Leu	Ala
			85						90					95	
Ser	Ser	Thr	Glu	Leu	Pro	Glu	Val	Glu	Lys	Glu	Phe	Asn	Gly	Lys	Tyr
			100					105					110		
Ser	Val	His	Ile	Tyr	Ser	Val	Gln	Ala	Ser	Ile	Pro	Met	Asp	Pro	Ala
	115						120					125			
Ala	Ile	Trp	Asn	Thr	Glu	Phe	Val	Gln	Ala	Glu	Glu	Leu	Phe	Arg	Gln
	130					135					140				
Pro	Ser	Ala	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Asn	Ser	Phe	Cys	Gly	Val
145					150					155					160
Ser	Asn	Ser	Cys	Val	Lys	Arg	Asn	Ile	Glu	Gly	Ala	Thr	Glu	Asn	Val
			165						170					175	
Thr	Ala	Pro	Arg	Thr	Glu	Ser	Val	Arg	Thr	Thr	Gly	Gln	Ser	Lys	Ser
			180					185					190		
Ser	Ser	Asn	Phe	Gln	Asn	Ser	Thr	Val	Pro	Ser	Asn	Gln	Gly	Lys	Asn
		195					200					205			
Phe	Gln	His	Ser	Ser	Ser	Asn	Val	Gly	His	Gln	Ala	Lys	Ser	Glu	Ser
	210					215					220				
Ile	Ala	Ala	Pro	Ala	Lys	Asn	Arg	Ser	Ala	Lys	Ser	Ser	Leu	Asp	Lys
225					230					235					240
Glu	Lys	Ala	Phe	His	Val	Pro	Ala	Asn	Lys	Lys	Asn	Gly	Gln	Gly	Glu
			245						250					255	
Lys	Ser	Val	Thr	Gly	Thr	Gly	Gly	Leu	Leu	Lys	Asn	Met	Trp	Gly	Arg
			260					265					270		
Val	Pro	Val	Lys	Thr	Glu	Asp	Asp	Ser	Pro	Thr	Val	Asp	Val	Lys	Asn
		275				280						285			
His	Ile	Thr	Asn	His	Ser	Glu	Pro	Gln	Lys	Pro	Ser	His	Asp	Ala	Asp
	290					295					300				
Lys	Lys	Gly	Gly	Ser	Asp	Glu	Thr	Arg	Asp	Ala	Asn	Phe	Met	Arg	
	305				310				315					320	
Ala	Pro	Lys	Asp	Asn	Arg	Lys	Arg	Lys	Val	Ile	Phe	Asp	Phe	Ser	Asp
			325						330					335	
Asp	Glu	Tyr	Glu	Asp	Val	Ile	Ser	Leu	Ala	Ser	His	Ser	Ser	Pro	Lys
		340						345					350		
Val	Asn	Ser	Arg	Pro	Asp	Val	Glu	Leu	Ser	Ser	Glu	Asp	Ser	Gly	Pro
	355					360						365			
Glu	Lys	Pro	Asp	Ala	Asp	Val	Ser	Pro	Glu	Ile	Lys	Ser	Glu	Glu	Pro
	370					375					380				
Glu	Ala	Ser	Lys	Glu	Asp	Arg	Gln	Asn	Thr	Ala	Ser	Val	Asp	Ala	Ser
385					390					395					400
Thr	Thr	Leu	Ser	Thr	Glu	Lys	Ile	Gln	Ala	Ile	Gly	Ser	Glu	Ala	Glu
				405					410					415	
Val	Asn	Pro	Ser	Lys	Arg	Arg	Thr	Thr	Ala	Val	Pro	Ser	Ser	Pro	Lys

420	425	430
Arg Lys Lys Val Leu Lys Ser Arg Ile Asp Asp Arg Gly Arg Glu Val		
435	440	445
Thr Glu Val Val Trp Glu Glu Thr Glu Thr Asn Ala Lys Lys Lys Glu		
450	455	460
Asp Thr Asn Thr Ser Lys Lys Leu Asp Asp Gly Lys Thr Ala Asn Ala		
465	470	475
Val Asn Arg Ala Val Ala Gln Lys Lys Ser Pro Ala Ile Gly Asn Thr		
485	490	495
Ala Ala Thr Asn Ala Gly Gly Lys Ala Gly Ser Lys Lys Gly Gly Asn		
500	505	510
Val Lys Asp Pro Lys Gln Gly Asn Ile Met Ser Phe Phe Lys Lys Val		
515	520	525

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

Met Thr His Thr Glu Thr Leu Asn Leu Leu Asp Glu Ile Glu Ser Leu		
1	5	10
Val Ser Asp Gln Leu Gln Val Val Ser Tyr Lys Trp Leu Ser Arg Asn		
20	25	30
Phe Ser Leu Ser Ser Asn Thr Ala Lys Arg Leu Leu Lys Asp Phe Ile		
35	40	45
Glu Lys His Gly Lys Gly Leu Glu Val Val Tyr Ile Val Ser Gly Leu		
50	55	60
Leu Lys Asn Gly Pro Ser Asp Tyr His Ala Arg Leu Ala Ser Ser Thr		
65	70	75
Glu Leu Pro Glu Val Glu Lys Glu Phe Asn Gly Lys Tyr Ser Val His		
85	90	95
Ile Tyr Ser Val Gln Ala Ser Ile Pro Met Asp Pro Ala Ala Ile Trp		
100	105	110
Asn Thr Glu Phe Val Gln Ala Glu Glu Leu Phe Arg Gln Pro Ser Ala		
115	120	125
Thr Asp Asn Cys Leu Lys Gly Asn Ser Phe Cys Gly Val Ser Asn Ser		
130	135	140
Cys Val Lys Arg Asn Ile Glu Gly Ala Thr Glu Asn Val Thr Ala Pro		
145	150	155
Arg Thr Glu Ser Val Arg Thr Thr Gly Gln Ser Lys Ser Ser Ser Asn		
165	170	175
Phe Gln Asn Ser Thr Val Pro Ser Asn Gln Gly Lys Asn Phe Gln His		
180	185	190
Ser Ser Ser Asn Val Gly His Gln Ala Lys Ser Glu Ser Ile Ala Ala		
195	200	205
Pro Ala Lys Asn Arg Ser Ala Lys Ser Ser Leu Asp Lys Glu Lys Ala		
210	215	220
Phe His Val Pro Ala Asn Lys Lys Asn Gly Gln Gly Glu Lys Ser Val		
225	230	235
Thr Gly Thr Gly Gly Leu Leu Lys Asn Met Trp Gly Arg Val Pro Val		
245	250	255
Lys Thr Glu Asp Asp Ser Pro Thr Val Asp Val Lys Asn His Ile Thr		
260	265	270

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Asn His Ser Glu Pro Gln Lys Pro Ser His Asp Ala Asp Lys Lys Gly
      275      280      285
Gly Ser Asp Asp Glu Thr Arg Asp Ala Asn Phe Met Arg Ala Pro Lys
      290      295      300
Asp Asn Arg Lys Arg Lys Val Ile Phe Asp Phe Ser Asp Asp Glu Tyr
      305      310      315      320
Glu Asp Val Ile Ser Leu Ala Ser His Ser Ser Pro Lys Val Asn Ser
      325      330      335
Arg Pro Asp Val Glu Leu Ser Ser Glu Asp Ser Gly Pro Glu Lys Pro
      340      345      350
Asp Ala Asp Val Ser Pro Glu Ile Lys Ser Glu Glu Pro Glu Ala Ser
      355      360      365
Lys Glu Asp Arg Gln Asn Thr Ala Ser Val Asp Ala Ser Thr Thr Leu
      370      375      380
Ser Thr Glu Lys Ile Gln Ala Ile Gly Ser Glu Ala Glu Val Asn Pro
      385      390      395      400
Ser Lys Arg Arg Thr Thr Ala Val Pro Ser Ser Pro Lys Arg Lys Lys
      405      410      415
Val Leu Lys Ser Arg Ile Asp Asp Arg Gly Arg Glu Val Thr Glu Val
      420      425      430
Val Trp Glu Thr Glu Thr Asn Ala Lys Lys Lys Glu Asp Thr Asn
      435      440      445
Thr Ser Lys Lys Leu Asp Asp Gly Lys Thr Ala Asn Ala Val Asn Arg
      450      455      460
Ala Val Ala Gln Lys Lys Ser Pro Ala Ile Gly Asn Thr Ala Ala Thr
      465      470      475      480
Asn Ala Gly Gly Lys Ala Gly Ser Lys Lys Gly Gly Asn Val Lys Asp
      485      490      495
Pro Lys Gln Gly Asn Ile Met Ser Phe Phe Lys Lys Val
      500      505

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(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..404
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

```

Met Asp Pro Ala Ala Ile Trp Asn Thr Glu Phe Val Gln Ala Glu Glu
1          5          10          15
Leu Phe Arg Gln Pro Ser Ala Thr Asp Asn Cys Leu Lys Gly Asn Ser
      20          25          30
Phe Cys Gly Val Ser Asn Ser Cys Val Lys Arg Asn Ile Glu Gly Ala
      35          40          45
Thr Glu Asn Val Thr Ala Pro Arg Thr Glu Ser Val Arg Thr Thr Gly
      50          55          60
Gln Ser Lys Ser Ser Ser Asn Phe Gln Asn Ser Thr Val Pro Ser Asn
      65          70          75          80
Gln Gly Lys Asn Phe Gln His Ser Ser Ser Asn Val Gly His Gln Ala
      85          90          95
Lys Ser Glu Ser Ile Ala Ala Pro Ala Lys Asn Arg Ser Ala Lys Ser
      100          105          110
Ser Leu Asp Lys Glu Lys Ala Phe His Val Pro Ala Asn Lys Lys Asn
      115          120          125
Gly Gln Gly Glu Lys Ser Val Thr Gly Thr Gly Gly Leu Leu Lys Asn
      130          135          140
Met Trp Gly Arg Val Pro Val Lys Thr Glu Asp Asp Ser Pro Thr Val

```

145 150 155 160  
Asp Val Lys Asn His Ile Thr Asn His Ser Glu Pro Gln Lys Pro Ser  
165 170 175  
His Asp Ala Asp Lys Lys Gly Gly Ser Asp Asp Glu Thr Arg Asp Ala  
180 185 190  
Asn Phe Met Arg Ala Pro Lys Asp Asn Arg Lys Arg Lys Val Ile Phe  
195 200 205  
Asp Phe Ser Asp Asp Glu Tyr Glu Asp Val Ile Ser Leu Ala Ser His  
210 215 220  
Ser Ser Pro Lys Val Asn Ser Arg Pro Asp Val Glu Leu Ser Ser Glu  
225 230 235 240  
Asp Ser Gly Pro Glu Lys Pro Asp Ala Asp Val Ser Pro Glu Ile Lys  
245 250 255  
Ser Glu Glu Pro Glu Ala Ser Lys Glu Asp Arg Gln Asn Thr Ala Ser  
260 265 270  
Val Asp Ala Ser Thr Thr Leu Ser Thr Glu Lys Ile Gln Ala Ile Gly  
275 280 285  
Ser Glu Ala Glu Val Asn Pro Ser Lys Arg Arg Thr Thr Ala Val Pro  
290 295 300  
Ser Ser Pro Lys Arg Lys Lys Val Leu Lys Ser Arg Ile Asp Asp Arg  
305 310 315 320  
Gly Arg Glu Val Thr Glu Val Val Trp Glu Glu Thr Glu Thr Asn Ala  
325 330 335  
Lys Lys Lys Glu Asp Thr Asn Thr Ser Lys Lys Leu Asp Asp Gly Lys  
340 345 350  
Thr Ala Asn Ala Val Asn Arg Ala Val Ala Gln Lys Lys Ser Pro Ala  
355 360 365  
Ile Gly Asn Thr Ala Ala Thr Asn Ala Gly Gly Lys Ala Gly Ser Lys  
370 375 380  
Lys Gly Gly Asn Val Lys Asp Pro Lys Gln Gly Asn Ile Met Ser Phe  
385 390 395 400  
Phe Lys Lys Val

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..779
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

atttctgttc atttcacctt tactaaaaag agaactcaca tcaaagaaac agtccatcat	60
tcacatgata tagatgagca tcattactaa ttatcttgta acgaatgata actaatgttt	120
ttgactattc tatgcagctc tagtggcact cctaccacag gaacaccaac tagtgggaca	180
ccaaccagtg ggaccccgac taccggaact ccgaccacog gaacccccac cactggaact	240
ccaaccagtg ggactccaac tagtggcttc ccaaataccg ggactccgaa cacagggact	300
aacactggga tgccaaattc caacgggatg ccaacttcat cgtcatcttc ggtgttcccg	360
gggactactc ttggaccgac tggtagcggg ggactaggcg atccaaatgc tggagagaag	420
ctgtctgttc gaactaacac atttgtcttc ttattaacog gtgtagcagc aatgcttgct	480
atatgagggc ttagatgtca caccggtta tggttgtaat tgggtttgct gagagatcag	540
atcttgcta cggctcatgg ttgatagagc catctttttt tcaactcgtc ttctaggatt	600
tggacttagg ttggccgaga gacataatgc ttgtagtagc tagtattttg gggtatgtac	660
aactttaact aagagcttta cttttgtaaa tccggaggat gagatgctct tttgtttctt	720
atattctttt taatcctttt actttgatct ttcattcttt aatacgtacc atcattgtc	

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499233  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

Met	Phe	Leu	Thr	Ile	Leu	Cys	Ser	Ser	Ser	Gly	Thr	Pro	Thr	Thr	Gly
1			5						10					15	
Thr	Pro	Thr	Ser	Gly	Thr	Pro	Thr	Ser	Gly	Thr	Pro	Thr	Thr	Gly	Thr
			20					25					30		
Pro	Thr	Thr	Gly	Thr	Pro	Thr	Thr	Gly	Thr	Pro	Thr	Ser	Gly	Thr	Pro
			35				40					45			
Thr	Ser	Gly	Phe	Pro	Asn	Thr	Gly	Thr	Pro	Asn	Thr	Gly	Thr	Asn	Thr
			50				55				60				
Gly	Met	Pro	Asn	Ser	Asn	Gly	Met	Pro	Thr	Ser	Ser	Ser	Ser	Ser	Val
65					70					75				80	
Phe	Pro	Gly	Thr	Thr	Leu	Gly	Pro	Thr	Gly	Ser	Gly	Gly	Leu	Gly	Asp
			85						90					95	
Pro	Asn	Ala	Gly	Glu	Lys	Leu	Ser	Val	Arg	Thr	Asn	Thr	Leu	Val	Phe
			100					105					110		
Leu	Leu	Thr	Gly	Val	Ala	Ala	Met	Leu	Val	Ile					
			115				120								

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1412  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

actccgagcg	tttcctttct	cacaagccaa	tggcgcaatt	tactaattcc	atcaattatc	60
tctttttctgt	ttctctctta	ttatttgtat	cgttccactg	cttatgtttt	cgtttttcat	120
tggttgacgc	ttgttcaaac	tccaccgacg	accaacagat	tcaacaccat	caccaccgga	180
aatgggttg	tccctcaggc	cacaaagtca	tcaccgtctc	acttaacggc	cacgctcagt	240
ttcgctccgt	ccaagacgct	gtggattcca	taccaaagav	caataacaag	agcatcacaa	300
tcaagattgc	tcccggattt	tacagagaga	aagtgggtgt	tccagctaca	aaaccgtaca	360
taaacgttca	aaggagctgg	tagggatgtg	accgctatag	agtggcacga	ccgtgcgtcc	420
gaccttgccg	ctaacggtca	acagttacgt	acctatcaaa	ccgcttccgt	caccgtctac	480
gctaattatt	tcaccgctag	aaacattagc	ttcacggtag	tctattcaat	tctaaccgcaa	540
ttatatatat	agggaaactt	tcacaaaaat	gcgagtcttt	ctttatttta	ttttaaattg	600
tgaagaatac	tgcgccggct	ccattgccgg	ggatgcaagg	gtggcaagcg	gtggcggtta	660
ggatctcccg	cgacaaagct	ttcttttccg	gctgcgggtt	ttacggtgca	caagacactt	720
tatgcgacga	tgtctggcgt	cattacttca	aggagtgtta	cattgaaggc	tctatcgact	780
ttatcttttg	taatggccgc	tccatgtata	aagattgtga	gttgcatcgc	atagcgtcaa	840
gattcgggtc	gatagcggcg	catggttaga	catgcccgga	agagaaaacg	ggtttcgcgt	900
tcgtgggttg	tcgggtaaca	ggtacgggtc	cattgtacgt	gggcccggcc	atgggacca	960
tactcacgta	tcgtttacgc	ctacacttac	tttgatgctc	tcgtcgctca	cggtgggttg	1020
gacgattggg	accacaaatc	caacaaaagc	aagacggcat	ttttcggagt	gtacaattgc	1080
tatgggccag	gagcagcagc	gacgagaggc	gtgtcttggg	ctagagcttt	ggactatgaa	1140
tcggccccatc	catttatcgc	taagagcttc	gttaatggga	gacattggat	cgctcctcga	1200
gatgcttaac	caacttcaaa	ccttgccggg	gtttcttttc	ctaattcctc	ggttcctccc	1260
agtcccaagt	cctaaaagct	tactatattt	ttatcattcg	tttatttctt	ttattgttta	1320
ttttttccaa	tttatttata	cattgtgtga	tagtacaaca	aagtattgct	tcttcttcat	1380
ctgtatccat	ttcagttaaa	tgttttgagc	tt			

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

Ser	Glu	Arg	Phe	Leu	Ser	His	Lys	Pro	Met	Ala	Gln	Phe	Thr	Asn	Ser	
1				5					10					15		
Ile	Asn	Tyr	Leu	Phe	Ser	Val	Ser	Leu	Leu	Leu	Phe	Val	Ser	Phe	His	
			20					25					30			
Cys	Leu	Cys	Phe	Arg	Phe	Ser	Leu	Val	Ala	Ala	Cys	Ser	Asn	Ser	Thr	
		35					40					45				
Asp	Asp	Gln	Gln	Ile	Gln	His	His	His	Arg	Lys	Trp	Val	Gly	Pro		
	50				55					60						
Ser	Gly	His	Lys	Val	Ile	Thr	Val	Ser	Leu	Asn	Gly	His	Ala	Gln	Phe	
65				70					75					80		
Arg	Ser	Val	Gln	Asp	Ala	Val	Asp	Ser	Ile	Pro	Lys	Xaa	Asn	Asn	Lys	
			85					90					95			
Ser	Ile	Thr	Ile	Lys	Ile	Ala	Pro	Gly	Phe	Tyr	Arg	Glu	Lys	Val	Val	
		100					105					110				
Val	Pro	Ala	Thr	Lys	Pro	Tyr	Ile	Asn	Val	Gln	Arg	Ser	Trp			
		115				120					125					

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

Met	Pro	Gly	Arg	Glu	Asn	Gly	Phe	Arg	Val	Arg	Gly	Leu	Ser	Gly	Asn	
1				5					10					15		
Arg	Tyr	Gly	Ser	Ile	Val	Arg	Gly	Pro	Gly	His	Gly	Thr	Asn	Thr	His	
			20					25					30			
Val	Ser	Phe	Thr	Pro	Thr	Leu	Thr	Leu	Met	Leu	Ser	Ser	Leu	Thr	Val	
		35				40					45					
Val	Gly	Thr	Ile	Gly	Thr	Thr	Asn	Pro	Thr	Lys	Ala	Arg	Arg	His	Phe	
	50					55				60						
Ser	Glu	Cys	Thr	Ile	Ala	Met	Gly	Gln	Glu	Gln	Gln	Arg	Arg	Glu	Ala	
65				70					75					80		
Cys	Leu	Gly	Leu	Glu	Leu	Trp	Thr	Met	Asn	Arg	Pro	Ile	His	Leu	Ser	
			85					90					95			
Leu	Arg	Ala	Ser	Leu	Met	Gly	Asp	Ile	Gly	Ser	Leu	Leu	Glu	Met	Leu	
		100				105						110				
Asn	Gln	Leu	Gln	Thr	Leu	Ala	Gly	Phe	Leu	Phe	Leu	Ile	Pro	Arg	Phe	
	115					120						125				
Leu	Pro	Val	Pro	Ser	Pro	Lys	Ser	Leu	Leu	Tyr	Phe	Tyr	His	Ser	Phe	
	130					135				140						
Ile	Ser	Phe	Ile	Val	Tyr	Phe	Phe	Gln	Phe	Ile	Tyr	Thr	Leu	Cys	Asp	
145				150					155					160		
Ser	Thr	Thr	Lys	Tyr	Cys	Phe	Phe	Phe	Ile	Cys	Ile	His	Phe	Ser		

165 170 175

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1499245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

Met	Leu	Ser	Ser	Leu	Thr	Val	Val	Gly	Thr	Ile	Gly	Thr	Thr	Asn	Pro
1				5					10					15	
Thr	Lys	Ala	Arg	Arg	His	Phe	Ser	Glu	Cys	Thr	Ile	Ala	Met	Gly	Gln
			20					25					30		
Glu	Gln	Gln	Arg	Arg	Glu	Ala	Cys	Leu	Gly	Leu	Glu	Leu	Trp	Thr	Met
		35					40					45			
Asn	Arg	Pro	Ile	His	Leu	Ser	Leu	Arg	Ala	Ser	Leu	Met	Gly	Asp	Ile
	50					55					60				
Gly	Ser	Leu	Leu	Glu	Met	Leu	Asn	Gln	Leu	Gln	Thr	Leu	Ala	Gly	Phe
65				70						75				80	
Leu	Phe	Leu	Ile	Pro	Arg	Phe	Leu	Pro	Val	Pro	Ser	Pro	Lys	Ser	Leu
			85					90						95	
Leu	Tyr	Phe	Tyr	His	Ser	Phe	Ile	Ser	Phe	Ile	Val	Tyr	Phe	Phe	Gln
		100					105					110			
Phe	Ile	Tyr	Thr	Leu	Cys	Asp	Ser	Thr	Thr	Lys	Tyr	Cys	Phe	Phe	Phe
		115					120					125			
Ile	Cys	Ile	His	Phe	Ser										
		130													

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1894
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

aacaccgtga	cagctcctta	gatctctcct	cggttacttc	ctttttaatt	tccatggctc	60
tctaaaaatc	tctctctctt	tctctctctc	ttacttgat	tggtacgatc	tctgcttgaa	120
gattatggac	ggcgccgatg	gaaccgttcg	cgtcaagcct	ggtcgcggat	tcgaaacgga	180
gacggatgtt	gcggtttcgt	cgccagtgc	acgtcagaaa	gctgctgcag	ctaagcaatt	240
catcgagaat	cattataaga	attacttgca	aggcttgac	gaacgaatgg	agagacgcag	300
ggagtttcag	aggaaagtgc	aagaagctca	gttacctgtt	gaggaacaag	acgagatgat	360
gaggaatctg	gctcgtcgtg	aaactgagta	tatgagactt	cagagacgta	aaattgggat	420
tgatgatttt	gagcttttga	ccgttattgg	caaagggtgc	tttggtgagg	ttagattatg	480
tcgtttgaga	tctacatctg	aagtttatgc	catgaagaaa	ttgaaaaaaa	ctgagatgct	540
tagccgtgga	caggtagagc	atgtcaggtc	cgagaggaac	ttacttgcag	aagttgacag	600
ccgttacatt	gtaaaacctt	tttactcttt	tcaagattct	gaatgtttgt	atcttatcat	660
ggagtattta	cctgggggtg	acatcatgac	actactcatg	agagaagaca	ttctttctga	720
agatgttgcc	cgtttttata	ttgctgagag	cattcttgcc	atccattcaa	ttcatcaaca	780
caactatgtt	cacaggggaca	tcaaacctga	taatttgata	ctagacaaaa	gtgggcattt	840
gaagctttca	gatttttggtt	tatgtaagcc	acttgatgac	aagtattctt	cattgctatt	900
agaagacgat	gaaatgttgt	ctcaggattc	agagaaccag	tcaggaaaaat	cagacgctga	960
caaagcacc	tggcaaatgc	ctaaagagca	gttactgcag	tggaaacgca	atcgccgtgc	1020
attggcttat	tcaaccgttg	gaactcttga	ttacatggct	ccagaagtac	tcctaaagaa	1080



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aggatatgga atggaatgtg attggtggtc tctcggcgca attttgtatg agatgttagt 1140
tgggtatccc ccattctgtt ctgatgaccc ccgtataaca tgccgcaaga taattaattg 1200
gagggtatgc ttgaagttcc ctgaacaacc aaaaatatca gatgaagcca gagacttgat 1260
ttgtcggttg ctttgtgatg ttgattcaag gttgggaacc agaggtgttg aggagataaa 1320
gtcgcatcca tggttcaaag gcaccccatg ggacaaactg tatgacatgg aggcagctta 1380
tagaccatt gtcgatggag aactagacac acaaaatattt gagaagtttc ctgaagtga 1440
aggatcacca tccgaagcac cacaagttgg tccttgagaga aagatgttga cgtccaagga 1500
caccaacttc ataggattta catttaagaa gtcagacatc acaagatcaa tggaaagttc 1560
agggtgcagac atgaaatcaa atggatcagg ggaagccccg tcgttgatat cattgttagg 1620
tcggatcaat atggaagaag gtgaagggtg tgagttaaac cacaagacat agggaaaata 1680
caaataattat tgatttttta tccgcttgca gttgttttga tcatttggca gaggcaatgg 1740
agaggcgatg gtagtttttt aaccacatca cttatgatgg ggttcataaa aacttctatt 1800
tccttttttt ttcttgtaac atatttgttt ttttttcaat ctaaaaaaga aactgtaaag 1860
catggaagaa taatttctgg aacattttac cccc
```

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

```
Met Asp Gly Ala Asp Gly Thr Val Arg Val Lys Pro Gly Arg Gly Phe
1          5          10          15
Glu Thr Glu Thr Asp Val Ala Val Ser Ser Pro Val Thr Arg Gln Lys
          20          25          30
Ala Ala Ala Ala Lys Gln Phe Ile Glu Asn His Tyr Lys Asn Tyr Leu
          35          40          45
Gln Gly Leu His Glu Arg Met Glu Arg Arg Arg Glu Phe Gln Arg Lys
          50          55          60
Val Gln Glu Ala Gln Leu Pro Val Glu Glu Gln Asp Glu Met Met Arg
65          70          75          80
Asn Leu Ala Arg Arg Glu Thr Glu Tyr Met Arg Leu Gln Arg Arg Lys
          85          90          95
Ile Gly Ile Asp Asp Phe Glu Leu Leu Thr Val Ile Gly Lys Gly Ala
          100          105          110
Phe Gly Glu Val Arg Leu Cys Arg Leu Arg Ser Thr Ser Glu Val Tyr
          115          120          125
Ala Met Lys Lys Leu Lys Lys Thr Glu Met Leu Ser Arg Gly Gln Val
          130          135          140
Glu His Val Arg Ser Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Arg
          145          150          155          160
Tyr Ile Val Lys Leu Phe Tyr Ser Phe Gln Asp Ser Glu Cys Leu Tyr
          165          170          175
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Ile Met Thr Leu Leu Met
          180          185          190
Arg Glu Asp Ile Leu Ser Glu Asp Val Ala Arg Phe Tyr Ile Ala Glu
          195          200          205
Ser Ile Leu Ala Ile His Ser Ile His Gln His Asn Tyr Val His Arg
          210          215          220
Asp Ile Lys Pro Asp Asn Leu Ile Leu Asp Lys Ser Gly His Leu Lys
          225          230          235          240
Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu Asp Asp Lys Tyr Ser Ser
          245          250          255
Leu Leu Leu Glu Asp Asp Glu Met Leu Ser Gln Asp Ser Glu Asn Gln
          260          265          270
Ser Gly Lys Ser Asp Ala Asp Lys Ala Pro Trp Gln Met Pro Lys Glu
```

275	280	285
Gln Leu Leu Gln Trp Lys Arg Asn Arg Arg Ala Leu Ala Tyr Ser Thr		
290	295	300
Val Gly Thr Leu Asp Tyr Met Ala Pro Glu Val Leu Leu Lys Lys Gly		
305	310	315
Tyr Gly Met Glu Cys Asp Trp Trp Ser Leu Gly Ala Ile Leu Tyr Glu		
	325	330
Met Leu Val Gly Tyr Pro Pro Phe Cys Ser Asp Asp Pro Arg Ile Thr		
	340	345
Cys Arg Lys Ile Ile Asn Trp Arg Val Cys Leu Lys Phe Pro Glu Gln		
	355	360
Pro Lys Ile Ser Asp Glu Ala Arg Asp Leu Ile Cys Arg Leu Leu Cys		
	370	375
Asp Val Asp Ser Arg Leu Gly Thr Arg Gly Val Glu Glu Ile Lys Ser		
385	390	395
His Pro Trp Phe Lys Gly Thr Pro Trp Asp Lys Leu Tyr Asp Met Glu		
	405	410
Ala Ala Tyr Arg Pro Ile Val Asp Gly Glu Leu Asp Thr Gln Asn Phe		
	420	425
Glu Lys Phe Pro Glu Val Glu Gly Ser Pro Ser Glu Ala Pro Gln Val		
	435	440
Gly Pro Trp Arg Lys Met Leu Thr Ser Lys Asp Thr Asn Phe Ile Gly		
	450	455
Phe Thr Phe Lys Lys Ser Asp Ile Thr Arg Ser Met Glu Ser Ser Gly		
465	470	475
Ala Asp Met Lys Ser Asn Gly Ser Gly Glu Ala Pro Ser Leu Ile Ser		
	485	490
Leu Leu Gly Arg Ile Asn Met Glu Glu Gly Glu Gly Glu Leu Asn		
	500	505
His Lys Thr		510
	515	

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

Met Glu Arg Arg Arg Glu Phe Gln Arg Lys Val Gln Glu Ala Gln Leu	
1	15
Pro Val Glu Glu Gln Asp Glu Met Met Arg Asn Leu Ala Arg Arg Glu	
	30
Thr Glu Tyr Met Arg Leu Gln Arg Arg Lys Ile Gly Ile Asp Asp Phe	
	45
Glu Leu Leu Thr Val Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Leu	
	60
Cys Arg Leu Arg Ser Thr Ser Glu Val Tyr Ala Met Lys Lys Leu Lys	
65	80
Lys Thr Glu Met Leu Ser Arg Gly Gln Val Glu His Val Arg Ser Glu	
	95
Arg Asn Leu Leu Ala Glu Val Asp Ser Arg Tyr Ile Val Lys Leu Phe	
	110
Tyr Ser Phe Gln Asp Ser Glu Cys Leu Tyr Leu Ile Met Glu Tyr Leu	
	125
Pro Gly Gly Asp Ile Met Thr Leu Leu Met Arg Glu Asp Ile Leu Ser	
130	140

Glu	Asp	Val	Ala	Arg	Phe	Tyr	Ile	Ala	Glu	Ser	Ile	Leu	Ala	Ile	His
145					150				155						160
Ser	Ile	His	Gln	His	Asn	Tyr	Val	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn
			165						170						175
Leu	Ile	Leu	Asp	Lys	Ser	Gly	His	Leu	Lys	Leu	Ser	Asp	Phe	Gly	Leu
			180						185						190
Cys	Lys	Pro	Leu	Asp	Asp	Lys	Tyr	Ser	Ser	Leu	Leu	Leu	Glu	Asp	Asp
			195				200						205		
Glu	Met	Leu	Ser	Gln	Asp	Ser	Glu	Asn	Gln	Ser	Gly	Lys	Ser	Asp	Ala
			210				215					220			
Asp	Lys	Ala	Pro	Trp	Gln	Met	Pro	Lys	Glu	Gln	Leu	Leu	Gln	Trp	Lys
225					230					235					240
Arg	Asn	Arg	Arg	Ala	Leu	Ala	Tyr	Ser	Thr	Val	Gly	Thr	Leu	Asp	Tyr
				245						250					255
Met	Ala	Pro	Glu	Val	Leu	Leu	Lys	Lys	Gly	Tyr	Gly	Met	Glu	Cys	Asp
			260					265					270		
Trp	Trp	Ser	Leu	Gly	Ala	Ile	Leu	Tyr	Glu	Met	Leu	Val	Gly	Tyr	Pro
			275					280					285		
Pro	Phe	Cys	Ser	Asp	Asp	Pro	Arg	Ile	Thr	Cys	Arg	Lys	Ile	Ile	Asn
					295							300			
Trp	Arg	Val	Cys	Leu	Lys	Phe	Pro	Glu	Gln	Pro	Lys	Ile	Ser	Asp	Glu
305					310						315				320
Ala	Arg	Asp	Leu	Ile	Cys	Arg	Leu	Leu	Cys	Asp	Val	Asp	Ser	Arg	Leu
				325					330						335
Gly	Thr	Arg	Gly	Val	Glu	Glu	Ile	Lys	Ser	His	Pro	Trp	Phe	Lys	Gly
				340				345						350	
Thr	Pro	Trp	Asp	Lys	Leu	Tyr	Asp	Met	Glu	Ala	Ala	Tyr	Arg	Pro	Ile
			355				360						365		
Val	Asp	Gly	Glu	Leu	Asp	Thr	Gln	Asn	Phe	Glu	Lys	Phe	Pro	Glu	Val
			370			375					380				
Glu	Gly	Ser	Pro	Ser	Glu	Ala	Pro	Gln	Val	Gly	Pro	Trp	Arg	Lys	Met
385					390					395					400
Leu	Thr	Ser	Lys	Asp	Thr	Asn	Phe	Ile	Gly	Phe	Thr	Phe	Lys	Lys	Ser
				405					410						415
Asp	Ile	Thr	Arg	Ser	Met	Glu	Ser	Ser	Gly	Ala	Asp	Met	Lys	Ser	Asn
				420					425				430		
Gly	Ser	Gly	Glu	Ala	Pro	Ser	Leu	Ile	Ser	Leu	Leu	Gly	Arg	Ile	Asn
			435				440					445			
Met	Glu	Gly	Glu	Gly	Gly	Gly	Glu	Leu	Asn	His	Lys	Thr			
450					455						460				

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1499253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Met	Met	Arg	Asn	Leu	Ala	Arg	Arg	Glu	Thr	Glu	Tyr	Met	Arg	Leu	Gln
1				5					10					15	
Arg	Arg	Lys	Ile	Gly	Ile	Asp	Asp	Phe	Glu	Leu	Leu	Thr	Val	Ile	Gly
			20					25					30		
Lys	Gly	Ala	Phe	Gly	Glu	Val	Arg	Leu	Cys	Arg	Leu	Arg	Ser	Thr	Ser
		35					40					45			
Glu	Val	Tyr	Ala	Met	Lys	Lys	Leu	Lys	Lys	Thr	Glu	Met	Leu	Ser	Arg
	50				55					60					
Gly	Gln	Val	Glu	His	Val	Arg	Ser	Glu	Arg	Asn	Leu	Leu	Ala	Glu	Val

65		70		75		80
Asp Ser Arg Tyr	Ile Val Lys Leu Phe Tyr Ser Phe Gln Asp Ser Glu					
	85		90		95	
Cys Leu Tyr Leu	Ile Met Glu Tyr Leu Pro Gly Gly Asp Ile Met Thr					
	100		105		110	
Leu Leu Met Arg	Glu Asp Ile Leu Ser Glu Asp Val Ala Arg Phe Tyr					
	115		120		125	
Ile Ala Glu Ser	Ile Leu Ala Ile His Ser Ile His Gln His Asn Tyr					
	130		135		140	
Val His Arg Asp	Ile Lys Pro Asp Asn Leu Ile Leu Asp Lys Ser Gly					
	145		150		155	
His Leu Lys Leu	Ser Asp Phe Gly Leu Cys Lys Pro Leu Asp Asp Lys					
	165		170		175	
Tyr Ser Ser Leu	Leu Leu Glu Asp Asp Glu Met Leu Ser Gln Asp Ser					
	180		185		190	
Glu Asn Gln Ser	Gly Lys Ser Asp Ala Asp Lys Ala Pro Trp Gln Met					
	195		200		205	
Pro Lys Glu Gln	Leu Leu Gln Trp Lys Arg Asn Arg Arg Ala Leu Ala					
	210		215		220	
Tyr Ser Thr Val	Gly Thr Leu Asp Tyr Met Ala Pro Glu Val Leu Leu					
	225		230		235	
Lys Lys Gly Tyr	Gly Met Glu Cys Asp Trp Trp Ser Leu Gly Ala Ile					
	245		250		255	
Leu Tyr Glu Met	Leu Val Gly Tyr Pro Pro Phe Cys Ser Asp Asp Pro					
	260		265		270	
Arg Ile Thr Cys	Arg Lys Ile Ile Asn Trp Arg Val Cys Leu Lys Phe					
	275		280		285	
Pro Glu Gln Pro	Lys Ile Ser Asp Glu Ala Arg Asp Leu Ile Cys Arg					
	290		295		300	
Leu Leu Cys Asp	Val Asp Ser Arg Leu Gly Thr Arg Gly Val Glu Glu					
	305		310		315	
Ile Lys Ser His	Pro Trp Phe Lys Gly Thr Pro Trp Asp Lys Leu Tyr					
	325		330		335	
Asp Met Glu Ala	Ala Tyr Arg Pro Ile Val Asp Gly Glu Leu Asp Thr					
	340		345		350	
Gln Asn Phe Glu	Lys Phe Pro Glu Val Glu Gly Ser Pro Ser Glu Ala					
	355		360		365	
Pro Gln Val Gly	Pro Trp Arg Lys Met Leu Thr Ser Lys Asp Thr Asn					
	370		375		380	
Phe Ile Gly Phe	Thr Phe Lys Lys Ser Asp Ile Thr Arg Ser Met Glu					
	385		390		395	
Ser Ser Gly Ala	Asp Met Lys Ser Asn Gly Ser Gly Glu Ala Pro Ser					
	405		410		415	
Leu Ile Ser Leu	Leu Gly Arg Ile Asn Met Glu Glu Gly Glu Gly Gly					
	420		425		430	
Glu Leu Asn His	Lys Thr					
	435					

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

aagcttttga agctttctcaa caatggcggc tattccttcc cacaacaacc ttcttaccat  
caaccacaaa aactccataa ccggttcttc ttcccttaat accaatttct cagaaatcaa

60  
120

ttttcccgcc	aaattccgag	tagctacgag	agctttgtcc	agaaccgacg	agtcgtcttt	180
atccgccgtg	attttctcgcc	tcgagcgaga	aaggcgggaa	agacaagggt	tattaatcga	240
ggaagcggaa	ggagctggag	aactatggat	gacggcggaa	gatattcgcc	ggcgagataa	300
aaaaaccgaa	gaagaaagaa	gactaagaga	cacgtggcgt	aagatccaag	gagaagacga	360
ttgggcccgg	ttaatggatc	caatggatcc	aattcttaga	tcggagctaa	tccgttacgg	420
cgaaatggct	caagcttggt	acgacgcttt	cgatttcgat	cccgcctcca	aatactgcgg	480
cacctccagg	ttcacgcgac	tcgagttctt	cgattctctc	ggaatgatcg	attccggtta	540
cgaggtggcg	cgttacctct	acgcgacgtc	gaacatcaat	ctcccgaact	tcttctcgaa	600
atcgcggtgg	tctaaagtct	ggagcaaaaa	cgctaattgg	atgggatacg	tcgccgtttc	660
agacgacgaa	acgtctcgta	accgactcgg	ccgccgtgat	atcgcgattg	cgtggagagg	720
aaccgttacg	aaacttgaat	ggatcgcgga	tctaaaggat	tatttaaaac	cggtaaccca	780
aaacaagatc	cgatgccccg	acccggccgt	taaagtcgaa	tccggattct	tagatctcta	840
cactgacaaa	gacacaacct	gcaaattcgc	gagattctca	gcgcgtgaac	agattttaac	900
ggaggtgaaa	cggttagtgg	aagaacacgg	cgacgacgat	gattccgatt	taagcatcac	960
cgtgacggga	cacagtctcg	gcggcgcggt	agcgatatta	agcgcgtacg	atatagcgga	1020
gatgagattg	aatcggagta	agaaagggaa	agtgattccg	gtgacgggtg	tgacatacgg	1080
aggaccgaga	gttgggaacg	ttaggtttag	ggagaggatg	gaggaattgg	gagtgaaggt	1140
gatgagagta	gtgaatgttc	acgacgtggt	tcccaagtcg	ccgggattgt	ttttgaacga	1200
gagtagacct	cacgcgctga	tgaagatagc	ggaggggttg	ccgtgggtgt	atagccacgt	1260
gggggaggag	ctggcggttg	atcatcagaa	ctcgcggttt	cttaaaccct	ccgttgatgt	1320
ttctactgct	cataatcttg	aagctatgct	tcatttactt	gacgggtatc	atggaaaagg	1380
agagagattt	gtgctgtcga	gtgggagaga	ccatgcgcta	gtgaacaaag	cgtcggaact	1440
tttgaagag	catttacaaa	ttccaccgtt	ttggcgtcaa	gacgcgaata	aaggaatggt	1500
tcggaacagt	gaaggtcggt	ggattcaagc	cgagcgtctc	cgttttgagg	atcatcattc	1560
tcctgatata	caccaccatc	tctctcagct	ccgtcttgat	catacttggt	aatcacacgc	1620
acatatatat	aatacacaca	ttttccctaa	tttgtaaagt	acgcataccat	cttttgaaaa	1680
taaaatgtca	caatcatctc	acttgacggc	tttggtcaac	gtacgttccc	tattaataaa	1740

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1499255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

Met	Ala	Ala	Ile	Pro	Ser	His	Asn	Asn	Leu	Leu	Thr	Ile	Asn	His	Lys
1				5					10					15	
Asn	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Leu	Asn	Thr	Asn	Phe	Ser	Glu	Ile
			20					25					30		
Asn	Phe	Pro	Ala	Lys	Phe	Arg	Val	Ala	Thr	Arg	Ala	Leu	Ser	Arg	Thr
		35					40					45			
Asp	Glu	Ser	Ser	Leu	Ser	Ala	Val	Ile	Ser	Arg	Leu	Glu	Arg	Glu	Arg
	50					55					60				
Arg	Glu	Arg	Gln	Gly	Leu	Leu	Ile	Glu	Glu	Ala	Glu	Gly	Ala	Gly	Glu
65					70					75				80	
Leu	Trp	Met	Thr	Ala	Glu	Asp	Ile	Arg	Arg	Arg	Asp	Lys	Lys	Thr	Glu
			85					90						95	
Glu	Glu	Arg	Arg	Leu	Arg	Asp	Thr	Trp	Arg	Lys	Ile	Gln	Gly	Glu	Asp
		100						105				110			
Asp	Trp	Ala	Gly	Leu	Met	Asp	Pro	Met	Asp	Pro	Ile	Leu	Arg	Ser	Glu
		115					120					125			
Leu	Ile	Arg	Tyr	Gly	Glu	Met	Ala	Gln	Ala	Cys	Tyr	Asp	Ala	Phe	Asp
		130					135					140			
Phe	Asp	Pro	Ala	Ser	Lys	Tyr	Cys	Gly	Thr	Ser	Arg	Phe	Thr	Arg	Leu
145					150					155				160	
Glu	Phe	Phe	Asp	Ser	Leu	Gly	Met	Ile	Asp	Ser	Gly	Tyr	Glu	Val	Ala

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..447
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1499256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

Met Thr Ala Glu Asp Ile Arg Arg Arg Asp Lys Lys Thr Glu Glu Glu  
1 5 10 15

Arg	Arg	Leu	Arg	Asp	Thr	Trp	Arg	Lys	Ile	Gln	Gly	Glu	Asp	Asp	Trp
		20						25					30		
Ala	Gly	Leu	Met	Asp	Pro	Met	Asp	Pro	Ile	Leu	Arg	Ser	Glu	Leu	Ile
		35					40					45			
Arg	Tyr	Gly	Glu	Met	Ala	Gln	Ala	Cys	Tyr	Asp	Ala	Phe	Asp	Phe	Asp
	50					55					60				
Pro	Ala	Ser	Lys	Tyr	Cys	Gly	Thr	Ser	Arg	Phe	Thr	Arg	Leu	Glu	Phe
65					70					75					80
Phe	Asp	Ser	Leu	Gly	Met	Ile	Asp	Ser	Gly	Tyr	Glu	Val	Ala	Arg	Tyr
			85					90						95	
Leu	Tyr	Ala	Thr	Ser	Asn	Ile	Asn	Leu	Pro	Asn	Phe	Phe	Ser	Lys	Ser
		100						105					110		
Arg	Trp	Ser	Lys	Val	Trp	Ser	Lys	Asn	Ala	Asn	Trp	Met	Gly	Tyr	Val
		115					120					125			
Ala	Val	Ser	Asp	Asp	Glu	Thr	Ser	Arg	Asn	Arg	Leu	Gly	Arg	Arg	Asp
	130					135					140				
Ile	Ala	Ile	Ala	Trp	Arg	Gly	Thr	Val	Thr	Lys	Leu	Glu	Trp	Ile	Ala
145					150					155					160
Asp	Leu	Lys	Asp	Tyr	Leu	Lys	Pro	Val	Thr	Glu	Asn	Lys	Ile	Arg	Cys
			165					170						175	
Pro	Asp	Pro	Ala	Val	Lys	Val	Glu	Ser	Gly	Phe	Leu	Asp	Leu	Tyr	Thr
		180						185					190		
Asp	Lys	Asp	Thr	Thr	Cys	Lys	Phe	Ala	Arg	Phe	Ser	Ala	Arg	Glu	Gln
		195					200					205			
Ile	Leu	Thr	Glu	Val	Lys	Arg	Leu	Val	Glu	Glu	His	Gly	Asp	Asp	Asp
	210					215					220				
Asp	Ser	Asp	Leu	Ser	Ile	Thr	Val	Thr	Gly	His	Ser	Leu	Gly	Gly	Ala
225					230					235					240
Leu	Ala	Ile	Leu	Ser	Ala	Tyr	Asp	Ile	Ala	Glu	Met	Arg	Leu	Asn	Arg
			245						250					255	
Ser	Lys	Lys	Gly	Lys	Val	Ile	Pro	Val	Thr	Val	Leu	Thr	Tyr	Gly	Gly
		260						265					270		
Pro	Arg	Val	Gly	Asn	Val	Arg	Phe	Arg	Glu	Arg	Met	Glu	Glu	Leu	Gly
		275					280					285			
Val	Lys	Val	Met	Arg	Val	Val	Asn	Val	His	Asp	Val	Val	Pro	Lys	Ser
	290					295					300				
Pro	Gly	Leu	Phe	Leu	Asn	Glu	Ser	Arg	Pro	His	Ala	Leu	Met	Lys	Ile
305					310					315					320
Ala	Glu	Gly	Leu	Pro	Trp	Cys	Tyr	Ser	His	Val	Gly	Glu	Glu	Leu	Ala
			325						330					335	
Leu	Asp	His	Gln	Asn	Ser	Pro	Phe	Leu	Lys	Pro	Ser	Val	Asp	Val	Ser
			340					345					350		
Thr	Ala	His	Asn	Leu	Glu	Ala	Met	Leu	His	Leu	Leu	Asp	Gly	Tyr	His
		355					360					365			
Gly	Lys	Gly	Glu	Arg	Phe	Val	Leu	Ser	Ser	Gly	Arg	Asp	His	Ala	Leu
	370					375				380					
Val	Asn	Lys	Ala	Ser	Asp	Phe	Leu	Lys	Glu	His	Leu	Gln	Ile	Pro	Pro
385					390					395					400
Phe	Trp	Arg	Gln	Asp	Ala	Asn	Lys	Gly	Met	Val	Arg	Asn	Ser	Glu	Gly
			405						410					415	
Arg	Trp	Ile	Gln	Ala	Glu	Arg	Leu	Arg	Phe	Glu	Asp	His	His	Ser	Pro
			420					425					430		
Asp	Ile	His	His	His	Leu	Ser	Gln	Leu	Arg	Leu	Asp	His	Pro	Cys	
		435					440					445			

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1499257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

Met	Asp	Pro	Met	Asp	Pro	Ile	Leu	Arg	Ser	Glu	Leu	Ile	Arg	Tyr	Gly
1			5						10					15	
Glu	Met	Ala	Gln	Ala	Cys	Tyr	Asp	Ala	Phe	Asp	Phe	Asp	Pro	Ala	Ser
		20					25						30		
Lys	Tyr	Cys	Gly	Thr	Ser	Arg	Phe	Thr	Arg	Leu	Glu	Phe	Phe	Asp	Ser
	35					40						45			
Leu	Gly	Met	Ile	Asp	Ser	Gly	Tyr	Glu	Val	Ala	Arg	Tyr	Leu	Tyr	Ala
	50				55						60				
Thr	Ser	Asn	Ile	Asn	Leu	Pro	Asn	Phe	Phe	Ser	Lys	Ser	Arg	Trp	Ser
65				70						75				80	
Lys	Val	Trp	Ser	Lys	Asn	Ala	Asn	Trp	Met	Gly	Tyr	Val	Ala	Val	Ser
			85						90					95	
Asp	Asp	Glu	Thr	Ser	Arg	Asn	Arg	Leu	Gly	Arg	Arg	Asp	Ile	Ala	Ile
			100					105					110		
Ala	Trp	Arg	Gly	Thr	Val	Thr	Lys	Leu	Glu	Trp	Ile	Ala	Asp	Leu	Lys
	115						120					125			
Asp	Tyr	Leu	Lys	Pro	Val	Thr	Glu	Asn	Lys	Ile	Arg	Cys	Pro	Asp	Pro
	130					135					140				
Ala	Val	Lys	Val	Glu	Ser	Gly	Phe	Leu	Asp	Leu	Tyr	Thr	Asp	Lys	Asp
145					150					155				160	
Thr	Thr	Cys	Lys	Phe	Ala	Arg	Phe	Ser	Ala	Arg	Glu	Gln	Ile	Leu	Thr
			165						170					175	
Glu	Val	Lys	Arg	Leu	Val	Glu	Glu	His	Gly	Asp	Asp	Asp	Asp	Ser	Asp
			180					185					190		
Leu	Ser	Ile	Thr	Val	Thr	Gly	His	Ser	Leu	Gly	Gly	Ala	Leu	Ala	Ile
	195					200						205			
Leu	Ser	Ala	Tyr	Asp	Ile	Ala	Glu	Met	Arg	Leu	Asn	Arg	Ser	Lys	Lys
	210				215						220				
Gly	Lys	Val	Ile	Pro	Val	Thr	Val	Leu	Thr	Tyr	Gly	Gly	Pro	Arg	Val
225					230					235				240	
Gly	Asn	Val	Arg	Phe	Arg	Glu	Arg	Met	Glu	Glu	Leu	Gly	Val	Lys	Val
			245						250					255	
Met	Arg	Val	Val	Asn	Val	His	Asp	Val	Val	Pro	Lys	Ser	Pro	Gly	Leu
		260					265						270		
Phe	Leu	Asn	Glu	Ser	Arg	Pro	His	Ala	Leu	Met	Lys	Ile	Ala	Glu	Gly
	275					280						285			
Leu	Pro	Trp	Cys	Tyr	Ser	His	Val	Gly	Glu	Glu	Leu	Ala	Leu	Asp	His
	290				295						300				
Gln	Asn	Ser	Pro	Phe	Leu	Lys	Pro	Ser	Val	Asp	Val	Ser	Thr	Ala	His
305					310					315				320	
Asn	Leu	Glu	Ala	Met	Leu	His	Leu	Leu	Asp	Gly	Tyr	His	Gly	Lys	Gly
			325						330					335	
Glu	Arg	Phe	Val	Leu	Ser	Ser	Gly	Arg	Asp	His	Ala	Leu	Val	Asn	Lys
		340					345						350		
Ala	Ser	Asp	Phe	Leu	Lys	Glu	His	Leu	Gln	Ile	Pro	Pro	Phe	Trp	Arg
	355					360						365			
Gln	Asp	Ala	Asn	Lys	Gly	Met	Val	Arg	Asn	Ser	Glu	Gly	Arg	Trp	Ile
	370				375						380				
Gln	Ala	Glu	Arg	Leu	Arg	Phe	Glu	Asp	His	His	Ser	Pro	Asp	Ile	His
385				390						395				400	
His	His	Leu	Ser	Gln	Leu	Arg	Leu	Asp	His	Pro	Cys				
			405						410						

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1361 base pairs

(B) TYPE: nucleic acid



- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1361  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

```
ggattagga gactcgcaact cttcttcttc ttctttgtac ccagaaagaa agtgagctcc      60
aacaatggct gcttgcgcta ctactcctc tctcatgcta gcatacgccg ccgcatccac      120
tcgttcccag gaccttacc ctaactccatc tcttttctct tttgccagct ccagacccaa      180
ccacttgagc gtcccgcctc ttctccttgg gggttccagg gaccggagat gtgctgctat      240
tgacagagct tccaaccaca agtttattgt ctccgcctg ggcgctgagg ctgacctcga      300
cacggaggag gacctggagc agaccgccac cgccgtcctt gatccgcca agcctaagaa      360
aggaaaagcc gctttgggtc tcaagagaga tagaacaagg tctaagaggt ttttggaat      420
ccaaaagcta agggaaacca aaaaggagta tgatgtcaac actgctatct ctttgcttaa      480
acaaactgcc aacacaaggt ttgttgagtc tggtgaagcc catttccgtc tcaacatcga      540
tcctaagtac aatgaccagc agctgcgtgc aacggtgagc ctgcctaagg gaactggcca      600
gactgttata gtcgctgttc ttgcacaagg tgagaagggt gatgaagcca aaagtgcagg      660
ggcagatatt gtgggcagtg atgatttaat cgaacagatt aaaggaggct tcatggagtt      720
tgacaagctg attgcatccc cggatatgat ggtcaagggt gctggcctgg gaaagattct      780
tgaccacggg gggctcatgc caaatcccaa ggctgggtaca gtcacagcga acattcccca      840
ggctattgaa gagttcaaga aggggaaagt tgaattcaga gcagacaaaa ctgggattgt      900
tcacattcca tttgggaaag ttaattttac agaggaagac cttctcataa acttccttgc      960
agcagtgaag tcggtggaga caaacaagcc aaaggagct aaaggagtgt actggaaaag     1020
cgctcacata tgctcgtaaa tggggccttc catcaagttg aacataagag agatgataga     1080
cttcaagcct cccactgcga actaatcgac aacgccattt gtaaattggg tcttttggg     1140
agacgggcaa tgccagtgtg gacagagaag agaaacacca agtctagtct gttagtaatc     1200
ttttcacgcc tcaactgctt gtatcacttt gatggccatt tacttcttgt cgttatttat     1260
ttactattgc ctattaaaat ttggcaaggg gctgtacatg tcaggacgca gaactcttta     1320
gtactctcta aaagaaaaga ccttacattg atctttaggc t
```

(2) INFORMATION FOR SEQ ID NO:957:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 346 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..346  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

```
Met Ala Ala Cys Ala Thr His Ser Ser Leu Met Leu Ala Tyr Ala Ala
1      5      10      15
Ala Ser Thr Arg Ser Gln Asp Leu Thr Pro Thr Pro Ser Leu Phe Ser
20     25     30
Phe Ala Ser Ser Arg Pro Asn His Leu Ser Val Pro Leu Leu Leu Leu
35     40     45
Gly Gly Ser Arg Asp Arg Arg Cys Ala Ala Ile Asp Arg Ala Ser Asn
50     55     60
His Lys Phe Ile Val Ser Ala Val Ala Ala Glu Ala Asp Leu Asp Thr
65     70     75     80
Glu Glu Asp Leu Glu Gln Thr Ala Thr Ala Val Leu Asp Pro Pro Lys
85     90     95
Pro Lys Lys Gly Lys Ala Ala Leu Val Leu Lys Arg Asp Arg Thr Arg
100    105    110
Ser Lys Arg Phe Leu Glu Ile Gln Lys Leu Arg Glu Thr Lys Lys Glu
115    120    125
Tyr Asp Val Asn Thr Ala Ile Ser Leu Leu Lys Gln Thr Ala Asn Thr
130    135    140
```

Arg	Phe	Val	Glu	Ser	Val	Glu	Ala	His	Phe	Arg	Leu	Asn	Ile	Asp	Pro
145					150					155					160
Lys	Tyr	Asn	Asp	Gln	Gln	Leu	Arg	Ala	Thr	Val	Ser	Leu	Pro	Lys	Gly
			165						170						175
Thr	Gly	Gln	Thr	Val	Ile	Val	Ala	Val	Leu	Ala	Gln	Gly	Glu	Lys	Val
			180						185						190
Asp	Glu	Ala	Lys	Ser	Ala	Gly	Ala	Asp	Ile	Val	Gly	Ser	Asp	Asp	Leu
		195					200					205			
Ile	Glu	Gln	Ile	Lys	Gly	Gly	Phe	Met	Glu	Phe	Asp	Lys	Leu	Ile	Ala
	210					215					220				
Ser	Pro	Asp	Met	Met	Val	Lys	Val	Ala	Gly	Leu	Gly	Lys	Ile	Leu	Gly
225					230					235					240
Pro	Arg	Gly	Leu	Met	Pro	Asn	Pro	Lys	Ala	Gly	Thr	Val	Thr	Ala	Asn
				245					250						255
Ile	Pro	Gln	Ala	Ile	Glu	Glu	Phe	Lys	Lys	Gly	Lys	Val	Glu	Phe	Arg
			260					265							270
Ala	Asp	Lys	Thr	Gly	Ile	Val	His	Ile	Pro	Phe	Gly	Lys	Val	Asn	Phe
		275					280					285			
Thr	Glu	Glu	Asp	Leu	Leu	Ile	Asn	Phe	Leu	Ala	Ala	Val	Lys	Ser	Val
	290					295					300				
Glu	Thr	Asn	Lys	Pro	Lys	Gly	Ala	Lys	Gly	Val	Tyr	Trp	Lys	Ser	Ala
305					310					315					320
His	Ile	Cys	Ser	Ser	Met	Gly	Pro	Ser	Ile	Lys	Leu	Asn	Ile	Arg	Glu
			325						330						335
Met	Ile	Asp	Phe	Lys	Pro	Pro	Thr	Ala	Asn						
			340					345							

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1499260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

Met	Leu	Ala	Tyr	Ala	Ala	Ala	Ser	Thr	Arg	Ser	Gln	Asp	Leu	Thr	Pro
1			5						10					15	
Thr	Pro	Ser	Leu	Phe	Ser	Phe	Ala	Ser	Ser	Arg	Pro	Asn	His	Leu	Ser
			20					25					30		
Val	Pro	Leu	Leu	Leu	Leu	Gly	Gly	Ser	Arg	Asp	Arg	Arg	Cys	Ala	Ala
		35				40					45				
Ile	Asp	Arg	Ala	Ser	Asn	His	Lys	Phe	Ile	Val	Ser	Ala	Val	Ala	Ala
	50					55					60				
Glu	Ala	Asp	Leu	Asp	Thr	Glu	Glu	Asp	Leu	Glu	Gln	Thr	Ala	Thr	Ala
65					70				75						80
Val	Leu	Asp	Pro	Pro	Lys	Pro	Lys	Lys	Gly	Lys	Ala	Ala	Leu	Val	Leu
			85						90					95	
Lys	Arg	Asp	Arg	Thr	Arg	Ser	Lys	Arg	Phe	Leu	Glu	Ile	Gln	Lys	Leu
			100					105					110		
Arg	Glu	Thr	Lys	Lys	Glu	Tyr	Asp	Val	Asn	Thr	Ala	Ile	Ser	Leu	Leu
		115					120					125			
Lys	Gln	Thr	Ala	Asn	Thr	Arg	Phe	Val	Glu	Ser	Val	Glu	Ala	His	Phe
		130				135					140				
Arg	Leu	Asn	Ile	Asp	Pro	Lys	Tyr	Asn	Asp	Gln	Gln	Leu	Arg	Ala	Thr
145					150				155						160
Val	Ser	Leu	Pro	Lys	Gly	Thr	Gly	Gln	Thr	Val	Ile	Val	Ala	Val	Leu
				165					170						175
Ala	Gln	Gly	Glu	Lys	Val	Asp	Glu	Ala	Lys	Ser	Ala	Gly	Ala	Asp	Ile

			180					185					190			
Val	Gly	Ser	Asp	Asp	Leu	Ile	Glu	Gln	Ile	Lys	Gly	Gly	Phe	Met	Glu	
		195					200					205				
Phe	Asp	Lys	Leu	Ile	Ala	Ser	Pro	Asp	Met	Met	Val	Lys	Val	Ala	Gly	
	210					215					220					
Leu	Gly	Lys	Ile	Leu	Gly	Pro	Arg	Gly	Leu	Met	Pro	Asn	Pro	Lys	Ala	
225					230					235					240	
Gly	Thr	Val	Thr	Ala	Asn	Ile	Pro	Gln	Ala	Ile	Glu	Glu	Phe	Lys	Lys	
				245					250					255		
Gly	Lys	Val	Glu	Phe	Arg	Ala	Asp	Lys	Thr	Gly	Ile	Val	His	Ile	Pro	
		260						265					270			
Phe	Gly	Lys	Val	Asn	Phe	Thr	Glu	Asp	Leu	Leu	Ile	Asn	Phe	Leu		
		275					280					285				
Ala	Ala	Val	Lys	Ser	Val	Glu	Thr	Asn	Lys	Pro	Lys	Gly	Ala	Lys	Gly	
		290				295					300					
Val	Tyr	Trp	Lys	Ser	Ala	His	Ile	Cys	Ser	Ser	Met	Gly	Pro	Ser	Ile	
305					310					315					320	
Lys	Leu	Asn	Ile	Arg	Glu	Met	Ile	Asp	Phe	Lys	Pro	Pro	Thr	Ala	Asn	
				325					330					335		

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

aatttcaccg	ctctttctct	ttcgcttctc	tgagaagttt	caaagcta	tcagctttcg	60
agaaattgca	acaatggaga	aactcgcggc	gtctactgtt	acagatctag	cttgcgtaac	120
ggcgataaac	tcaccaccgc	ctccactatc	accgatctct	gaacaaagct	tcagcaacaa	180
acaccaagaa	gagttcgcag	caagcttcgc	atcactctac	aactcaattt	tctcaccgga	240
atctcaattc	tctccttctc	ctccgctctc	ttcctcacca	ccatctcgcg	tcgatacaac	300
tacagagcat	cgtcttcttc	aagcgaaact	tatcctcgag	tacgatgaac	tcaacgatca	360
ttacgagctt	tgctttaacc	gtcttcaatc	tctaattgacg	gaacttgact	ctcttcgtca	420
cgaaaacgat	tctctccgct	ttgaaaactc	agatctactc	aaacttattc	atatctctac	480
ttcatctctc	tctctcgtct	ctcctccggc	gccgatccat	aaccgtcaat	tccgtcacca	540
gatctccgat	tctcgctccg	cgaagagaaa	caatcaagag	agaaactcgt	tgcttaagag	600
catctccgtc	agatctcaag	gatattctcaa	gatcaaccat	ggatttgaag	cttcagatcg	660
ccaaacgagt	caactcagct	ctaactcggg	gttgtcttct	caaaagggtg	gtgtagtaca	720
aaccaaaggg	gagagagaag	cattagagct	tgaggatat	cgtcaaggga	tgatgaagac	780
ggagctttgt	aacaaatggc	aagagactgg	agcttggtgt	tacggcgata	attgccaat	840
cgctcacgga	atcgacgagc	tacgtcctgt	gattaggtat	ccacgctaca	aaactgaggt	900
ttgcagaatg	attgtcaccg	gagctatgtg	tccttacggg	caccgttgcc	atttccgtca	960
ctcacttact	gatcaagaga	ggatgatgat	gatgatgctt	actcgctgat	ctggagaaga	1020
agaagaaagg	tcattgaaaa	agagaaataa	ttagtggttg	tgtacagatt	tcagatttga	1080
taccttataa	atatcgtaac	ttttctgggt	atttgctata	ggaataagga	agagaaagtg	1140
tttaataaat	gtttgatagg	attataggaa	tataattagg	gttgaagaaa	tgtgtggttc	1200
tcggataaaag	ctggagagac	ctgaaagagg	atttagattt	aacaaagata	tggaatttgc	1260
attgataaaa	gtttttgact	ttgtgcaaaa	ctatgcaact	ttcttcc		

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1499262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

Met	Glu	Lys	Leu	Ala	Ala	Ser	Thr	Val	Thr	Asp	Leu	Ala	Cys	Val	Thr
1			5					10					15		
Ala	Ile	Asn	Ser	Pro	Pro	Pro	Pro	Leu	Ser	Pro	Ile	Ser	Glu	Gln	Ser
		20						25				30			
Phe	Ser	Asn	Lys	His	Gln	Glu	Glu	Phe	Ala	Ala	Ser	Phe	Ala	Ser	Leu
	35					40					45				
Tyr	Asn	Ser	Ile	Phe	Ser	Pro	Glu	Ser	Gln	Phe	Ser	Pro	Ser	Pro	Pro
	50					55					60				
Ser	Ser	Ser	Ser	Pro	Pro	Ser	Arg	Val	Asp	Thr	Thr	Thr	Glu	His	Arg
65				70					75					80	
Leu	Leu	Gln	Ala	Lys	Leu	Ile	Leu	Glu	Tyr	Asp	Glu	Leu	Asn	Asp	His
		85						90					95		
Tyr	Glu	Leu	Cys	Leu	Asn	Arg	Leu	Gln	Ser	Leu	Met	Thr	Glu	Leu	Asp
	100							105					110		
Ser	Leu	Arg	His	Glu	Asn	Asp	Ser	Leu	Arg	Phe	Glu	Asn	Ser	Asp	Leu
	115						120					125			
Leu	Lys	Leu	Ile	His	Ile	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Val	Ser	Pro
	130						135					140			
Pro	Ala	Pro	Ile	His	Asn	Arg	Gln	Phe	Arg	His	Gln	Ile	Ser	Asp	Ser
145					150					155				160	
Arg	Ser	Ala	Lys	Arg	Asn	Asn	Gln	Glu	Arg	Asn	Ser	Leu	Pro	Lys	Ser
			165					170						175	
Ile	Ser	Val	Arg	Ser	Gln	Gly	Tyr	Leu	Lys	Ile	Asn	His	Gly	Phe	Glu
		180						185					190		
Ala	Ser	Asp	Arg	Gln	Thr	Ser	Gln	Leu	Ser	Ser	Asn	Ser	Val	Leu	Ser
	195						200					205			
Ser	Gln	Lys	Val	Cys	Val	Val	Gln	Thr	Lys	Gly	Glu	Arg	Glu	Ala	Leu
	210						215					220			
Glu	Leu	Glu	Val	Tyr	Arg	Gln	Gly	Met	Met	Lys	Thr	Glu	Leu	Cys	Asn
225					230					235				240	
Lys	Trp	Gln	Glu	Thr	Gly	Ala	Cys	Cys	Tyr	Gly	Asp	Asn	Cys	Gln	Phe
		245							250					255	
Ala	His	Gly	Ile	Asp	Glu	Leu	Arg	Pro	Val	Ile	Arg	His	Pro	Arg	Tyr
		260						265					270		
Lys	Thr	Glu	Val	Cys	Arg	Met	Ile	Val	Thr	Gly	Ala	Met	Cys	Pro	Tyr
	275						280					285			
Gly	His	Arg	Cys	His	Phe	Arg	His	Ser	Leu	Thr	Asp	Gln	Glu	Arg	Met
	290					295					300				
Met	Met	Met	Met	Leu	Thr	Arg									
305				310											

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1499263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met	Thr	Glu	Leu	Asp	Ser	Leu	Arg	His	Glu	Asn	Asp	Ser	Leu	Arg	Phe
1			5					10					15		
Glu	Asn	Ser	Asp	Leu	Leu	Lys	Leu	Ile	His	Ile	Ser	Thr	Ser	Ser	Ser



(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..398  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

Met	Glu	Ser	Ser	Ser	Pro	His	His	Ser	His	Ile	Val	Glu	Val	Asn	Val
1			5						10					15	
Gly	Lys	Ser	Asp	Glu	Glu	Arg	Ile	Ile	Val	Ala	Ser	Lys	Val	Cys	Gly
			20				25						30		
Glu	Ala	Pro	Cys	Gly	Phe	Ser	Asp	Ser	Lys	Asn	Ala	Ser	Gly	Asp	Ala
			35				40						45		
His	Glu	Arg	Ser	Ala	Ser	Met	Arg	Lys	Leu	Cys	Ile	Ala	Val	Val	Leu
						55					60				
Cys	Leu	Val	Phe	Met	Ser	Val	Glu	Val	Val	Gly	Gly	Ile	Lys	Ala	Asn
65						70				75					80
Ser	Leu	Ala	Ile	Leu	Thr	Asp	Ala	Ala	His	Leu	Leu	Ser	Asp	Val	Ala
				85					90					95	
Ala	Phe	Ala	Ile	Ser	Leu	Phe	Ser	Leu	Trp	Ala	Ala	Gly	Trp	Glu	Ala
			100					105					110		
Thr	Pro	Arg	Gln	Thr	Tyr	Gly	Phe	Phe	Arg	Ile	Glu	Ile	Leu	Gly	Ala
			115				120						125		
Leu	Val	Ser	Ile	Gln	Leu	Ile	Trp	Leu	Leu	Thr	Gly	Ile	Leu	Val	Tyr
			130				135					140			
Glu	Ala	Ile	Ile	Arg	Ile	Val	Thr	Glu	Thr	Ser	Glu	Val	Asn	Gly	Phe
145						150				155					160
Leu	Met	Phe	Leu	Val	Ala	Ala	Phe	Gly	Leu	Val	Val	Asn	Ile	Ile	Met
				165					170					175	
Ala	Val	Leu	Leu	Gly	His	Asp	His	Gly	His	Ser	His	Gly	His	Gly	His
			180					185					190		
Gly	His	Gly	His	Asp	His	His	Asn	His	Ser	His	Gly	Val	Thr	Val	Thr
			195				200					205			
Thr	His	His	His	His	His	Asp	His	Glu	His	Gly	His	Ser	His	Gly	His
			210			215					220				
Gly	Glu	Asp	Lys	His	His	Ala	His	Gly	Asp	Val	Thr	Glu	Gln	Leu	Leu
225						230				235					240
Asp	Lys	Ser	Lys	Thr	Gln	Val	Ala	Ala	Lys	Glu	Lys	Arg	Lys	Arg	Asn
				245					250					255	
Ile	Asn	Leu	Gln	Gly	Ala	Tyr	Leu	His	Val	Leu	Gly	Asp	Ser	Ile	Gln
			260					265					270		
Ser	Val	Gly	Val	Met	Ile	Gly	Gly	Ala	Ile	Ile	Trp	Tyr	Asn	Pro	Glu
			275				280					285			
Trp	Lys	Ile	Val	Asp	Leu	Ile	Cys	Thr	Leu	Ala	Phe	Ser	Val	Ile	Val
			290				295				300				
Leu	Gly	Thr	Thr	Ile	Asn	Met	Ile	Arg	Asn	Ile	Leu	Glu	Val	Leu	Met
305					310					315					320
Glu	Ser	Thr	Pro	Arg	Glu	Ile	Asp	Ala	Thr	Lys	Leu	Glu	Lys	Gly	Leu
				325					330					335	
Leu	Glu	Met	Glu	Glu	Val	Val	Ala	Val	His	Glu	Leu	His	Ile	Trp	Ala
			340					345					350		
Ile	Thr	Val	Gly	Lys	Val	Leu	Leu	Ala	Cys	His	Val	Asn	Ile	Arg	Pro
			355				360					365			
Glu	Ala	Asp	Ala	Asp	Met	Val	Leu	Asn	Lys	Val	Ile	Asp	Tyr	Ile	Arg
			370			375					380				
Arg	Glu	Tyr	Asn	Ile	Ser	His	Val	Thr	Ile	Gln	Ile	Glu	Arg		
385					390					395					

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..344  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499266  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

Met	Arg	Lys	Leu	Cys	Ile	Ala	Val	Val	Leu	Cys	Leu	Val	Phe	Met	Ser
1			5						10					15	
Val	Glu	Val	Val	Gly	Gly	Ile	Lys	Ala	Asn	Ser	Leu	Ala	Ile	Leu	Thr
			20					25					30		
Asp	Ala	Ala	His	Leu	Leu	Ser	Asp	Val	Ala	Ala	Phe	Ala	Ile	Ser	Leu
		35					40					45			
Phe	Ser	Leu	Trp	Ala	Ala	Gly	Trp	Glu	Ala	Thr	Pro	Arg	Gln	Thr	Tyr
	50					55					60				
Gly	Phe	Phe	Arg	Ile	Glu	Ile	Leu	Gly	Ala	Leu	Val	Ser	Ile	Gln	Leu
65				70						75					80
Ile	Trp	Leu	Leu	Thr	Gly	Ile	Leu	Val	Tyr	Glu	Ala	Ile	Ile	Arg	Ile
			85						90					95	
Val	Thr	Glu	Thr	Ser	Glu	Val	Asn	Gly	Phe	Leu	Met	Phe	Leu	Val	Ala
			100					105					110		
Ala	Phe	Gly	Leu	Val	Val	Asn	Ile	Ile	Met	Ala	Val	Leu	Leu	Gly	His
		115					120					125			
Asp	His	Gly	His	Ser	His	Gly	His	Gly	His	Gly	His	Gly	His	Asp	His
	130					135					140				
His	Asn	His	Ser	His	Gly	Val	Thr	Val	Thr	Thr	His	His	His	His	His
145				150						155					160
Asp	His	Glu	His	Gly	His	Ser	His	Gly	His	Gly	Glu	Asp	Lys	His	His
			165						170					175	
Ala	His	Gly	Asp	Val	Thr	Glu	Gln	Leu	Leu	Asp	Lys	Ser	Lys	Thr	Gln
		180						185					190		
Val	Ala	Ala	Lys	Glu	Lys	Arg	Lys	Arg	Asn	Ile	Asn	Leu	Gln	Gly	Ala
	195						200					205			
Tyr	Leu	His	Val	Leu	Gly	Asp	Ser	Ile	Gln	Ser	Val	Gly	Val	Met	Ile
	210					215					220				
Gly	Gly	Ala	Ile	Ile	Trp	Tyr	Asn	Pro	Glu	Trp	Lys	Ile	Val	Asp	Leu
225				230						235					240
Ile	Cys	Thr	Leu	Ala	Phe	Ser	Val	Ile	Val	Leu	Gly	Thr	Thr	Ile	Asn
			245						250					255	
Met	Ile	Arg	Asn	Ile	Leu	Glu	Val	Leu	Met	Glu	Ser	Thr	Pro	Arg	Glu
		260						265					270		
Ile	Asp	Ala	Thr	Lys	Leu	Glu	Lys	Gly	Leu	Leu	Glu	Met	Glu	Glu	Val
	275						280					285			
Val	Ala	Val	His	Glu	Leu	His	Ile	Trp	Ala	Ile	Thr	Val	Gly	Lys	Val
	290					295					300				
Leu	Leu	Ala	Cys	His	Val	Asn	Ile	Arg	Pro	Glu	Ala	Asp	Ala	Asp	Met
305				310						315					320
Val	Leu	Asn	Lys	Val	Ile	Asp	Tyr	Ile	Arg	Arg	Glu	Tyr	Asn	Ile	Ser
			325						330					335	
His	Val	Thr	Ile	Gln	Ile	Glu	Arg								
			340												

(2) INFORMATION FOR SEQ ID NO:965:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 330 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

```
Met Ser Val Glu Val Val Gly Gly Ile Lys Ala Asn Ser Leu Ala Ile
1      5      10      15
Leu Thr Asp Ala Ala His Leu Leu Ser Asp Val Ala Ala Phe Ala Ile
20      25      30
Ser Leu Phe Ser Leu Trp Ala Ala Gly Trp Glu Ala Thr Pro Arg Gln
35      40      45
Thr Tyr Gly Phe Phe Arg Ile Glu Ile Leu Gly Ala Leu Val Ser Ile
50      55      60
Gln Leu Ile Trp Leu Leu Thr Gly Ile Leu Val Tyr Glu Ala Ile Ile
65      70      75      80
Arg Ile Val Thr Glu Thr Ser Glu Val Asn Gly Phe Leu Met Phe Leu
85      90      95
Val Ala Ala Phe Gly Leu Val Val Asn Ile Ile Met Ala Val Leu Leu
100     105     110
Gly His Asp His Gly His Ser His Gly His Gly His Gly His Gly His
115     120     125
Asp His His Asn His Ser His Gly Val Thr Val Thr Thr His His His
130     135     140
His His Asp His Glu His Gly His Ser His Gly His Gly Glu Asp Lys
145     150     155     160
His His Ala His Gly Asp Val Thr Glu Gln Leu Leu Asp Lys Ser Lys
165     170     175
Thr Gln Val Ala Ala Lys Glu Lys Arg Lys Arg Asn Ile Asn Leu Gln
180     185     190
Gly Ala Tyr Leu His Val Leu Gly Asp Ser Ile Gln Ser Val Gly Val
195     200     205
Met Ile Gly Gly Ala Ile Ile Trp Tyr Asn Pro Glu Trp Lys Ile Val
210     215     220
Asp Leu Ile Cys Thr Leu Ala Phe Ser Val Ile Val Leu Gly Thr Thr
225     230     235     240
Ile Asn Met Ile Arg Asn Ile Leu Glu Val Leu Met Glu Ser Thr Pro
245     250     255
Arg Glu Ile Asp Ala Thr Lys Leu Glu Lys Gly Leu Leu Glu Met Glu
260     265     270
Glu Val Val Ala Val His Glu Leu His Ile Trp Ala Ile Thr Val Gly
275     280     285
Lys Val Leu Leu Ala Cys His Val Asn Ile Arg Pro Glu Ala Asp Ala
290     295     300
Asp Met Val Leu Asn Lys Val Ile Asp Tyr Ile Arg Arg Glu Tyr Asn
305     310     315     320
Ile Ser His Val Thr Ile Gln Ile Glu Arg
325     330
```

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 945 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..945

(D) OTHER INFORMATION: / Ceres Seq. ID 1499310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

```
accaaaccga cacctgcctc aactaatcgg gtcagatcag gtcacgggga aggccgccat
ggacgacgag gacgacgagg ttacggcca ggagatccct gaggacggcg atatggacgg
```

60  
120



```
cgctgacgtt gatatggccg ccgccgggga cgacgcggcg aacttcagga gcttgacgag 180
atgaagcgca astganagga gatggaggag gaggccgccg ccctccgcga tatgcaggcc 240
aaggctcgcca aggagatgca aggaggtgac cctagtatat ctacagctga rgcgaaggag 300
cagggtggatg cccgggtctgt gtatggttga aatggttgatt atgcttgacac cccagaagaa 360
gtgcagcagc atttccaagc ttgtggaact gtcaacaggg tgacaatctt gactgacaag 420
tttgggcagc caaaaggttt tgcttatggt gaatttctgg aacaagaagc tgtccaggaa 480
gctctgaact tgaatgaatc ggaattgcat ggtcgacaga ttaaggttgc gccgaagagg 540
actaatgtcc ctgggatgaa gcagcgtcca ccacgcgggt ataatcccta ccatggctac 600
ccttatagat catatggagc accgtacttc cccccatacg gttatggggag ggctcctaga 660
ttccgccgcc ctatgcgcta cagaccttac ttctgaagta cgtgcggggg aataatgttc 720
aatgcaaaac cagccatggt tagtggtcag tctcgggaat aattaaacct actgctgtat 780
cgtttgcgct gttcaatagt tgacatcggt gcggttcaat gctcctttac cagctgcctt 840
ttctgacctc tgttctcgca taagcgacat gtagacacag gacgtagggt tacaattggt 900
tgcattttct gtcattcttg attctgatga ccctatacag cactc
```

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

```
Met Glu Glu Glu Ala Ala Ala Leu Arg Asp Met Gln Ala Lys Val Ala
1      5      10      15
Lys Glu Met Gln Gly Gly Asp Pro Ser Ile Ser Thr Ala Xaa Ala Lys
20     25     30
Glu Gln Val Asp Ala Arg Ser Val Tyr Val Gly Asn Val Asp Tyr Ala
35     40     45
Cys Thr Pro Glu Glu Val Gln Gln His Phe Gln Ala Cys Gly Thr Val
50     55     60
Asn Arg Val Thr Ile Leu Thr Asp Lys Phe Gly Gln Pro Lys Gly Phe
65     70     75     80
Ala Tyr Val Glu Phe Leu Glu Gln Glu Ala Val Gln Glu Ala Leu Asn
85     90     95
Leu Asn Glu Ser Glu Leu His Gly Arg Gln Ile Lys Val Ala Pro Lys
100    105    110
Arg Thr Asn Val Pro Gly Met Lys Gln Arg Pro Pro Arg Gly Tyr Asn
115    120    125
Pro Tyr His Gly Tyr Pro Tyr Arg Ser Tyr Gly Ala Pro Tyr Phe Pro
130    135    140
Pro Tyr Gly Tyr Gly Arg Ala Pro Arg Phe Arg Arg Pro Met Arg Tyr
145    150    155    160
Arg Pro Tyr Phe
```

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

```
Met Gln Ala Lys Val Ala Lys Glu Met Gln Gly Gly Asp Pro Ser Ile
```

1		5		10		15									
Ser	Thr	Ala	Xaa	Ala	Lys	Glu	Gln	Val	Asp	Ala	Arg	Ser	Val	Tyr	Val
		20						25					30		
Gly	Asn	Val	Asp	Tyr	Ala	Cys	Thr	Pro	Glu	Glu	Val	Gln	Gln	His	Phe
		35					40					45			
Gln	Ala	Cys	Gly	Thr	Val	Asn	Arg	Val	Thr	Ile	Leu	Thr	Asp	Lys	Phe
	50					55					60				
Gly	Gln	Pro	Lys	Gly	Phe	Ala	Tyr	Val	Glu	Phe	Leu	Glu	Gln	Glu	Ala
65					70					75					80
Val	Gln	Glu	Ala	Leu	Asn	Leu	Asn	Glu	Ser	Glu	Leu	His	Gly	Arg	Gln
			85						90					95	
Ile	Lys	Val	Ala	Pro	Lys	Arg	Thr	Asn	Val	Pro	Gly	Met	Lys	Gln	Arg
		100						105					110		
Pro	Pro	Arg	Gly	Tyr	Asn	Pro	Tyr	His	Gly	Tyr	Pro	Tyr	Arg	Ser	Tyr
		115					120					125			
Gly	Ala	Pro	Tyr	Phe	Pro	Pro	Tyr	Gly	Tyr	Gly	Arg	Ala	Pro	Arg	Phe
	130					135					140				
Arg	Arg	Pro	Met	Arg	Tyr	Arg	Pro	Tyr	Phe						
145				150											

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1499313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

Met	Gln	Gly	Gly	Asp	Pro	Ser	Ile	Ser	Thr	Ala	Xaa	Ala	Lys	Glu	Gln
1			5					10						15	
Val	Asp	Ala	Arg	Ser	Val	Tyr	Val	Gly	Asn	Val	Asp	Tyr	Ala	Cys	Thr
		20						25				30			
Pro	Glu	Glu	Val	Gln	Gln	His	Phe	Gln	Ala	Cys	Gly	Thr	Val	Asn	Arg
		35					40					45			
Val	Thr	Ile	Leu	Thr	Asp	Lys	Phe	Gly	Gln	Pro	Lys	Gly	Phe	Ala	Tyr
	50					55					60				
Val	Glu	Phe	Leu	Glu	Gln	Glu	Ala	Val	Gln	Glu	Ala	Leu	Asn	Leu	Asn
65					70					75					80
Glu	Ser	Glu	Leu	His	Gly	Arg	Gln	Ile	Lys	Val	Ala	Pro	Lys	Arg	Thr
				85					90					95	
Asn	Val	Pro	Gly	Met	Lys	Gln	Arg	Pro	Pro	Arg	Gly	Tyr	Asn	Pro	Tyr
		100						105					110		
His	Gly	Tyr	Pro	Tyr	Arg	Ser	Tyr	Gly	Ala	Pro	Tyr	Phe	Pro	Pro	Tyr
		115					120					125			
Gly	Tyr	Gly	Arg	Ala	Pro	Arg	Phe	Arg	Arg	Pro	Met	Arg	Tyr	Arg	Pro
	130					135					140				
Tyr	Phe														
145															

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..917

(D) OTHER INFORMATION: / Ceres Seq. ID 1499314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

atgggggttrg	cctagttgtg	cccgttgagc	actagcagcc	tccttgaaac	ctccagatct	60
gtgcctccaa	ggcccccggt	cctcggaac	aagtcccatc	tgamggacct	tgttccctgt	120
ccccgsccac	gtggcctcct	ctgcagccgt	ccagatggac	accgccgcgc	ccctgcaact	180
gaaagcctgc	gccggcgacg	ccgcggagaa	gctgctgctc	gccgtcgcag	ccgaggggtcc	240
tatctgtrgt	gtgccagact	tcaagatgag	gggaaagaag	agtgatgarc	tcgaacctgt	300
cgatrctggc	gatgaagatg	atgatggtgg	tgacgatggg	gacgaggatg	gtgacttttg	360
ggaggagggt	gaagaggacg	tctcagaagg	ggagggatat	gacaacccaa	agggcaatga	420
gaccaagawg	camagagggt	atcctgagga	aaatggtgag	gaagatgagg	aagaaccaga	480
agatcaggag	ggtggcgggc	acgacgatga	tgacgacgat	gacgatgatg	agaacgggga	540
tgacgaggac	gacgacaatg	gggatgacga	tgaggagggt	gtagatgaag	aagacgatga	600
ccaggacgag	gatgaggagg	aagatgatga	tgaagactcg	ctccagcccc	caaagaagag	660
gaagaagtga	agatcttctg	ccgctttagt	taccgtgcgc	tgagttctgc	ctggcttttc	720
gtcatatcct	cgcattttcaa	ctttcccata	gagagttaag	aaggatccac	acgttcagca	780
gcacgtgtgg	gcttgttaga	gctttatgat	ttgaggcaat	tagggacaac	tcttatgtca	840
ttgttgcttg	cttctgtgga	gtcgaacaga	tgtttcgcta	acataattcg	acttgagtga	900
tgaaagcctc	cagattg					

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1499315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

Met	Asp	Thr	Ala	Ala	Pro	Leu	Gln	Leu	Lys	Ala	Cys	Ala	Gly	Asp	Ala	
1			5						10					15		
Ala	Glu	Lys	Leu	Leu	Leu	Ala	Val	Ala	Ala	Glu	Gly	Pro	Ile	Cys	Xaa	
			20					25					30			
Val	Pro	Asp	Phe	Lys	Met	Arg	Gly	Lys	Lys	Ser	Asp	Xaa	Leu	Glu	Pro	
			35				40					45				
Val	Asp	Xaa	Gly	Asp	Glu	Asp	Asp	Gly	Gly	Asp	Asp	Gly	Asp	Glu		
	50				55					60						
Asp	Gly	Asp	Phe	Gly	Glu	Gly	Glu	Glu	Asp	Val	Ser	Glu	Gly	Glu		
			70				75							80		
Gly	Tyr	Asp	Asn	Pro	Lys	Gly	Asn	Glu	Thr	Lys	Xaa	Xaa	Arg	Gly	Asp	
			85				90						95			
Pro	Glu	Glu	Asn	Gly	Glu	Glu	Asp	Glu	Glu	Pro	Glu	Asp	Gln	Glu		
			100				105						110			
Gly	Gly	Gly	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Glu	Asn	Gly	
			115				120						125			
Asp	Asp	Glu	Asp	Asp	Asp	Asn	Gly	Asp	Asp	Asp	Glu	Glu	Gly	Val	Asp	
			130				135				140					
Glu	Glu	Asp	Asp	Asp	Gln	Asp	Glu	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Glu	
			145			150				155					160	
Asp	Ser	Leu	Gln	Pro	Pro	Lys	Lys	Arg	Lys	Lys						
			165				170									

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1499316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

```
Met Arg Gly Lys Ser Asp Xaa Leu Glu Pro Val Asp Xaa Gly Asp
1          5          10          15
Glu Asp Asp Asp Gly Gly Asp Asp Gly Asp Glu Asp Gly Asp Phe Gly
20          25          30
Glu Glu Gly Glu Glu Asp Val Ser Glu Gly Glu Gly Tyr Asp Asn Pro
35          40          45
Lys Gly Asn Glu Thr Lys Xaa Xaa Arg Gly Asp Pro Glu Glu Asn Gly
50          55          60
Glu Glu Asp Glu Glu Glu Pro Glu Asp Gln Glu Gly Gly Gly Asp Asp
65          70          75          80
Asp Asp Asp Asp Asp Asp Asp Asp Glu Asn Gly Asp Asp Glu Asp Asp
85          90          95
Asp Asn Gly Asp Asp Asp Glu Glu Gly Val Asp Glu Glu Asp Asp Asp
100         105         110
Gln Asp Glu Asp Glu Glu Glu Asp Asp Asp Glu Asp Ser Leu Gln Pro
115         120         125
Pro Lys Lys Arg Lys Lys
130
```

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1499317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

```
Met Xaa Ser Asn Leu Ser Xaa Leu Ala Met Lys Met Met Met Val Val
1          5          10          15
Thr Met Gly Thr Arg Met Val Thr Leu Gly Arg Arg Val Lys Arg Thr
20          25          30
Ser Gln Lys Gly Arg Asp Met Thr Gln Arg Ala Met Arg Pro Arg
35          40          45
Xaa Xaa Glu Val Ile Leu Arg Lys Met Val Arg Lys Met Arg Lys Asn
50          55          60
Gln Lys Ile Arg Arg Val Ala Ala Thr Thr Met Met Thr Thr Met Thr
65          70          75          80
Met Met Arg Thr Gly Met Thr Arg Thr Thr Thr Met Gly Met Thr Met
85          90          95
Arg Arg Val
```

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 948 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..948

(D) OTHER INFORMATION: / Ceres Seq. ID 1499344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

```
ctycgtyccc ctctcgvt cctcgcgatc cttctttact gcccgagagt tctgactagc
cacatccagt caagcagtaa aggcgcacca tggaggcggc ggcggagaat aaggaggccg
```

60  
120

```
agcaggagga gcagcagcta ccgcacgcgc agaaggataa cgcgcccgcc gccgccgagg 180
aagacgaagc ggattcggag gagaccgagc gccgcaaccg cgacctcaag tccggccttc 240
acccccttag gcacaaactc gtgctctggt acactcgccg gacgcctgga gcgaggtcgc 300
agtcgtacga ggacaacatc aagaagatca tcgatttcag cacagtcgaa tcgtttctggg 360
tttgctactg ccaccttgcg cgcccttctt ccctgccgag cccactgac cttcatctct 420
tcaaggatgg catccgtccc ctctgggagg atcctgcaaa ccagaatggg ggcaagtggg 480
taattagatt caaaaaggca gtttcaggtc gattttggga ggatttggtg ctagtggtag 540
taggcgacca gcttgagtat agcgatgatg tctgtggtgt tgtgcttagt gtccgtttca 600
atgaagacat tctgagcgtc tggaaccgga acgcatcaga ccatcaggct gtgatggcat 660
tgagggattc tatcaagagg cacctcaagc tgccgcacag ctatctgatg gagtaciaaac 720
cccatgatst tcgcggcgtg acaactcgtc ctacaggaac acatggctga gaggatagat 780
aaacctcatg atactcggca gcttactgac gacggttctg aagcaaagag actcttttat 840
gtaccaagaa cgcagactat tatgcaatgt agtactacta ctactactac tcaaaagccc 900
ctacaatgtg acgcgcaaca attttactat ctaatgtgtt ttttttgc
```

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

```
Xaa Arg Xaa Pro Pro Xaa Leu Leu Ala Ile Leu Leu Tyr Cys Pro Arg
1          5          10          15
Val Leu Thr Ser His Ile Gln Ser Ser Ser Lys Gly Ala Pro Trp Arg
20          25          30
Arg Arg Arg Arg Ile Arg Arg Pro Ser Arg Arg Ser Ser Ser Tyr Arg
35          40          45
Thr Arg Arg Arg Ile Thr Arg Pro Pro Pro Pro Arg Lys Thr Lys Arg
50          55          60
Ile Arg Arg Arg Pro Ser Ala Ala Thr Ala Thr Ser Ser Pro Ala Phe
65          70          75          80
Thr Pro Leu Gly Thr Asn Ser Cys Ser Gly Thr Leu Ala Gly Arg Leu
85          90          95
Glu Arg Gly Arg Ser Arg Thr Arg Thr Thr Ser Arg Arg Ser Ser Ile
100          105          110
Ser Ala Gln Ser Asn Arg Ser Gly Phe Ala Thr Ala Thr Leu Arg Ala
115          120          125
Leu Leu Pro Cys Arg Ala Pro Leu Thr Phe Ile Ser Ser Arg Met Ala
130          135          140
Ser Val Pro Ser Gly Arg Ile Leu Gln Thr Arg Met Val Ala Ser Gly
145          150          155          160
```

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

Met Glu Ala Ala Ala Glu Asn Lys Glu Ala Glu Gln Glu Glu Gln Gln

1 5 10 15  
Leu Pro His Ala Gln Lys Asp Asn Ala Pro Ala Ala Glu Glu Asp  
20 25 30  
Glu Ala Asp Ser Glu Glu Thr Glu Arg Arg Asn Arg Asp Leu Lys Ser  
35 40 45  
Gly Leu His Pro Leu Arg His Lys Leu Val Leu Trp Tyr Thr Arg Arg  
50 55 60  
Thr Pro Gly Ala Arg Ser Gln Ser Tyr Glu Asp Asn Ile Lys Lys Ile  
65 70 75 80  
Ile Asp Phe Ser Thr Val Glu Ser Phe Trp Val Cys Tyr Cys His Leu  
85 90 95  
Ala Arg Pro Ser Ser Leu Pro Ser Pro Thr Asp Leu His Leu Phe Lys  
100 105 110  
Asp Gly Ile Arg Pro Leu Trp Glu Asp Pro Ala Asn Gln Asn Gly Gly  
115 120 125  
Lys Trp Ile Ile Arg Phe Lys Lys Ala Val Ser Gly Arg Phe Trp Glu  
130 135 140  
Asp Leu Val Leu Val Val Val Gly Asp Gln Leu Glu Tyr Ser Asp Asp  
145 150 155 160  
Val Cys Gly Val Val Leu Ser Val Arg Phe Asn Glu Asp Ile Leu Ser  
165 170 175  
Val Trp Asn Arg Asn Ala Ser Asp His Gln Ala Val Met Ala Leu Arg  
180 185 190  
Asp Ser Ile Lys Arg His Leu Lys Leu Pro His Ser Tyr Leu Met Glu  
195 200 205  
Tyr Lys Pro His Asp Xaa Arg Gly Val Thr Thr Arg Pro Thr Gly Thr  
210 215 220  
His Gly  
225

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

aaaaacacca cacaacacaa cacaataata cagcaaagga ggctagcaga agtgcaggat	60
taataagcta agctagtaga aattaagcaa agcataggca cagccatggc tacctcctct	120
ggttcttgcc ttattattag cctgtwggg gtgggtggg cggcggcgct gtcggcctca	180
acggcgctcg cagagctgtc gtcgacgttc tacgacacgt cgtgccccag cgcgatgtcc	240
accatcagca gggcggtgaa ctccgccgtg gcgcasaggc tcgtgtgggg gcgtcgctgc	300
tccggctcca cttccacgac tgcttcgtcc aaggctgcga cgcgtccatt ctgctgaacg	360
acacgtccgg ggagcagacc cagccgccga acctaacctt gaacccgagg gccttcgacg	420
tcgtcaacag catcaaggcg caggtggagg cggcggtgcc gggcgctcgt tcctgcgcgcg	480
acatcctcgc cgtcgccgcc cgcgacgagt tgtcgcgctc ggcgggcctt cgtggac	

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:  
Met Ala Thr Ser Ser Gly Ser Cys Leu Ile Ile Ser Leu Xaa Val Val  
1 5 10 15  
Val Val Ala Ala Ala Leu Ser Ala Ser Thr Ala Ser Ala Gln Leu Ser  
20 25 30  
Ser Thr Phe Tyr Asp Thr Ser Cys Pro Ser Ala Met Ser Thr Ile Ser  
35 40 45  
Ser Gly Val Asn Ser Ala Val Ala Xaa Arg Leu Val Trp Gly Arg Arg  
50 55 60  
Cys Ser Gly Ser Thr Ser Thr Thr Ala Ser Ser Lys Ala Ala Thr Arg  
65 70 75 80  
Pro Phe Cys

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..460
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

acccatagca gccagtcgcc cgcacgactc tttcccggct acccacaccg cgcgagatct	60
ccgatccccg cccaaatccc acgacgccgg cggsgccatg ggcggcaagg acctgacgga	120
ggaccagatc gcctcgatgc gggaggcctt ctcgctgttc gacacggacg gggacggccg	180
catcgcgccc tcggagctgg gcgtcctcat gcgtccctc ggcgggaacc ccacgcaggc	240
gcastccggg acatcgcggc gcaggagaag ctcaccgcac ccttcgactt cccgcgcttt	300
ctcgacctca tgcgcgcca cctcaagccc gagcccttcg accgchcgt cgcgcamgcc	360
ttcmgcgctc tcgacaagga cggctccggc accgtcgccg tmgcmrasct ccgccacgtc	420
ctcacctcca tcggcgagaa gctcgaggcc cagagttcg	

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

Thr His Ser Ser Gln Ser Pro Ala Arg Leu Phe Pro Gly Tyr Pro His	
1 5 10 15	
Arg Ala Arg Ser Pro Ile Pro Ala Gln Ile Pro Arg Arg Arg Arg Xaa	
20 25 30	
His Gly Arg Gln Gly Pro Asp Gly Gly Pro Asp Arg Leu Asp Ala Gly	
35 40 45	
Gly Leu Leu Ala Val Arg His Gly Arg Gly Arg Pro His Arg Ala Leu	
50 55 60	
Gly Ala Gly Arg Pro His Ala Leu Pro Arg Arg Glu Pro His Ala Gly	
65 70 75 80	
Ala Xaa Arg Asp Ile Ala Ala Gln Glu Lys Leu Thr Ala Pro Phe Asp	
85 90 95	
Phe Pro Arg Phe Leu Asp Leu Met Arg Ala His Leu Lys Pro Glu Pro	
100 105 110	
Phe Asp Arg Xaa Leu Arg Xaa Ala Phe Xaa Val Leu Asp Lys Asp Gly	
115 120 125	

Ser Gly Thr Val Ala Xaa Xaa Xaa Leu Arg His Val Leu Thr Ser Ile  
130 135 140  
Gly Glu Lys Leu Glu Ala His Glu Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

Pro Ile Ala Ala Ser Arg Pro His Asp Ser Phe Pro Ala Thr His Thr  
1 5 10 15  
Ala Arg Asp Leu Arg Ser Pro Pro Lys Ser His Asp Ala Gly Xaa Ala  
20 25 30  
Met Gly Gly Lys Asp Leu Thr Glu Asp Gln Ile Ala Ser Met Arg Glu  
35 40 45  
Ala Phe Ser Leu Phe Asp Thr Asp Gly Asp Gly Arg Ile Ala Pro Ser  
50 55 60  
Glu Leu Gly Val Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala  
65 70 75 80  
Xaa Ser Gly Thr Ser Arg Arg Arg Arg Ser Ser Pro His Pro Ser Thr  
85 90 95  
Ser Arg Ala Phe Ser Thr Ser Cys Ala Pro Thr Ser Ser Pro Ser Pro  
100 105 110  
Ser Thr Xaa Arg Ser Ala Xaa Pro Xaa Ala Ser Ser Thr Arg Thr Ala  
115 120 125  
Pro Ala Pro Ser Pro Xaa Xaa Xaa Ser Ala Thr Ser Ser Pro Pro Ser  
130 135 140  
Ala Arg Ser Ser Arg Pro Thr Ser Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Met Gly Gly Lys Asp Leu Thr Glu Asp Gln Ile Ala Ser Met Arg Glu  
1 5 10 15  
Ala Phe Ser Leu Phe Asp Thr Asp Gly Asp Gly Arg Ile Ala Pro Ser  
20 25 30  
Glu Leu Gly Val Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala  
35 40 45  
Xaa Ser Gly Thr Ser Arg Arg Arg Ser Ser Pro His Pro Ser Thr  
50 55 60  
Ser Arg Ala Phe Ser Thr Ser Cys Ala Pro Thr Ser Ser Pro Ser Pro  
65 70 75 80  
Ser Thr Xaa Arg Ser Ala Xaa Pro Xaa Ala Ser Ser Thr Arg Thr Ala  
85 90 95  
Pro Ala Pro Ser Pro Xaa Xaa Xaa Ser Ala Thr Ser Ser Pro Pro Ser



100 105 110  
Ala Arg Ser Ser Arg Pro Thr Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..736
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

gcattcgtac aaccgcagcc gagacggttg accaacgctg ccacgattcc gtccacacgc	60
cgacgcggcg ggctcctggc cgacgagcac tcccctccga acgcccgcgtt ggccggcccc	120
gccccacgag gccacgatgc agtagcagcg ttcacaccat ctgtctgtct caagtgtcac	180
ggcggtccgtc attcgattca accccaacc ccccatgggc ctggccgtat aaatcaaccg	240
ccggtgaagt ctagtctgtc cgtcgctcgg tccaccacct cagctccgcc gcttgccgcg	300
ttttgtcttc tccctcccgc ctctcggctt ctctacacg ctaccgtctc acagccgtaa	360
acgccccctc cggatcccgc tagttcgcca cgcgcgccg cccgcccgc gttcgcccta	420
tcattggcgc ctcgtcgacc gccacacctc gtccatgact tcacgtcaa ggatggagggt	480
ggcgcccggt gaggcggcgg tggcgatac ggtggcgggc gccgtgatgg aggcggctac	540
ggcggtggcg gtggaggcta cggcggtggt cgtggaggct acggcggcgg tgggggatac	600
ggtggtgcaa accgcggcgg cggctacggc aacaacgac ggaactggag gaactgagcg	660
gtgggggtccg ctgaggccta gttatcttgt tcgcttctgc taccgtgttc accctagtct	720
agaggggggtt tatctt	

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

Ala Phe Val Gln Pro Gln Pro Arg Arg Leu Thr Asn Ala Ala Thr Ile	
1 5 10 15	
Pro Ser Thr Arg Arg Arg Gly Gly Leu Leu Ala Asp Glu His Ser Pro	
20 25 30	
Pro Asn Ala Ala Leu Ala Gly Pro Ala Pro Arg Gly His Asp Ala Val	
35 40 45	
Ala Ala Phe Thr Pro Ser Val Cys Leu Lys Cys His Gly Val Arg His	
50 55 60	
Ser Ile Gln Pro Pro Thr Pro His Gly Pro Gly Arg Ile Asn Gln Pro	
65 70 75 80	
Pro Val Lys Ser Ser Arg Leu Val Ala Arg Ser Thr Thr Ser Ala Pro	
85 90 95	
Pro Leu Ala Arg Phe Cys Ser Leu Pro Pro Gly Ser Arg Leu Leu Leu	
100 105 110	
His Ala Thr Val Ser Gln Pro	
115	

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..94  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499372  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:  
Met Thr Ser Ser Ser Arg Met Glu Val Ala Ala Val Glu Ala Ala Val  
1                    5                    10                    15  
Ala Asp Thr Val Ala Gly Ala Val Met Glu Ala Ala Thr Ala Val Ala  
                    20                    25                    30  
Val Glu Ala Thr Ala Val Val Val Glu Ala Thr Ala Ala Val Gly Asp  
                    35                    40                    45  
Thr Val Val Gln Thr Ala Ala Ala Thr Ala Thr Thr Thr Gly Thr  
                    50                    55                    60  
Gly Gly Thr Glu Arg Trp Gly Pro Leu Arg Pro Ser Tyr Leu Val Arg  
65                    70                    75                    80  
Phe Cys Tyr Arg Val His Pro Ser Leu Glu Gly Val Tyr Leu  
                    85                    90

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1499373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

Met Glu Val Ala Ala Val Glu Ala Ala Val Ala Asp Thr Val Ala Gly  
1                    5                    10                    15  
Ala Val Met Glu Ala Ala Thr Ala Val Ala Val Glu Ala Thr Ala Val  
                    20                    25                    30  
Val Val Glu Ala Thr Ala Ala Val Gly Asp Thr Val Val Gln Thr Ala  
                    35                    40                    45  
Ala Ala Ala Thr Ala Thr Thr Thr Gly Thr Gly Thr Thr Glu Arg Trp  
50                    55                    60  
Gly Pro Leu Arg Pro Ser Tyr Leu Val Arg Phe Cys Tyr Arg Val His  
65                    70                    75                    80  
Pro Ser Leu Glu Gly Val Tyr Leu  
                    85

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..914

(D) OTHER INFORMATION: / Ceres Seq. ID 1499380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

gnacccctgc gccgcaccgc cacggcaaca gcatcgacct aggcccggtc ccgtgtcgct	60
tcgtagttcg tccccttccc cgcgccccca gcagcagcgg attcccctcg agagatccgg	120
cccttggcgc ggtcgccgga gagagcggca tggggctctg ggactcgctc ctcaactggc	180
tccggagctt gtttttcaag caagaaatgg agctctccct cgttgggttg cagaatgctg	240
ggaagacgtc gctggtcaat gctgttgcta caggtggcta cagcgaggac atgattccaa	300
cggtaggctt caatatgcgg aaggtcacca agggaaatgt cacgattaag ctttgggatc	360

```
ttggtgggca gcggagattc cgcactatgt gggagcgcta ttgccgtgga gtttctgcta 420
ttctatatgt tgtggacgct gctgaccgag atagtgtccc aatcgcgaaa agtgagttgc 480
atgatctgct gacgaaacag tctttggctg ggattccctt gcttgctcctt ggcaacaaaa 540
ttgacaagtc agaagcgctt tcgaagcagg ccttggttga tcaacttgga ctggaattga 600
taaaggaccg tgaggtttgt tgctacatga tctcctgtaa ggattctgtg aacatagacg 660
tcgtcatcga ctggccttctc aagcactcta gaacagcgaa gtaggctttc tgtgtgtttg 720
tatcgcttga tgcacggtgt tttatctttt gtgaatctga gcctggttcc ttgggtcccga 780
tgttaaaagc ggccaccttg taatttatga cctcttttgt gtcacagacg aactgcatgg 840
tatctagact agaaacatgt cttccctttg taaatccttt gaacctttga ttattcttac 900
tgtgaatgcc gtcc
```

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1499381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

```
Thr Pro Ala Pro His Pro His Gly Asn Ser Ile Asp Leu Gly Pro Val
1          5          10          15
Pro Cys Arg Phe Val Val Arg Pro Leu Pro Arg Ala Pro Ser Ser Ser
20          25          30
Gly Phe Pro Ser Arg Asp Pro Ala Leu Gly Ala Val Ala Gly Glu Ser
35          40          45
Gly Met Gly Leu Trp Asp Ser Leu Leu Asn Trp Leu Arg Ser Leu Phe
50          55          60
Phe Lys Gln Glu Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly
65          70          75          80
Lys Thr Ser Leu Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp
85          90          95
Met Ile Pro Thr Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn
100          105          110
Val Thr Ile Lys Leu Trp Asp Leu Gly Gly Gln Arg Arg Phe Arg Thr
115          120          125
Met Trp Glu Arg Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val
130          135          140
Asp Ala Ala Asp Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His
145          150          155          160
Asp Leu Leu Thr Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu
165          170          175
Gly Asn Lys Ile Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val
180          185          190
Asp Gln Leu Gly Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr
195          200          205
Met Ile Ser Cys Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp
210          215          220
Leu Ile Lys His Ser Arg Thr Ala Lys
225          230
```

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1499382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

Met Gly Leu Trp Asp Ser Leu Leu Asn Trp Leu Arg Ser Leu Phe Phe  
1 5 10 15  
Lys Gln Glu Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly Lys  
20 25 30  
Thr Ser Leu Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp Met  
35 40 45  
Ile Pro Thr Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn Val  
50 55 60  
Thr Ile Lys Leu Trp Asp Leu Gly Gly Gln Arg Phe Arg Thr Met  
65 70 75 80  
Trp Glu Arg Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val Asp  
85 90 95  
Ala Ala Asp Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His Asp  
100 105 110  
Leu Leu Thr Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu Gly  
115 120 125  
Asn Lys Ile Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val Asp  
130 135 140  
Gln Leu Gly Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr Met  
145 150 155 160  
Ile Ser Cys Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp Leu  
165 170 175  
Ile Lys His Ser Arg Thr Ala Lys  
180

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1499383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly Lys Thr Ser Leu  
1 5 10 15  
Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp Met Ile Pro Thr  
20 25 30  
Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn Val Thr Ile Lys  
35 40 45  
Leu Trp Asp Leu Gly Gly Gln Arg Arg Phe Arg Thr Met Trp Glu Arg  
50 55 60  
Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val Asp Ala Ala Asp  
65 70 75 80  
Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His Asp Leu Leu Thr  
85 90 95  
Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu Gly Asn Lys Ile  
100 105 110  
Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val Asp Gln Leu Gly  
115 120 125  
Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr Met Ile Ser Cys  
130 135 140  
Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp Leu Ile Lys His  
145 150 155 160  
Ser Arg Thr Ala Lys  
165

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

acacagcgag	ccaatcgccg	taatcatgaa	ggctcctcatc	gttctcgccg	cgtgcgttgc	60
cgccgccctg	gctggcatcc	cctccgagtc	tgagatccag	gctcattggg	agagcttcaa	120
ggctacccac	ggcaagacct	acgccaatgc	cgtcgaggag	gcctacaggg	ccaaggtgtt	180
caaggaaaac	gccatcagga	tcgccaaagca	caatgaccgt	ttcgccagcg	gsagngtcac	240
cttcaaggtc	ggctacaacc	agtacgtga	catgcacacc	cacgaggtca	ccgagaagat	300
gaacggtttc	cgcatggaga	tgaagaaacc	ctccgctaac	gtgcacgagg	gcaacgactc	360
ctggcccttg	agcaagaagg	tcgactggag	atccaagggc	tacgtcaccc	ccatcaagga	420
ccagggacag	tgcggttcct	gctggctctt	ctctgccact	ggttccctcg	agggtcagct	480
cttcaagata	ccggcaagct	ggctctccctc	tctgagcaga	acctggtcga	ctgctc	

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

His	Ser	Glu	Pro	Ile	Ala	Val	Ile	Met	Lys	Val	Leu	Ile	Val	Leu	Ala
1				5					10					15	
Ala	Cys	Val	Ala	Ala	Ala	Leu	Ala	Gly	Ile	Pro	Ser	Glu	Ser	Glu	Ile
			20					25						30	
Gln	Ala	His	Trp	Glu	Ser	Phe	Lys	Ala	Thr	His	Gly	Lys	Thr	Tyr	Ala
		35					40					45			
Asn	Ala	Val	Glu	Glu	Ala	Tyr	Arg	Ala	Lys	Val	Phe	Lys	Glu	Asn	Ala
		50				55					60				
Ile	Arg	Ile	Ala	Lys	His	Asn	Asp	Arg	Phe	Ala	Ser	Xaa	Xaa	Val	Thr
65					70				75					80	
Phe	Lys	Val	Gly	Tyr	Asn	Gln	Tyr	Ala	Asp	Met	His	Thr	His	Glu	Val
			85					90						95	
Thr	Glu	Lys	Met	Asn	Gly	Phe	Arg	Met	Glu	Met	Lys	Lys	Pro	Ser	Ala
			100					105					110		
Asn	Val	His	Glu	Gly	Asn	Asp	Ser	Trp	Pro	Trp	Ser	Lys	Lys	Val	Asp
		115				120						125			
Trp	Arg	Ser	Lys	Gly	Tyr	Val	Thr	Pro	Ile	Lys	Asp	Gln	Gly	Gln	Cys
		130				135					140				
Gly	Ser	Cys	Trp	Ser	Phe	Ser	Ala	Thr	Gly	Ser	Leu	Glu	Gly	Gln	Leu
145					150					155				160	
Phe	Lys	Ile	Pro	Ala	Ser	Trp	Ser	Pro	Ser	Leu	Ser	Arg	Thr	Trp	Ser
			165					170						175	
Thr	Ala														

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..170  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499386  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:  
Met Lys Val Leu Ile Val Leu Ala Ala Cys Val Ala Ala Ala Leu Ala  
1 5 10 15  
Gly Ile Pro Ser Glu Ser Glu Ile Gln Ala His Trp Glu Ser Phe Lys  
20 25 30  
Ala Thr His Gly Lys Thr Tyr Ala Asn Ala Val Glu Glu Ala Tyr Arg  
35 40 45  
Ala Lys Val Phe Lys Glu Asn Ala Ile Arg Ile Ala Lys His Asn Asp  
50 55 60  
Arg Phe Ala Ser Xaa Xaa Val Thr Phe Lys Val Gly Tyr Asn Gln Tyr  
65 70 75 80  
Ala Asp Met His Thr His Glu Val Thr Glu Lys Met Asn Gly Phe Arg  
85 90 95  
Met Glu Met Lys Lys Pro Ser Ala Asn Val His Glu Gly Asn Asp Ser  
100 105 110  
Trp Pro Trp Ser Lys Lys Val Asp Trp Arg Ser Lys Gly Tyr Val Thr  
115 120 125  
Pro Ile Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ser Phe Ser Ala  
130 135 140  
Thr Gly Ser Leu Glu Gly Gln Leu Phe Lys Ile Pro Ala Ser Trp Ser  
145 150 155 160  
Pro Ser Leu Ser Arg Thr Trp Ser Thr Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..470  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

gaccctttct ttcccaaagc cgagcagcga ccagcgaggg tgccactgcc accgcccgcc 60  
ccccagtccc ccaactcactc actagctagc ttgctagctg cgcactacgg gctacgccga 120  
gctagagtcc ggcgatcaca gcccggcagg ccggccatgg ccaccgcgcc cgctgctgctc 180  
ctagtccctgc acgtttctgct aggcgctgca gcggccgcct gcgccgcggc ggcagggagt 240  
agcagcaagg tgccggcgat gtacgtgttc ggcgactcca cggcggacgt gggcaccaac 300  
aactacttgc cgggcgggcg cgaagtgccg cgtgccaaact tccccacaa cggcgtcgac 360  
ttccccasgg sgcgcmccac cggcaggttc agcaacgggt tcaacggcgt cgacttcttg 420  
gccgtgaaca tgggcttcaa gcgcasmccc cgccgttctt cgcmtgggcc

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..156  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Asp Pro Phe Phe Pro Lys Ala Glu Gln Arg Pro Ala Arg Val Pro Leu  
1 5 10 15  
Pro Pro Pro Ala Pro Gln Ser Pro Thr His Ser Leu Ala Ser Leu Leu  
20 25 30  
Ala Ala His Tyr Gly Leu Arg Arg Ala Arg Val Arg Arg Ser Gln Pro  
35 40 45  
Gly Arg Pro Ala Met Ala Thr Ala Pro Val Val Val Leu Val Leu His  
50 55 60  
Val Leu Leu Gly Ala Ala Ala Ala Cys Ala Ala Ala Gly Ser  
65 70 75 80  
Ser Ser Lys Val Pro Ala Met Tyr Val Phe Gly Asp Ser Thr Ala Asp  
85 90 95  
Val Gly Thr Asn Asn Tyr Leu Pro Gly Gly Ala Glu Val Pro Arg Ala  
100 105 110  
Asn Phe Pro His Asn Gly Val Asp Phe Pro Xaa Xaa Arg Xaa Thr Gly  
115 120 125  
Arg Phe Ser Asn Gly Phe Asn Gly Val Asp Phe Leu Ala Val Asn Met  
130 135 140  
Gly Phe Lys Arg Xaa Pro Arg Arg Ser Ser Xaa Trp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

Met Ala Thr Ala Pro Val Val Val Leu Val Leu His Val Leu Leu Gly  
1 5 10 15  
Ala Ala Ala Ala Ala Cys Ala Ala Ala Gly Ser Ser Ser Lys Val  
20 25 30  
Pro Ala Met Tyr Val Phe Gly Asp Ser Thr Ala Asp Val Gly Thr Asn  
35 40 45  
Asn Tyr Leu Pro Gly Gly Ala Glu Val Pro Arg Ala Asn Phe Pro His  
50 55 60  
Asn Gly Val Asp Phe Pro Xaa Xaa Arg Xaa Thr Gly Arg Phe Ser Asn  
65 70 75 80  
Gly Phe Asn Gly Val Asp Phe Leu Ala Val Asn Met Gly Phe Lys Arg  
85 90 95  
Xaa Pro Arg Arg Ser Ser Xaa Trp  
100

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

cagascagaa ascagccgca gccccagccc ccacaagacg aggcaacaat ggcgctagaa  
gcagccaccg cccccgcgc actcctcgcc gcgtgcctcg tctgctggt cctcggcgcc

60  
120

```
ggcaccggcc cgtcgtcggg gctgcgcggc gccggggcgc aggcgggcag gggagccgga 180
tccaggatac gtcattgtatc cggcatgggg ccccgccgtc cactaatcgt cgtcgttcga 240
gggcgacgac gacgtccgc cgccaacgac ggcgagtgcc acatgcctat gctctcgtgt 300
gggccccgta cgttattgag cgctactagt actagggaaa gtgtacgtgt gatgtgtgtc 360
actcagtgtc gattgatcaa tgatgctcat ttctcgagcag acccaggaat gctgagtga 420
gagagcagag cgtntgttct acaagtgcac cgaggaataa agtggacaga aatgttggct 480
ggttcacgtg ccttctgagt aataaaatgg acatcttcg
```

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1499403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```
Gln Xaa Arg Xaa Gln Pro Gln Pro Gln Pro Pro Gln Asp Glu Ala Thr
1      5      10
Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys
20      25      30
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu
35      40      45
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
50      55      60
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
65      70      75      80
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro
85      90      95
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg
100     105     110
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp
115     120     125
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala
130     135     140
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala
145     150     155     160
Gly Ser Arg Ala Phe
165
```

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1499404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

```
Xaa Gln Lys Xaa Ala Ala Ala Pro Ala Pro Thr Arg Arg Gly Asn Asn
1      5      10      15
Gly Ala Arg Ser Ser His Arg Pro Pro Arg Thr Pro Arg Arg Val Pro
20      25      30
Arg Pro Ala Gly Pro Arg Arg Arg His Arg Pro Val Val Gly Ala Ala
35      40      45
Arg Arg Arg Gly Ala Gly Arg Gln Gly Ser Arg Ile Gln Asp Thr Ser
50      55      60
```



Cys Ile Arg His Gly Ala Pro Pro Ser Thr Asn Arg Arg Arg Ser Arg  
65 70 75 80  
Ala Thr Thr Thr Thr Leu Arg Arg Gln Arg Arg Val Pro His Ala Tyr  
85 90 95  
Ala Leu Val Trp Ala Pro Tyr Val Ile Glu Arg Tyr  
100 105

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1499405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys  
1 5 10 15  
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu  
20 25 30  
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg  
35 40 45  
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg  
50 55 60  
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro  
65 70 75 80  
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg  
85 90 95  
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp  
100 105 110  
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala  
115 120 125  
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala  
130 135 140  
Gly Ser Arg Ala Phe  
145

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1040

(D) OTHER INFORMATION: / Ceres Seq. ID 1499406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

gcattctcct cggcgcgggg tgccgagacg cgtacgggca ttctccttag gtgcgggggt 60  
tcctctcgag tctcggcaac gacgaaaacg aaaataccga gtcgagtcag cgatgaatcc 120  
cttcgcaaaa aaaccaactc cgcgagagggt gatgcggasa gcaagcggga cctgacgaat 180  
gctacgcgag ggatcgagag ggacattgcg tcattacagc aggaggagaa gaaactcgtt 240  
gctgaaatta aaaggacagc aaaaactggc aatgaggcag caacgaaaat tctagcccgt 300  
cagctgatca ggttaaggca gcagatttct aatttgcaag gtagccgagc tcagattcgg 360  
gggattgca cacataactc ggcaatgcat gccaacactt cagtggctac tggtttacia 420  
agtgcgagca aagcaatggg agctttgaat aagcaaatgg aacctaccaa gcagatgaaa 480  
ataatgcaag aattccaaaa gcagtcagca caaatggata tgacaaatga gatgatgtct 540  
gattcaatcg atgatgtctt agacgatgac caggccgagg aagaaactga agaacttgct 600  
aatcaggttc tggatgagat tgggtgtagac attgcatcac agttgtcctc ggctcccaaa 660

```
ggaaaaattg ctgggaagaa ggttcaggtt gatggaagtt cggagttgga ggaactagag 720
aagagactgg ctgctctaaa aaatgcataa gatcagttta caaccctctc ctctatgcac 780
atagcaagcc tgccgtgtac cttaattcca aatcttcatt cgacacgcaa agtcactgtg 840
atttgtatgt atcaaaagga agatgatgca aacccccaag tttttgggcg aatcgatggt 900
gctgctgttc gtacacactc acgcataaga tggggctgtg ctgccttatt agcgacatga 960
ttcagagcaa gggattccat agtcttgtaa agaagtttga ttattttttac atgacagcct 1020
tttgtttttg gtcgttcggt
```

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1499407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

```
Ala Phe Ser Ser Ala Arg Val Ala Glu Thr Arg Thr Gly Ile Leu Leu
1      5      10      15
Arg Cys Gly Gly Ser Ser Arg Val Ser Ala Thr Thr Lys Thr Lys Ile
20      25      30
Pro Ser Arg Val Ser Asp Glu Ser Leu Arg Gln Lys Thr Asn Ser Ala
35      40      45
Arg Gly Asp Ala Xaa Ser Lys Arg Asp Leu Thr Asn Ala Thr Arg Gly
50      55      60
Ile Glu Arg Asp Ile Ala Ser Leu Gln Gln Glu Lys Lys Leu Val
65      70      75      80
Ala Glu Ile Lys Arg Thr Ala Lys Thr Gly Asn Glu Ala Ala Thr Lys
85      90      95
Ile Leu Ala Arg Gln Leu Ile Arg Leu Arg Gln Gln Ile Ser Asn Leu
100      105      110
Gln Gly Ser Arg Ala Gln Ile Arg Gly Ile Ala Thr His Thr Gln Ala
115      120      125
Met His Ala Asn Thr Ser Val Ala Thr Gly Leu Gln Ser Ala Ser Lys
130      135      140
Ala Met Gly Ala Leu Asn Lys Gln Met Glu Pro Thr Lys Gln Met Lys
145      150      155      160
Ile Met Gln Glu Phe Gln Lys Gln Ser Ala Gln Met Asp Met Thr Asn
165      170      175
Glu Met Met Ser Asp Ser Ile Asp Asp Val Leu Asp Asp Asp Gln Ala
180      185      190
Glu Glu Glu Thr Glu Glu Leu Ala Asn Gln Val Leu Asp Glu Ile Gly
195      200      205
Val Asp Ile Ala Ser Gln Leu Ser Ser Ala Pro Lys Gly Lys Ile Ala
210      215      220
Gly Lys Lys Val Gln Val Asp Gly Ser Ser Glu Leu Glu Glu Leu Glu
225      230      235      240
Lys Arg Leu Ala Ala Leu Lys Asn Ala
245
```

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

(2) INFORMATION FOR SEQ ID NO:1004:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1499409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1499410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

Cys 1	Ser	Leu	Ser	Arg 5	Val	Pro	Ala	Phe	Gln 10	Trp	Gly	Ala	Phe	Met 15	Ala
Gly	Gln	Ser	Asp 20	Pro	His	Leu	Ser	Ile 25	Phe	Ser	Pro	Ser	Glu 30	Val	Glu
Phe	Val	Ala 35	Glu	Asp	Glu	Ile 40	Val	Glu	Ile	Val	Pro	Asn 45	Ile	Arg	Met
Asp	Ala 50	Leu	Asn	Met	Ile	Cys 55	Gly	Asp	Phe	Gly	Pro 60	Phe	Phe	Pro	Gln
Ile 65	Pro	Thr	Lys	Val 70	Pro	Leu	Trp	Leu	Ala	Val 75	Ala	Leu	Lys	Lys	Arg 80
Xaa	Ser	Ala	Pro	Ser 85	Ala	Pro	Arg	Thr	Gly 90						

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499411  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:  
Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu  
1                    5                    10                    15  
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile  
                    20                    25                    30  
Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe  
                    35                    40                    45  
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys  
                    50                    55                    60  
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly  
65                    70                    75

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

agcctctatc tcattccact ccgacattca cgtgcagctg tcgggagcag gcaatggcgc	60
cggatctaag cgaactcgcc gccgccgctc cagcccgtgg cgcctacctc gccggcgctc	120
gtgtggaaag agaaagagag agagaggaga ggtgcgagct ggtgagatgg atcgggtgga	180
ggagcggaac attaagaara aggavaagga ggatgganga ngcgcgcaag gaagangagc	240
ggaargagga ggccgggggac aggaataccc aggagccgca gcaaggtcaa ggcctcarcc	300
tmwvactcgm caacggcgagc kacasgncag gtctgcaatg ttgccgatgt cgaacccttc	360
agctaattccc acacagctta caattttcta tgggtgatca gtatgtgtgt atgactcggg	420
tgccaccaga aaaggctcag gcaatcatgc ttatagctgc agctgcgg	

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

Ala Ser Ile Ser Phe His Ser Asp Ile His Val Gln Leu Ser Gly Ala	
1                    5                    10                    15	
Gly Asn Gly Ala Gly Ser Lys Arg Thr Arg Arg Arg Arg Ser Ser Pro	
20                    25                    30	
Trp Arg Leu Pro Arg Arg Arg Arg Cys Gly Lys Arg Lys Arg Glu Arg	
35                    40                    45	
Gly Glu Val Arg Ala Gly Glu Met Asp Arg Leu Glu Arg Asn Ile	
50                    55                    60	
Lys Xaa Lys Xaa Lys Glu Asp Gly Xaa Xaa Ala Gln Gly Arg Xaa Ala	
65                    70                    75                    80	
Glu Xaa Gly Gly Gly Gly Gln Glu Tyr Pro Gly Ala Ala Ala Arg Ser	
85                    90                    95	
Arg Pro Xaa Pro Xaa Thr Xaa Gln Arg Gln Xaa Xaa Xaa Arg Ser Ala	

		100						105						110	
Met	Leu	Pro	Met	Ser	Asn	Pro	Ser	Ala	Asn	Pro	Thr	Gln	Leu	Thr	Ile
		115						120					125		
Phe	Tyr	Gly	Gly	Ser	Val	Cys	Val	Tyr	Asp	Ser	Gly	Ala	Thr	Arg	Lys
		130						135					140		
Gly	Ser	Gly	Asn	His	Ala	Tyr	Ser	Cys	Ser	Cys					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1499414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

Pro	Leu	Ser	His	Ser	Thr	Pro	Thr	Phe	Thr	Cys	Ser	Cys	Arg	Glu	Gln
1			5						10					15	
Ala	Met	Ala	Pro	Asp	Leu	Ser	Glu	Leu	Ala	Ala	Ala	Ala	Pro	Ala	Arg
			20					25					30		
Gly	Ala	Tyr	Leu	Ala	Gly	Val	Gly	Val	Glu	Arg	Glu	Arg	Glu	Arg	Glu
		35					40					45			
Glu	Arg	Cys	Glu	Leu	Val	Arg	Trp	Ile	Gly	Trp	Arg	Ser	Gly	Thr	Leu
		50				55					60				
Arg	Xaa	Arg	Xaa	Arg	Arg	Met	Xaa	Xaa	Ala	Arg	Lys	Glu	Xaa	Glu	Arg
65					70					75				80	
Xaa	Glu	Glu	Ala	Gly	Asp	Arg	Asn	Thr	Gln	Glu	Pro	Gln	Gln	Gly	Gln
			85						90					95	
Gly	Leu	Xaa	Xaa	Xaa	Leu	Xaa	Asn	Gly	Ser	Xaa	Xaa	Xaa	Gly	Leu	Gln
			100					105					110		
Cys	Cys	Arg	Cys	Arg	Thr	Leu	Gln	Leu	Ile	Pro	His	Ser	Leu	Gln	Phe
		115					120					125			
Ser	Met	Val	Asp	Gln	Tyr	Val	Cys	Met	Thr	Arg	Val	Pro	Pro	Glu	Lys
		130				135						140			
Ala	Gln	Ala	Ile	Met	Leu	Ile	Ala	Ala	Ala	Ala					
145					150						155				

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1499415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

Met	Ala	Pro	Asp	Leu	Ser	Glu	Leu	Ala	Ala	Ala	Ala	Pro	Ala	Arg	Gly
1				5						10				15	
Ala	Tyr	Leu	Ala	Gly	Val	Gly	Val	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Glu
			20					25					30		
Arg	Cys	Glu	Leu	Val	Arg	Trp	Ile	Gly	Trp	Arg	Ser	Gly	Thr	Leu	Arg
		35					40					45			
Xaa	Arg	Xaa	Arg	Arg	Met	Xaa	Xaa	Ala	Arg	Lys	Glu	Xaa	Glu	Arg	Xaa
		50				55					60				
Glu	Glu	Ala	Gly	Asp	Arg	Asn	Thr	Gln	Glu	Pro	Gln	Gln	Gly	Gln	Gly
65					70					75				80	

Leu Xaa Xaa Xaa Leu Xaa Asn Gly Ser Xaa Xaa Xaa Gly Leu Gln Cys  
85 90 95  
Cys Arg Cys Arg Thr Leu Gln Leu Ile Pro His Ser Leu Gln Phe Ser  
100 105 110  
Met Val Asp Gln Tyr Val Cys Met Thr Arg Val Pro Pro Glu Lys Ala  
115 120 125  
Gln Ala Ile Met Leu Ile Ala Ala Ala Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..392
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

cgtgccacac atccatcccc gttcgctct tctctccct cctgccgggt ccttaataaa	60
gagcagcagc gcaagaggtt ggtagagcga gcgagaagaa ggcaatggcg gcggagagct	120
tcctgttcac ctcggagtcc gtgaacgarg ggcacccaga caagctgtgc gaccaggtgt	180
cggacgcggt gctggacgcc tgcctggcgc aggaccccgga cagcaaggtg gcctgcgaga	240
cctgcaccaa gacgaacatg gtgatgggtg tcggcgagat caccaccaag gcgagcgtgg	300
actacgagaa gatcgtdcgc gacacctgcc gcgagatcgg gttcacctcc gacgacgtgg	360
ggctcgacgc cgaccgctgc aargtgctgg tg	

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

Arg Ala Thr His Ser Pro Phe Ala Ser Ser Pro Pro Ser Cys Arg	
1 5 10 15	
Val Leu Asn Lys Glu Gln Gln Arg Lys Arg Leu Val Glu Arg Ala Arg	
20 25 30	
Arg Arg Gln Trp Arg Arg Arg Ala Ser Cys Ser Pro Arg Ser Pro	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

Met Ala Ala Glu Ser Phe Leu Phe Thr Ser Glu Ser Val Asn Xaa Gly	
1 5 10 15	
His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp Ala	
20 25 30	

Cys	Leu	Ala	Gln	Asp	Pro	Asp	Ser	Lys	Val	Ala	Cys	Glu	Thr	Cys	Thr
	35						40					45			
Lys	Thr	Asn	Met	Val	Met	Val	Phe	Gly	Glu	Ile	Thr	Thr	Lys	Ala	Ser
	50					55					60				
Val	Asp	Tyr	Glu	Lys	Ile	Xaa	Arg	Asp	Thr	Cys	Arg	Glu	Ile	Gly	Phe
65					70					75					80
Thr	Ser	Asp	Asp	Val	Gly	Leu	Asp	Ala	Asp	Arg	Cys	Xaa	Val	Leu	Val
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..486

(D) OTHER INFORMATION: / Ceres Seq. ID 1499422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

gaacaggttt	acaggcgcg	tcccgacgc	atgcccac	ccttttttga	caagctcagc	60
gtccaccact	aaatggcgg	ggagaccaa	cgggtgcg	ccatcggggt	tgccggcgag	120
atggaggtgg	aggcatacc	ccgcctatt	ccagtggcct	tcctggagcg	ccacctgggt	180
gagtcggtcc	gcacgatgc	ccgcgcctg	aragaggccc	gcaccaccac	cgtcgccctc	240
ggcgccgtgt	cctccgcgc	tggttccgct	ctcgtccgcg	ttggcgacac	cgccatgctc	300
gcgtcggtca	agctcgaggt	gatgtcgccc	tgggcccagt	acccagacga	aggatccgtc	360
tctgttgagt	tccacatgcc	gcccacgtgc	tccccgctgg	ttaggccagg	ccgatctgcg	420
gaggtggcac	cagtcacatc	caaggccctt	gaagacgttt	tggatgagtt	ccagaatgct	480
aaatttt						

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1499423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

Asn	Arg	Phe	Thr	Gly	Ala	Leu	Pro	His	Ala	Cys	Pro	Asn	Pro	Phe	Leu
1				5					10					15	
Thr	Ser	Ser	Ala	Ser	Thr	Thr	Lys	Trp	Arg	Arg	Arg	Pro	Asn	Arg	Leu
			20					25					30		
Arg	Pro	Ser	Gly	Leu	Pro	Ala	Arg	Trp	Arg	Trp	Arg	His	Thr	Ala	Ala
		35				40					45				
Tyr	Ser	Gln	Trp	Pro	Ser	Trp	Ser	Ala	Thr	Trp	Val	Ser	Pro	Ser	Ala
	50				55						60				
Ser	Met	Pro	Ala	Ala											
65															

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

```
Met Ala Ala Glu Thr Lys Pro Ala Ala Ala Ile Gly Val Ala Gly Glu
1          5          10          15
Met Glu Val Glu Ala Tyr Arg Arg Leu Phe Pro Val Ala Phe Leu Glu
          20          25          30
Arg His Leu Gly Glu Ser Val Arg Ile Asp Ala Arg Arg Leu Xaa Glu
          35          40          45
Ala Arg Thr Thr Thr Val Ala Leu Gly Ala Val Ser Ser Ala His Gly
          50          55          60
Ser Ala Leu Val Arg Val Gly Asp Thr Ala Met Leu Ala Ser Val Lys
65          70          75          80
Leu Glu Val Met Ser Pro Ser Ala Glu Tyr Pro Asp Glu Gly Ser Val
          85          90          95
Ser Val Glu Phe His Met Pro Pro Ile Cys Ser Pro Leu Val Arg Pro
          100          105          110
Gly Arg Ser Ala Glu Val Ala Pro Val Ile Ser Lys Ala Leu Glu Asp
          115          120          125
Val Leu Asp Glu Phe Gln Asn Ala Lys Phe
          130          135
```

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

```
Met Glu Val Glu Ala Tyr Arg Arg Leu Phe Pro Val Ala Phe Leu Glu
1          5          10          15
Arg His Leu Gly Glu Ser Val Arg Ile Asp Ala Arg Arg Leu Xaa Glu
          20          25          30
Ala Arg Thr Thr Thr Val Ala Leu Gly Ala Val Ser Ser Ala His Gly
          35          40          45
Ser Ala Leu Val Arg Val Gly Asp Thr Ala Met Leu Ala Ser Val Lys
          50          55          60
Leu Glu Val Met Ser Pro Ser Ala Glu Tyr Pro Asp Glu Gly Ser Val
65          70          75          80
Ser Val Glu Phe His Met Pro Pro Ile Cys Ser Pro Leu Val Arg Pro
          85          90          95
Gly Arg Ser Ala Glu Val Ala Pro Val Ile Ser Lys Ala Leu Glu Asp
          100          105          110
Val Leu Asp Glu Phe Gln Asn Ala Lys Phe
          115          120
```

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1617
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499446



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

aaactgaaag	ttaggacctt	tcatttccaa	tctctaaacc	catttctcta	cgattagaga	60
agctgacatc	aaaattgaaa	cttggaatt	tttagatttg	ttcttcttct	atggcaactg	120
aagacgatgg	tgaattgtca	gctcgttacc	agaacacggt	ggatgcattg	tcgtctttga	180
tcacaaaacg	tggccgttta	gctagtaaca	accaatctca	ccgattccgt	ttgctctttc	240
attatctcaa	ggttcttgag	cttgaagatg	cagtttcaca	aatgaaaatc	attcatgtgg	300
ccggaactaa	aggaaaggga	tcaacatgta	catttgcgga	gtctattctt	cgttgttacg	360
gtcttcgaac	tggctctctc	acatctcctc	acttaatcga	tgtccgagag	agattccgctc	420
ttaacggcat	tgagataagc	caggagaaat	ttgtgaacta	cttttggtgt	tcctttcata	480
agctcaagga	gaaaaccagc	aatgaggttg	atgttggtat	actagaagtt	ggcttaggtg	540
ggagattcga	tgcgactaat	gtgattcaga	aacctgtcgt	ctgtggtatt	tcttctctag	600
ggtatgacca	tatggagatt	cttgataaca	cacttgctga	aattgctgca	gagaaagccg	660
gtatcttcaa	gagtggagtt	cctgctttta	cagtggctca	acctgatgaa	gcaatgcgtg	720
tactcaatga	aaaagcttca	aaattggagg	tgaatcttca	ggtggtggaa	ccgttggact	780
caagccagag	actcgggctt	caaggcgaac	atcaatatct	aaacgctggt	cttgctgttg	840
cgttgtgctc	tacatttctt	aaagagattg	gtattgagga	caagaatggt	ttggatcaga	900
caaacggttt	acccgaaaaa	ttcatctctg	gattgtcaaa	tgcttatttg	atgggacgag	960
ctatgatagt	gcctgattca	gaactccctg	aagagattgt	gtattacctt	gatggagctc	1020
atagtcctga	aagcatggaa	gcttgcgcta	tatggttttc	aaaacagatc	aaacaaaacc	1080
aagaaagaaa	ccagaaaaga	tcagagcaga	tactcttggt	caattgtatg	tctgttcgtg	1140
acccgagttt	gcttcttccg	cgattaagga	gtaaatgcat	tgatcaagga	gttgatttca	1200
agagagccgt	ttttgtgcca	aacgtatcag	tgtacaacca	agtgggatct	tcgacaaaacg	1260
ttggcacacg	tgtcgagtcg	atgtcgtggc	agttcgttct	tcagaggatt	tgggagagtt	1320
tagctcgagg	tgaagcaaaa	tctaattcaa	aaagtgattc	taaaggcaaa	gaagaagaga	1380
agagtttctg	tttctcgtca	cttcctgtgg	ctggtgactg	gctccggggac	aatgctcgcc	1440
aaagtaaaca	agttcgtttt	caggtgttgg	taactggttc	attacatttg	gtgggtgatc	1500
tcttgagatt	tatcaagaaa	tgaatatgtt	tctgccatgt	attcttggcc	aatctttgcc	1560
tgtaatgact	atatatctca	caacatgatt	taacaaaaga	aaagaaaaga	tatttctg	

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

Met	Ala	Thr	Glu	Asp	Asp	Gly	Glu	Leu	Ser	Ala	Arg	Tyr	Gln	Asn	Thr
1				5					10					15	
Leu	Asp	Ala	Leu	Ser	Ser	Leu	Ile	Thr	Lys	Arg	Gly	Arg	Leu	Ala	Ser
			20					25					30		
Asn	Asn	Gln	Ser	His	Arg	Phe	Arg	Leu	Leu	Phe	His	Tyr	Leu	Lys	Val
		35				40					45				
Leu	Glu	Leu	Glu	Asp	Ala	Val	Ser	Gln	Met	Lys	Ile	Ile	His	Val	Ala
	50					55					60				
Gly	Thr	Lys	Gly	Lys	Gly	Ser	Thr	Cys	Thr	Phe	Ala	Glu	Ser	Ile	Leu
65					70					75				80	
Arg	Cys	Tyr	Gly	Leu	Arg	Thr	Gly	Leu	Phe	Thr	Ser	Pro	His	Leu	Ile
				85					90					95	
Asp	Val	Arg	Glu	Arg	Phe	Arg	Leu	Asn	Gly	Ile	Glu	Ile	Ser	Gln	Glu
		100						105					110		
Lys	Phe	Val	Asn	Tyr	Phe	Trp	Cys	Ser	Phe	His	Lys	Leu	Lys	Glu	Lys
		115				120						125			
Thr	Ser	Asn	Glu	Val	Asp	Val	Val	Ile	Leu	Glu	Val	Gly	Leu	Gly	Gly
		130				135						140			
Arg	Phe	Asp	Ala	Thr	Asn	Val	Ile	Gln	Lys	Pro	Val	Val	Cys	Gly	Ile
145					150					155				160	
Ser	Ser	Leu	Gly	Tyr	Asp	His	Met	Glu	Ile	Leu	Gly	Tyr	Thr	Leu	Ala

Met	Lys	Ile	Ile	His	Val	Ala	Gly	Thr	Lys	Gly	Lys	Gly	Ser	Thr	Cys
1				5					10					15	
Thr	Phe	Ala	Glu	Ser	Ile	Leu	Arg	Cys	Tyr	Gly	Leu	Arg	Thr	Gly	Leu
			20					25					30		
Phe	Thr	Ser	Pro	His	Leu	Ile	Asp	Val	Arg	Glu	Arg	Phe	Arg	Leu	Asn
			35				40					45			
Gly	Ile	Glu	Ile	Ser	Gln	Glu	Lys	Phe	Val	Asn	Tyr	Phe	Trp	Cys	Ser
	50					55				60					
Phe	His	Lys	Leu	Lys	Glu	Lys	Thr	Ser	Asn	Glu	Val	Asp	Val	Val	Ile
65					70					75					80

```

Leu Glu Val Gly Leu Gly Gly Arg Phe Asp Ala Thr Asn Val Ile Gln
      85                      90                      95
Lys Pro Val Val Cys Gly Ile Ser Ser Leu Gly Tyr Asp His Met Glu
      100                    105                    110
Ile Leu Gly Tyr Thr Leu Ala Glu Ile Ala Ala Glu Lys Ala Gly Ile
      115                    120                    125
Phe Lys Ser Gly Val Pro Ala Phe Thr Val Ala Gln Pro Asp Glu Ala
      130                    135                    140
Met Arg Val Leu Asn Glu Lys Ala Ser Lys Leu Glu Val Asn Leu Gln
      145                    150                    155                    160
Val Val Glu Pro Leu Asp Ser Ser Gln Arg Leu Gly Leu Gln Gly Glu
      165                    170                    175
His Gln Tyr Leu Asn Ala Gly Leu Ala Val Ala Leu Cys Ser Thr Phe
      180                    185                    190
Leu Lys Glu Ile Gly Ile Glu Asp Lys Asn Gly Leu Asp Gln Thr Asn
      195                    200                    205
Gly Leu Pro Glu Lys Phe Ile Ser Gly Leu Ser Asn Ala Tyr Leu Met
      210                    215                    220
Gly Arg Ala Met Ile Val Pro Asp Ser Glu Leu Pro Glu Glu Ile Val
      225                    230                    235                    240
Tyr Tyr Leu Asp Gly Ala His Ser Pro Glu Ser Met Glu Ala Cys Ala
      245                    250                    255
Ile Trp Phe Ser Lys Gln Ile Lys Gln Asn Gln Glu Arg Asn Gln Lys
      260                    265                    270
Arg Ser Glu Gln Ile Leu Leu Phe Asn Cys Met Ser Val Arg Asp Pro
      275                    280                    285
Ser Leu Leu Leu Pro Arg Leu Arg Ser Lys Cys Ile Asp Gln Gly Val
      290                    295                    300
Asp Phe Lys Arg Ala Val Phe Val Pro Asn Val Ser Val Tyr Asn Gln
      305                    310                    315                    320
Val Gly Ser Ser Thr Asn Val Gly Thr Arg Val Glu Ser Met Ser Trp
      325                    330                    335
Gln Phe Gly Leu Gln Arg Ile Trp Glu Ser Leu Ala Arg Gly Glu Ala
      340                    345                    350
Lys Ser Asn Ser Lys Ser Asp Ser Lys Gly Lys Glu Glu Glu Lys Ser
      355                    360                    365
Phe Val Phe Ser Ser Leu Pro Val Ala Val Asp Trp Leu Arg Asp Asn
      370                    375                    380
Ala Arg Gln Ser Lys Gln Val Arg Phe Gln Val Leu Val Thr Gly Ser
      385                    390                    395                    400
Leu His Leu Val Gly Asp Leu Leu Arg Phe Ile Lys Lys
      405                    410

```

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1499449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

```

Met Glu Ile Leu Gly Tyr Thr Leu Ala Glu Ile Ala Ala Glu Lys Ala
1      5      10      15
Gly Ile Phe Lys Ser Gly Val Pro Ala Phe Thr Val Ala Gln Pro Asp
      20      25      30
Glu Ala Met Arg Val Leu Asn Glu Lys Ala Ser Lys Leu Glu Val Asn
      35      40      45
Leu Gln Val Val Glu Pro Leu Asp Ser Ser Gln Arg Leu Gly Leu Gln

```

50	55	60
Gly Glu His Gln Tyr Leu Asn Ala Gly Leu Ala Val Ala Leu Cys Ser		
65	70	75
Thr Phe Leu Lys Glu Ile Gly Ile Glu Asp Lys Asn Gly Leu Asp Gln		80
	85	90
Thr Asn Gly Leu Pro Glu Lys Phe Ile Ser Gly Leu Ser Asn Ala Tyr		95
	100	105
Leu Met Gly Arg Ala Met Ile Val Pro Asp Ser Glu Leu Pro Glu Glu		110
	115	120
Ile Val Tyr Tyr Leu Asp Gly Ala His Ser Pro Glu Ser Met Glu Ala		125
	130	135
Cys Ala Ile Trp Phe Ser Lys Gln Ile Lys Gln Asn Gln Glu Arg Asn		140
	145	150
Gln Lys Arg Ser Glu Gln Ile Leu Leu Phe Asn Cys Met Ser Val Arg		155
	165	170
Asp Pro Ser Leu Leu Leu Pro Arg Leu Arg Ser Lys Cys Ile Asp Gln		175
	180	185
Gly Val Asp Phe Lys Arg Ala Val Phe Val Pro Asn Val Ser Val Tyr		190
	195	200
Asn Gln Val Gly Ser Ser Thr Asn Val Gly Thr Arg Val Glu Ser Met		205
	210	215
Ser Trp Gln Phe Gly Leu Gln Arg Ile Trp Glu Ser Leu Ala Arg Gly		220
	225	230
Glu Ala Lys Ser Asn Ser Lys Ser Asp Ser Lys Gly Lys Glu Glu Glu		235
	245	250
Lys Ser Phe Val Phe Ser Ser Leu Pro Val Ala Val Asp Trp Leu Arg		255
	260	265
Asp Asn Ala Arg Gln Ser Lys Gln Val Arg Phe Gln Val Leu Val Thr		270
	275	280
Gly Ser Leu His Leu Val Gly Asp Leu Leu Arg Phe Ile Lys Lys		285
	290	295
		300

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

atctcacaca	ccgaaagtta	ttttogaato	cactaacgaa	tcttccacag	caaaaaactt	60
tcgtgttcct	ctgtaatttc	tcagtatata	tagataccaa	atcgagcagt	gaaaaaatgg	120
ctatggcgag	tttatatcgg	cgatctcttc	cttctcctcc	ggccattgac	ttttcttccg	180
ccgaagaagn	ctaattctca	atgaagcgct	tcagaaagga	actatggaag	gatttttcag	240
gttgatttcg	tatttttcaga	cacaatccga	acctgcgtat	tgtggttttg	ctagtctctc	300
agtgggtgtg	aatgctcttt	ctatcgatcc	tggacgtaaa	tggaaagggc	cttggagggtg	360
gtttgatgaa	tcaatgtttg	attgctgcga	acctctggaa	gtagtgaagg	aaaaagggcat	420
ttcatttgga	aaagttgtct	gtttggctca	ttgttcagga	gcaaaagttg	aggctttccg	480
tacaagtcag	agcaccattg	atgattttcc	gcamayttgt	cgtagaatgc	acgagttctg	540
agaattgcc	tatgatctca	acatatcaca	gaggtgtatt	taagcagact	gggactggtc	600
acttttcacc	tattggtggc	tataatgctg	agagagatat	ggctttgatt	cttgatgttg	660
ctcgtttcaa	gtatccccct	cactgggttc	ctcttaaact	tctttgggaa	gccatggaca	720
gtattgatca	gtcaacaggg	aaacgtagag	ggttcattgct	catatctaga	ccacacagag	780
aaccggatt	gctctatact	ctgagctgca	aggatgaaag	ctggatcgaa	atagccaagt	840
atttgaagga	agatgttcc	cgtcttgtaa	gttcacagca	tgtagattct	gtggagaaaa	900
tcatatcagt	tgtgttcaag	tcacttccat	caaatttcaa	ccaattcatc	agatgggttg	960
ctgagatccg	aattacagag	gactcaaacc	aaaatctcag	cgcagaggag	aagtctaggc	1020
tgaactaaa	gcaattggtg	ctgaaggaag	tgcacgaaac	tgaactgttc	aaacacatca	1080

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ataagttctt atccacagtg ggttatgaag acagtctgac ttatgctgct gcaaaggctt 1140
gttgccaagg agctgaaatc ttatccggaa gctcatcaaa agagttttgt tgtcgggaaa 1200
cttgcgtaga atgcatcaaa ggtcctgatg actctgaagg cacagtgggtg actggagttg 1260
tggtgcgtga tgggaatgaa caaaagggtt atctgttagt gccatcgacg caaactgagt 1320
gtgaatgtgg tcctgaagca acttatccag caggaaacga tgtgttctact gcacttctat 1380
tggctttacc tccacagaca tggtcaggga tcaaagacca agctcttatg catgaaatga 1440
agcagctcat ttccatgggt tccctcccaa ctttgcttca agaagaggta ttgcatcttc 1500
gacggcaact tcagctgcta aaacgatgcc aagagaacaa ggaagaggat gatctcgctg 1560
ctcctgccta ttagttcatt gtcccaaatc cactctcttc cccatttgaa tcccacgttc 1620
tcaacacttg attgttagaa agtctcttta ttgtctgtac gattcaaact ctatttgcaa 1680
tgagagatat ttgtaaacad attcattcta tgaattgtta atcacaataa gtaaagaatc 1740
ttagaatcat atttc
```

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

```
Met Ile Phe Arg Xaa Xaa Val Val Lys Cys Thr Ser Ser Glu Asn Cys
1         5         10        15
His Met Ile Ser Thr Tyr His Arg Gly Val Phe Lys Gln Thr Gly Thr
20        25        30
Gly His Phe Ser Pro Ile Gly Gly Tyr Asn Ala Glu Arg Asp Met Ala
35        40        45
Leu Ile Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp Val Pro
50        55        60
Leu Lys Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser Thr Gly
65        70        75        80
Lys Arg Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu Pro Gly
85        90        95
Leu Leu Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu Ile Ala
100       105       110
Lys Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val
115       120       125
Asp Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser
130       135       140
Asn Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu
145       150       155       160
Asp Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu
165       170       175
Lys Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His
180       185       190
Ile Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr
195       200       205
Ala Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser
210       215       220
Ser Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys
225       230       235       240
Gly Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Val Arg
245       250       255
Asp Gly Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr Gln Thr
260       265       270
Glu Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val
275       280       285
Phe Thr Ala Leu Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser Gly Ile
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290 295 300  
Lys Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala  
305 310 315 320  
Ser Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln  
325 330 335  
Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu  
340 345 350  
Ala Ala Pro Ala Tyr  
355

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1499452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

Met Ile Ser Thr Tyr His Arg Gly Val Phe Lys Gln Thr Gly Thr Gly  
1 5 10 15  
His Phe Ser Pro Ile Gly Gly Tyr Asn Ala Glu Arg Asp Met Ala Leu  
20 25 30  
Ile Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp Val Pro Leu  
35 40 45  
Lys Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser Thr Gly Lys  
50 55 60  
Arg Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu Pro Gly Leu  
65 70 75 80  
Leu Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu Ile Ala Lys  
85 90 95  
Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val Asp  
100 105 110  
Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser Asn  
115 120 125  
Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu Asp  
130 135 140  
Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu Lys  
145 150 155 160  
Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His Ile  
165 170 175  
Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr Ala  
180 185 190  
Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser Ser  
195 200 205  
Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys Gly  
210 215 220  
Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Val Arg Asp  
225 230 235 240  
Gly Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr Gln Thr Glu  
245 250 255  
Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val Phe  
260 265 270  
Thr Ala Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser Gly Ile Lys  
275 280 285  
Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala Ser  
290 295 300  
Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln Leu  
305 310 315 320

Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu Ala  
325 330 335  
Ala Pro Ala Tyr  
340

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1499453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

Met	Ala	Leu	Ile	Leu	Asp	Val	Ala	Arg	Phe	Lys	Tyr	Pro	Pro	His	Trp
1			5						10					15	
Val	Pro	Leu	Lys	Leu	Leu	Trp	Glu	Ala	Met	Asp	Ser	Ile	Asp	Gln	Ser
		20						25					30		
Thr	Gly	Lys	Arg	Arg	Gly	Phe	Met	Leu	Ile	Ser	Arg	Pro	His	Arg	Glu
		35					40					45			
Pro	Gly	Leu	Leu	Tyr	Thr	Leu	Ser	Cys	Lys	Asp	Glu	Ser	Trp	Ile	Glu
	50					55				60					
Ile	Ala	Lys	Tyr	Leu	Lys	Glu	Asp	Val	Pro	Arg	Leu	Val	Ser	Ser	Gln
65					70					75					80
His	Val	Asp	Ser	Val	Glu	Lys	Ile	Ile	Ser	Val	Val	Phe	Lys	Ser	Leu
			85						90				95		
Pro	Ser	Asn	Phe	Asn	Gln	Phe	Ile	Arg	Trp	Val	Ala	Glu	Ile	Arg	Ile
		100						105					110		
Thr	Glu	Asp	Ser	Asn	Gln	Asn	Leu	Ser	Ala	Glu	Glu	Lys	Ser	Arg	Leu
		115					120					125			
Lys	Leu	Lys	Gln	Leu	Val	Leu	Lys	Glu	Val	His	Glu	Thr	Glu	Leu	Phe
	130					135					140				
Lys	His	Ile	Asn	Lys	Phe	Leu	Ser	Thr	Val	Gly	Tyr	Glu	Asp	Ser	Leu
145					150					155					160
Thr	Tyr	Ala	Ala	Ala	Lys	Ala	Cys	Cys	Gln	Gly	Ala	Glu	Ile	Leu	Ser
			165						170					175	
Gly	Ser	Ser	Ser	Lys	Glu	Phe	Cys	Cys	Arg	Glu	Thr	Cys	Val	Lys	Cys
		180					185						190		
Ile	Lys	Gly	Pro	Asp	Asp	Ser	Glu	Gly	Thr	Val	Val	Thr	Gly	Val	Val
	195						200					205			
Val	Arg	Asp	Gly	Asn	Glu	Gln	Lys	Val	Asp	Leu	Leu	Val	Pro	Ser	Thr
	210					215						220			
Gln	Thr	Glu	Cys	Glu	Cys	Gly	Pro	Glu	Ala	Thr	Tyr	Pro	Ala	Gly	Asn
225					230					235					240
Asp	Val	Phe	Thr	Ala	Leu	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Thr	Trp	Ser
			245						250					255	
Gly	Ile	Lys	Asp	Gln	Ala	Leu	Met	His	Glu	Met	Lys	Gln	Leu	Ile	Ser
		260					265						270		
Met	Ala	Ser	Leu	Pro	Thr	Leu	Leu	Gln	Glu	Glu	Val	Leu	His	Leu	Arg
	275						280					285			
Arg	Gln	Leu	Gln	Leu	Leu	Lys	Arg	Cys	Gln	Glu	Asn	Lys	Glu	Glu	Asp
	290					295					300				
Asp	Leu	Ala	Ala	Pro	Ala	Tyr									
305				310											

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1283  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

gaaggaccag	acccgagaga	agttgagctg	tatgtggaag	agatactgtc	actgatgcag	60
ttgggtgagg	actataccga	gttcatggtg	tcaaaaatca	agtctttgac	gtcggtagat	120
cctgaattgt	tgccaacggc	tacaaaggca	tttagaaata	agagttttag	caaagcgatt	180
caggatgtga	cgagatatta	tgttatacta	gaagggttct	ttatggttga	gaatgtgagg	240
aaagctatta	ggatcgatga	gcatgtacct	gacagcctta	ccacttcaat	ggtggacgat	300
gtgttctacg	tgttgcagag	ttgtctgagg	agagcgattt	caacttcaaa	cataagttct	360
gtgattgctg	tgttgagcta	tgctggtagc	ttgttgggca	atgattacca	tgaagctcta	420
caacagaaga	ttagagagcc	taaccttggg	gctaggttgt	tcttgggtgg	tataggtatg	480
gaaaacaccg	gaactgagat	tgcaactgct	ttgaacaata	tggacgtgag	ctgcgagtac	540
attctcaaac	taaaacatga	aatcgaggag	caatgtactg	aggtatttcc	tgcaccagca	600
gatcgagaga	ggataaaatc	atgtctatcc	gagctaggcg	agttaagcag	cacgttcaag	660
cagttactca	actcaggcat	ggaacagcta	gtagcaaccg	taacaccaag	aatccgtccg	720
gttctagaca	ccgtggctac	cataagctac	gagttaacag	aaaccgagta	cgcagagaat	780
gaggtgaacg	acccttgggt	ccaaagactt	ctccactcag	tcgaaacaaa	tgccgcgtgg	840
ctccaaccac	taatgacatc	caacaactac	gactcgtttc	tgcatctcat	aattgatttc	900
atagtttaaga	gactcgaagt	cataatgatg	cagaaacggg	ttanccagct	tggtgggctt	960
cagcttgatc	gagacacaag	ggctttgggt	agccatttct	cgggtatgac	tcaaagaaca	1020
gtgagagata	agtttgctcg	gttaacgcag	atggcgacga	tactgaactt	ggaaaagggtc	1080
tcagagattt	tggacttttg	gggagaaaac	tcaggaccca	tgacttggag	actcacacca	1140
gctgagggtta	gacgggtttt	gggtctccgg	gtcaggttca	aacccgaatc	aattgctgct	1200
ctcaagttgt	gatgttactt	cttttcttta	ttatgtcatc	tacacaactc	gaaccaattc	1260
tttcgaaatc	tgattggttc	ccc				

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..403  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

Glu	Gly	Pro	Asp	Pro	Arg	Glu	Val	Glu	Leu	Tyr	Val	Glu	Glu	Ile	Leu	
1				5					10					15		
Ser	Leu	Met	Gln	Leu	Gly	Glu	Asp	Tyr	Thr	Glu	Phe	Met	Val	Ser	Lys	
		20						25					30			
Ile	Lys	Ser	Leu	Thr	Ser	Val	Asp	Pro	Glu	Leu	Leu	Pro	Thr	Ala	Thr	
		35					40					45				
Lys	Ala	Phe	Arg	Asn	Lys	Ser	Phe	Ser	Lys	Ala	Ile	Gln	Asp	Val	Thr	
		50				55					60					
Arg	Tyr	Tyr	Val	Ile	Leu	Glu	Gly	Phe	Phe	Met	Val	Glu	Asn	Val	Arg	
65				70					75				80			
Lys	Ala	Ile	Arg	Ile	Asp	Glu	His	Val	Pro	Asp	Ser	Leu	Thr	Thr	Ser	
			85					90					95			
Met	Val	Asp	Asp	Val	Phe	Tyr	Val	Leu	Gln	Ser	Cys	Leu	Arg	Arg	Ala	
		100						105				110				
Ile	Ser	Thr	Ser	Asn	Ile	Ser	Ser	Val	Ile	Ala	Val	Leu	Ser	Tyr	Ala	
		115				120						125				
Gly	Ser	Leu	Leu	Gly	Asn	Asp	Tyr	His	Glu	Ala	Leu	Gln	Gln	Lys	Ile	
		130				135					140					
Arg	Glu	Pro	Asn	Leu	Gly	Ala	Arg	Leu	Phe	Leu	Gly	Gly	Ile	Gly	Met	
145				150						155					160	



Glu Asn Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn Asn Met Asp Val  
165 170 175  
Ser Cys Glu Tyr Ile Leu Lys Leu Lys His Glu Ile Glu Glu Gln Cys  
180 185 190  
Thr Glu Val Phe Pro Ala Pro Ala Asp Arg Glu Arg Ile Lys Ser Cys  
195 200 205  
Leu Ser Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys Gln Leu Leu Asn  
210 215 220  
Ser Gly Met Glu Gln Leu Val Ala Thr Val Thr Pro Arg Ile Arg Pro  
225 230 235 240  
Val Leu Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu Thr Glu Thr Glu  
245 250 255  
Tyr Ala Glu Asn Glu Val Asn Asp Pro Trp Val Gln Arg Leu Leu His  
260 265 270  
Ser Val Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu Met Thr Ser Asn  
275 280 285  
Asn Tyr Asp Ser Phe Leu His Leu Ile Ile Asp Phe Ile Val Lys Arg  
290 295 300  
Leu Glu Val Ile Met Met Gln Lys Arg Phe Xaa Gln Leu Gly Gly Leu  
305 310 315 320  
Gln Leu Asp Arg Asp Thr Arg Ala Leu Val Ser His Phe Ser Gly Met  
325 330 335  
Thr Gln Arg Thr Val Arg Asp Lys Phe Ala Arg Leu Thr Gln Met Ala  
340 345 350  
Thr Ile Leu Asn Leu Glu Lys Val Ser Glu Ile Leu Asp Phe Trp Gly  
355 360 365  
Glu Asn Ser Gly Pro Met Thr Trp Arg Leu Thr Pro Ala Glu Val Arg  
370 375 380  
Arg Val Leu Gly Leu Arg Val Glu Phe Lys Pro Glu Ser Ile Ala Ala  
385 390 395 400  
Leu Lys Leu

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

Met Gln Leu Gly Glu Asp Tyr Thr Glu Phe Met Val Ser Lys Ile Lys  
1 5 10 15  
Ser Leu Thr Ser Val Asp Pro Glu Leu Pro Thr Ala Thr Lys Ala  
20 25 30  
Phe Arg Asn Lys Ser Phe Ser Lys Ala Ile Gln Asp Val Thr Arg Tyr  
35 40 45  
Tyr Val Ile Leu Glu Gly Phe Phe Met Val Glu Asn Val Arg Lys Ala  
50 55 60  
Ile Arg Ile Asp Glu His Val Pro Asp Ser Leu Thr Thr Ser Met Val  
65 70 75 80  
Asp Asp Val Phe Tyr Val Leu Gln Ser Cys Leu Arg Arg Ala Ile Ser  
85 90 95  
Thr Ser Asn Ile Ser Ser Val Ile Ala Val Leu Ser Tyr Ala Gly Ser  
100 105 110  
Leu Leu Gly Asn Asp Tyr His Glu Ala Leu Gln Gln Lys Ile Arg Glu  
115 120 125  
Pro Asn Leu Gly Ala Arg Leu Phe Leu Gly Gly Ile Gly Met Glu Asn

```

      130              135              140
Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn Asn Met Asp Val Ser Cys
145              150              155              160
Glu Tyr Ile Leu Lys Leu Lys His Glu Ile Glu Glu Gln Cys Thr Glu
      165              170              175
Val Phe Pro Ala Pro Ala Asp Arg Glu Arg Ile Lys Ser Cys Leu Ser
      180              185              190
Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys Gln Leu Leu Asn Ser Gly
      195              200              205
Met Glu Gln Leu Val Ala Thr Val Thr Pro Arg Ile Arg Pro Val Leu
      210              215              220
Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu Thr Glu Thr Glu Tyr Ala
225              230              235              240
Glu Asn Glu Val Asn Asp Pro Trp Val Gln Arg Leu Leu His Ser Val
      245              250              255
Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu Met Thr Ser Asn Asn Tyr
      260              265              270
Asp Ser Phe Leu His Leu Ile Ile Asp Phe Ile Val Lys Arg Leu Glu
      275              280              285
Val Ile Met Met Gln Lys Arg Phe Xaa Gln Leu Gly Gly Leu Gln Leu
      290              295              300
Asp Arg Asp Thr Arg Ala Leu Val Ser His Phe Ser Gly Met Thr Gln
305              310              315              320
Arg Thr Val Arg Asp Lys Phe Ala Arg Leu Thr Gln Met Ala Thr Ile
      325              330              335
Leu Asn Leu Glu Lys Val Ser Glu Ile Leu Asp Phe Trp Gly Glu Asn
      340              345              350
Ser Gly Pro Met Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Arg Val
      355              360              365
Leu Gly Leu Arg Val Glu Phe Lys Pro Glu Ser Ile Ala Ala Leu Lys
      370              375              380
Leu
385
```

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

```

Met Val Ser Lys Ile Lys Ser Leu Thr Ser Val Asp Pro Glu Leu Leu
1      5      10      15
Pro Thr Ala Thr Lys Ala Phe Arg Asn Lys Ser Phe Ser Lys Ala Ile
      20      25      30
Gln Asp Val Thr Arg Tyr Tyr Val Ile Leu Glu Gly Phe Phe Met Val
      35      40      45
Glu Asn Val Arg Lys Ala Ile Arg Ile Asp Glu His Val Pro Asp Ser
      50      55      60
Leu Thr Thr Ser Met Val Asp Asp Val Phe Tyr Val Leu Gln Ser Cys
      65      70      75      80
Leu Arg Arg Ala Ile Ser Thr Ser Asn Ile Ser Ser Val Ile Ala Val
      85      90      95
Leu Ser Tyr Ala Gly Ser Leu Leu Gly Asn Asp Tyr His Glu Ala Leu
      100     105     110
Gln Gln Lys Ile Arg Glu Pro Asn Leu Gly Ala Arg Leu Phe Leu Gly
      115     120     125
```

Gly Ile Gly Met Glu Asn Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn  
130 135 140  
Asn Met Asp Val Ser Cys Glu Tyr Ile Leu Lys Leu Lys His Glu Ile  
145 150 155 160  
Glu Glu Gln Cys Thr Glu Val Phe Pro Ala Pro Ala Asp Arg Glu Arg  
165 170 175  
Ile Lys Ser Cys Leu Ser Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys  
180 185 190  
Gln Leu Leu Asn Ser Gly Met Glu Gln Leu Val Ala Thr Val Thr Pro  
195 200 205  
Arg Ile Arg Pro Val Leu Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu  
210 215 220  
Thr Glu Thr Glu Tyr Ala Glu Asn Glu Val Asn Asp Pro Trp Val Gln  
225 230 235 240  
Arg Leu Leu His Ser Val Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu  
245 250 255  
Met Thr Ser Asn Asn Tyr Asp Ser Phe Leu His Leu Ile Ile Asp Phe  
260 265 270  
Ile Val Lys Arg Leu Glu Val Ile Met Met Gln Lys Arg Phe Xaa Gln  
275 280 285  
Leu Gly Gly Leu Gln Leu Asp Arg Asp Thr Arg Ala Leu Val Ser His  
290 295 300  
Phe Ser Gly Met Thr Gln Arg Thr Val Arg Asp Lys Phe Ala Arg Leu  
305 310 315 320  
Thr Gln Met Ala Thr Ile Leu Asn Leu Glu Lys Val Ser Glu Ile Leu  
325 330 335  
Asp Phe Trp Gly Glu Asn Ser Gly Pro Met Thr Trp Arg Leu Thr Pro  
340 345 350  
Ala Glu Val Arg Arg Val Leu Gly Leu Arg Val Glu Phe Lys Pro Glu  
355 360 365  
Ser Ile Ala Ala Leu Lys Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

atattattca cgattctcat caaatcatct cggatactca caaccgaaat aactaacccc	60
tcctcaacaa aaaacaacaa aacatgtaca ctccatcata cttaaaatat tcaataatct	120
caattatata cgtattattc ctccaaggaa ctcatggaga cgacggaggt tggcaagggtg	180
gtcacgccgt aaaacgtggc gtgaccacct tgccaacctc cgtcgtccct tattaaaatt	240
acctgccagt ttacttttct ctcttcttgt tttctgtgtt ggaagattct caagttattt	300
attccgcaaa aaacggttta tcatttacaa ttagttgaat tttggtcg	

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:  
Ile Leu Phe Thr Ile Leu Ile Lys Ser Ser Pro Ile Leu Thr Thr Glu  
1 5 10 15  
Ile Thr Asn Pro Ser Ser Thr Lys Asn Asn Lys Thr Cys Thr Leu His  
20 25 30  
His Thr

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

Met Tyr Thr Pro Ser Tyr Leu Lys Tyr Ser Ile Ile Ser Ile Ile Ser  
1 5 10 15  
Val Leu Phe Leu Gln Gly Thr His Gly Asp Asp Gly Gly Trp Gln Gly  
20 25 30  
Gly His Ala Val Lys Arg Gly Val Thr Thr Leu Pro Thr Ser Val Val  
35 40 45  
Pro Tyr  
50

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1004
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

aaagaccaaa agaaaaaaaa atcttttttct tttctgatga atcgtatcta ttagctatga 60  
gcctgagggtg atgatacatgt caacataacc atcaacgttc taccatggct agtcctagca 120  
acaaaggcaa aggcataagca gaaggatcgt ctcaaccgca atcgcaaccg caaccacaac 180  
cacaccaact gcaatcacct cctaaccgcg cagcggttaag ccggtacgag tcacagaaac 240  
gacgagactg gaacacgttt tgtoaatacc tgcgtaacca acagccaccg gttcacatct 300  
cgcagtgtgg atcaaaccac atcctcgatt tcctccaata tctcgaccag tttgggaaga 360  
caaaggttca tatccatgga tgcgttttct tcggacaggt tgagccagcg ggacagtgt 420  
actgtccttt aaaacaagcg tgggggagtt tagatgcttt gatcggacgg ctaagagcgg 480  
ctttcgagga gaacggagga ttgccggaga gaaacccttt tgccggcggc ggaattaggg 540  
tttttctgag ggaagtgaga gattcacagg cgaaggcaag aggagttccg tacaagaaaa 600  
gaaaaaagag gaagaagagg aatcctatga agagtcatga tgggtgaagat ggtactacgg 660  
gaactagtag tagctccaac ttggcttctt agcgggaagca aacaaaaaat ctataataaa 720  
acaaaagtgg aattagttaa tggttaagcat ttaatactct ccataatctc tattaatattt 780  
cagtacttta atcctatttt gtgatctatt tacaatttta catatagagt gaaaagaaac 840  
aattctacat ttgtttcttg atagtcagct cttaatgcat agttgaattt tatacgtatc 900  
ataccctaac tataagatta atcttgatct tagatcatat acatatatca tcatggtgtg 960  
taccctaagt ttcataatca tttttcttaa ctatttatgt ggat

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..195  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499466  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:  
Met Ala Ser Pro Ser Asn Lys Gly Lys Gly Ile Ala Glu Gly Ser Ser  
1                    5                    10                    15  
Gln Pro Gln Ser Gln Pro Gln Pro Gln Pro His Gln Leu Gln Ser Pro  
                    20                    25                    30  
Pro Asn Pro Pro Ala Leu Ser Arg Tyr Glu Ser Gln Lys Arg Arg Asp  
                    35                    40                    45  
Trp Asn Thr Phe Cys Gln Tyr Leu Arg Asn Gln Gln Pro Pro Val His  
50                    55                    60  
Ile Ser Gln Cys Gly Ser Asn His Ile Leu Asp Phe Leu Gln Tyr Leu  
65                    70                    75                    80  
Asp Gln Phe Gly Lys Thr Lys Val His Ile His Gly Cys Val Phe Phe  
                    85                    90                    95  
Gly Gln Val Glu Pro Ala Gly Gln Cys Asn Cys Pro Leu Lys Gln Ala  
                    100                    105                    110  
Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Phe Glu  
                    115                    120                    125  
Glu Asn Gly Gly Leu Pro Glu Arg Asn Pro Phe Ala Gly Gly Gly Ile  
130                    135                    140  
Arg Val Phe Leu Arg Glu Val Arg Asp Ser Gln Ala Lys Ala Arg Gly  
145                    150                    155                    160  
Val Pro Tyr Lys Lys Arg Lys Lys Arg Lys Lys Arg Asn Pro Met Lys  
                    165                    170                    175  
Ser His Asp Gly Glu Asp Gly Thr Thr Gly Thr Ser Ser Ser Ser Asn  
180                    185                    190  
Leu Ala Ser  
195

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1049  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

actttgtaat	aataaccaca	acttcccaat	cttcttcac	agattttgct	agttcgtcac	60
acacacggat	caacgtcatc	atcttctctt	cttcttctcc	acaagcccac	ctacaatttc	120
catttcgccc	cttcctctgt	tcccacttac	atcaattccg	ctcgatttcg	aatttcgagc	180
tcaatcttcc	ctttggatcg	aagaagaaga	agaagaatct	ggtctgtctc	tggctttaaa	240
tctatggccg	atttagtaaa	aaccaatgct	cgcagagacg	gtgaagaacg	atttcaagcg	300
cttgagcaag	aggctttcat	caataattcg	tctccggagc	tccagaacga	gttggtatcc	360
gacgccggag	gtgggattga	agcaatcgct	aatcgctctga	ctgcattttt	gtcaaatggc	420
agagcaaagt	gattgtagca	gctctgtttg	gatccgttct	gcttctacga	catgatgggtg	480
cagcttttgt	ggctgtgatt	ggatcgggtt	caaattccgt	gctctcagta	gctttgaaac	540
gtatacttaa	ccaagagaga	cctgttgcta	ctctccgttc	tgatcctggg	atgccttctt	600
ctcatgcccc	atccatttct	ttcatctctg	tgttttctgt	cttctccgtt	atggagtggc	660
ttggaaccaa	tgtactctct	ctgttcctta	cggtcttcac	cctcgcattg	ggttcttatt	720
tcacgtgggt	aagggtttct	cagaagcttc	acacgacaag	tcaagtggtc	gtaggtgcaa	780
tcgtgggttc	tgtttactcc	accttatggg	atgtaacttg	gaactctctt	gttcttgaag	840
cctttacctc	aacattctca	gtacaaatag	ctgtctttct	ggttgctgct	gcgtctgctt	900
taggttttgc	agtttatgtg	ctacttaact	ggtttaaaga	tgacagatga	cagatgacag	960

aatgataatt ttcagtactt aggatgtata aggaatgcat ttgattctcc ttataattca 1020  
tattgattga gctatttttaa cattcaatg

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

Phe	Val	Ile	Ile	Thr	Thr	Ser	Gln	Ser	Ser	Ser	Ser	Asp	Phe	Ala
1				5				10					15	
Ser	Ser	Ser	His	Thr	Arg	Ile	Asn	Val	Ile	Ile	Phe	Ser	Ser	Ser
			20					25					30	
Pro	Gln	Ala	His	Leu	Gln	Phe	Pro	Phe	Arg	Arg	Phe	Leu	Cys	Ser
			35					40					45	
Leu	His	Gln	Phe	Arg	Ser	Ile	Ser	Asn	Phe	Glu	Leu	Asn	Leu	Pro
			50					55					60	
Gly	Ser	Lys	Lys	Lys	Lys	Lys	Asn	Leu	Val	Cys	Leu	Trp	Leu	
65							70						75	

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

Met	Pro	Ser	Ser	His	Ala	Gln	Ser	Ile	Ser	Phe	Ile	Ser	Val	Phe	Ser
1				5					10					15	
Val	Phe	Ser	Val	Met	Glu	Trp	Leu	Gly	Thr	Asn	Val	Leu	Ser	Leu	Phe
			20					25						30	
Leu	Ser	Gly	Phe	Ile	Leu	Ala	Leu	Gly	Ser	Tyr	Phe	Thr	Trp	Leu	Arg
			35					40						45	
Val	Ser	Gln	Lys	Leu	His	Thr	Thr	Ser	Gln	Val	Val	Val	Gly	Ala	Ile
			50					55						60	
Val	Gly	Ser	Val	Tyr	Ser	Thr	Leu	Trp	Tyr	Val	Thr	Trp	Asn	Ser	Leu
65							70							80	
Val	Leu	Glu	Ala	Phe	Thr	Ser	Thr	Phe	Ser	Val	Gln	Ile	Ala	Val	Phe
			85					90						95	
Leu	Val	Ala	Ala	Ala	Ser	Ala	Leu	Gly	Phe	Ala	Val	Tyr	Val	Leu	Leu
			100					105						110	
Asn	Trp	Phe	Lys	Asp	Asp	Arg									
							115								

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1499470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

```
Met Glu Trp Leu Gly Thr Asn Val Leu Ser Leu Phe Leu Ser Gly Phe
1          5          10          15
Ile Leu Ala Leu Gly Ser Tyr Phe Thr Trp Leu Arg Val Ser Gln Lys
20          25          30
Leu His Thr Thr Ser Gln Val Val Val Gly Ala Ile Val Gly Ser Val
35          40          45
Tyr Ser Thr Leu Trp Tyr Val Thr Trp Asn Ser Leu Val Leu Glu Ala
50          55          60
Phe Thr Ser Thr Phe Ser Val Gln Ile Ala Val Phe Leu Val Ala Ala
65          70          75          80
Ala Ser Ala Leu Gly Phe Ala Val Tyr Val Leu Leu Asn Trp Phe Lys
85          90          95
Asp Asp Arg
```

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1232

(D) OTHER INFORMATION: / Ceres Seq. ID 1499474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

```
tcttcttctc ccacacagct agaaacacag tctcctcatc ttctgagcaa aaaaatggaa 60
gtggctcttc tatnvtcttc ttcttctctg tctcctctct gtcaccagcg aatctcaact 120
ctcacaccca aaacctcgaa ttccccaat taccctcgcc tcccggtcat cagatccgag 180
gtgacagaga ggagacaagg aagaagagaa ggagatgttg aactagggga acaacaaggt 240
ggagatcaag gattggaaga tttttttcaa aaaggttcaa gtgattgaca aacagtatga 300
taagctagac aagcttctaa agaaactgca ggcttcccat gaggagtcaa aatctgtgac 360
caaagctcct gccatgaagg cgataaagaa gacaatggaa aaagacgttg atgaagtgtg 420
aagtattgcc cgtttcrtaa aggggaaact cgaggagttg gacagagaga acttgggcaa 480
atagacaaaa acctggatgt gcaaaaggat ctggtgtgga tcgatcaaga acagcaacaa 540
cactttcctt aaagaagaag ttgaaagaca agatggccga gtttcagggt ctacgagaga 600
acattcaaca agagtatcgc gatgttggtg ataggcgagt ttatacagta actggggagc 660
gggcgagatga agatactatt gatgaattga ttgaaactgg aaacagcgaa cagatcttcc 720
agaaagcgat tcaggagcaa ggaagaggac aggtaatgga caccttggcg gaaatccaag 780
aacgtcatga tgctgtcaga gacttggaaa agaaacttct tgacttacia caaatattct 840
tgatgatggc agttttggtt gatgcacaag gagaaatgct tgacaatata gaatctcagg 900
tgtcaagtgc agtagatcac gtgcaatcgg gaaacacggc acttcaaaga gcaaagagct 960
tgcakgaaga actcaagaaa atggatgtgt attgcaatta tcctcctcct cattgtgggt 1020
gcagtgatcg ttgttggtgt tctcaagcct tggaaaaaca aagagtgttt gaggaagaa 1080
agaatgtaca aaaagaatat caaatcctta ttcacggctt tgagtgtgag tgttttgttt 1140
atgatgtgtg tgtttttttt ttaccaagaa acgaaaaaaa aagaacacaa attctacatt 1200
cttttaattg gatcaaacaa accaatttcc cc
```

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1499475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

Ser	Ser	Ser	Ser	Thr	Gln	Leu	Glu	Thr	Gln	Ser	Pro	His	Leu	Leu	Ser
1				5				10					15		
Lys	Lys	Met	Glu	Val	Ala	Leu	Leu	Xaa	Phe	Ser	Ser	Ser	Leu	Ser	Pro
			20					25					30		
Leu	Cys	His	Gln	Arg	Ile	Ser	Thr	Leu	Thr	Pro	Lys	Thr	Ser	Asn	Ser
			35				40					45			
Pro	Asn	Tyr	Pro	Arg	Leu	Pro	Val	Ile	Arg	Ser	Ala	Val	Thr	Glu	Arg
			50				55				60				
Arg	Gln	Gly	Arg	Arg	Glu	Gly	Asp	Val	Glu	Leu	Gly	Glu	Gln	Gln	Gly
65					70				75						80
Gly	Asp	Gln	Gly	Leu	Glu	Asp	Phe	Phe	Gln	Lys	Gly	Ser	Ser	Asp	
				85				90						95	

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

Met	Ala	Glu	Phe	Gln	Val	Leu	Arg	Glu	Asn	Ile	Gln	Gln	Glu	Tyr	Arg
1				5				10					15		
Asp	Val	Val	Asp	Arg	Arg	Val	Tyr	Thr	Val	Thr	Gly	Glu	Arg	Ala	Asp
			20					25					30		
Glu	Asp	Thr	Ile	Asp	Glu	Leu	Ile	Glu	Thr	Gly	Asn	Ser	Glu	Gln	Ile
			35				40					45			
Phe	Gln	Lys	Ala	Ile	Gln	Glu	Gln	Gly	Arg	Gly	Gln	Val	Met	Asp	Thr
			50				55				60				
Leu	Ala	Glu	Ile	Gln	Glu	Arg	His	Asp	Ala	Val	Arg	Asp	Leu	Glu	Lys
65					70				75					80	
Lys	Leu	Leu	Asp	Leu	Gln	Gln	Ile	Phe	Leu	Asp	Met	Ala	Val	Leu	Val
				85				90						95	
Asp	Ala	Gln	Gly	Glu	Met	Leu	Asp	Asn	Ile	Glu	Ser	Gln	Val	Ser	Ser
			100					105					110		
Ala	Val	Asp	His	Val	Gln	Ser	Gly	Asn	Thr	Ala	Leu	Gln	Arg	Ala	Lys
			115				120						125		
Ser	Leu	Xaa	Glu	Glu	Leu	Lys	Lys	Met	Asp	Val	Tyr	Cys	Asn	Tyr	His
			130				135					140			
Pro	Pro	His	Cys	Gly	Cys	Ser	Asp	Arg	Cys	Trp	Cys	Ser	Gln	Ala	Leu
145					150				155					160	
Glu	Lys	Gln	Arg	Val	Leu	Glu	Glu	Arg	Lys	Asn	Val	Gln	Lys	Glu	Tyr
				165				170						175	
Gln	Ile	Leu	Ile	His	Gly	Phe	Glu								
				180											

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:



Met Asp Thr Leu Ala Glu Ile Gln Glu Arg His Asp Ala Val Arg Asp  
1 5 10 15  
Leu Glu Lys Lys Leu Leu Asp Leu Gln Ile Phe Leu Asp Met Ala  
20 30  
Val Leu Val Asp Ala Gln Gly Glu Met Leu Asp Asn Ile Glu Ser Gln  
35 40 45  
Val Ser Ser Ala Val Asp His Val Gln Ser Gly Asn Thr Ala Leu Gln  
50 55 60  
Arg Ala Lys Ser Leu Xaa Glu Glu Leu Lys Lys Met Asp Val Tyr Cys  
65 70 75 80  
Asn Tyr His Pro Pro His Cys Gly Cys Ser Asp Arg Cys Trp Cys Ser  
85 90 95  
Gln Ala Leu Glu Lys Gln Arg Val Leu Glu Glu Arg Lys Asn Val Gln  
100 105 110  
Lys Glu Tyr Gln Ile Leu Ile His Gly Phe Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

gccttttagtt aaaccacacg atctaaaaat cccttctctc tttctttctt tctttttttc	60
tctccctctc ttctcaggcg agtatgcaaa gcaagaacat gatcgtggct tcatctcatc	120
agcagcaaca acaacagcaa ccgcagcagc cacaaccgca acttaaatgc cctcggttgcg	180
attcttccaa cacaaagttc tgctactaca acaactacag cctctctcaa ccacggcact	240
tttgcaaggc ttgcaagagg tactggacga gaggtgggac tctcaggaac gttcccggtan	300
gggntagcta tcggaagaac aaacgtgtaa agcggccatc aaccgcaacc acaaccactg	360
cctccaccgt ctgcagcact aattcttcat cccctaataa ccctcatcag atctctcatt	420
tctcttccat gaatcatcat cctttgttct atggtttatc agatcatatg agcagttgta	480
ataataaata ttccaatgat cccaagccgt ttcagtgatt cttcaaagac ttgttcatca	540
agtgggttag agagtgaagt tctctcatct ggktttagca gtcttagtgc b	

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

Met Gln Ser Lys Asn Met Ile Val Ala Ser Ser His Gln Gln Gln Gln  
1 5 10 15  
Gln Gln Gln Pro Gln Gln Pro Gln Pro Gln Leu Lys Cys Pro Arg Cys  
20 25 30  
Asp Ser Ser Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser  
35 40 45  
Gln Pro Arg His Phe Cys Lys Ala Cys Lys Arg Tyr Trp Thr Arg Gly  
50 55 60  
Gly Thr Leu Arg Asn Val Pro Val Xaa Xaa Ser Tyr Arg Lys Asn Lys  
65 70 75 80  
Arg Val Lys Arg Pro Ser Thr Ala Thr Thr Thr Thr Ala Ser Thr Val

	85	90	95
Ser Thr Thr Asn Ser Ser Ser Pro Asn Asn Pro His Gln Ile Ser His			
	100	105	110
Phe Ser Ser Met Asn His His Pro Leu Phe Tyr Gly Leu Ser Asp His			
	115	120	125
Met Ser Ser Cys Asn Asn Lys Ser Ser Asn Asp Pro Lys Pro Phe Gln			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1499488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

Met Ile Val Ala Ser Ser His Gln Gln Gln Gln Gln Pro Gln			
1	5	10	15
Gln Pro Gln Pro Gln Leu Lys Cys Pro Arg Cys Asp Ser Ser Asn Thr			
	20	25	30
Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser Gln Pro Arg His Phe			
	35	40	45
Cys Lys Ala Cys Lys Arg Tyr Trp Thr Arg Gly Gly Thr Leu Arg Asn			
	50	55	60
Val Pro Val Xaa Xaa Ser Tyr Arg Lys Asn Lys Arg Val Lys Arg Pro			
65	70	75	80
Ser Thr Ala Thr Thr Thr Thr Ala Ser Thr Val Ser Thr Thr Asn Ser			
	85	90	95
Ser Ser Pro Asn Asn Pro His Gln Ile Ser His Phe Ser Ser Met Asn			
	100	105	110
His His Pro Leu Phe Tyr Gly Leu Ser Asp His Met Ser Ser Cys Asn			
	115	120	125
Asn Lys Ser Ser Asn Asp Pro Lys Pro Phe Gln			
	130	135	

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1762

(D) OTHER INFORMATION: / Ceres Seq. ID 1499501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

agaccgctag tttttttttt cactctctt cgtctctctc ttgtagcaat gccgcttctt	60
catccacagt cgttgcgcca tcttctttc gagattcaga cccaaagaag aagcaattcc	120
acaacaagat tgcttctttc tcacaagttt ctccattctc aagcttccat tatctcaatc	180
tccaggacaa gaatcctcaa acgggtctct cagaatctct ctgtagctaa agctgcttca	240
gctcaagcta gtagtagtgt tggtagagat gttgctcaaa catcagaaaa agatgtgttg	300
aaggctctgt ctcagattat tgatcctgat tttgggacag atattgtttc ttgtggtttt	360
gtgaaagatt tggggattaa tgaagctttg ggtgaggttt cgttccgttt ggagctgaca	420
acaccgcat gtccagtc aaacatgttt gagaacaagg caaatgaggt agttgcagcc	480
cttccatggg tgaagaaggt aaatctgaca atgtcagcac aaccagccaa gccattttt	540
gcagggcagc ttcccttttg attatcaaga atttcgaaca tcatcgctgt ttctagttgc	600

aaggggtggtg ttgggaaatc aacagtagct gtaaattcttg cttatacatt agctggtatg 660  
ggtgctagag ttggtatctt tgatgctgat gtctatggtc caagtctacc aaccatggtc 720  
aatcctgaga gccgtatatt ggaaatgaac ccggagaaga agaccatcat tccaacagaa 780  
tacatgggcg tcaagctagt ctcatcttga ttgacaggac aagggcgtgc cattatgaga 840  
ggtcctatgg tgtctggtgt tataaaccac ctctttacaa caactgaatg gggagagctg 900  
gactatcttg ttatcgacat gcctcctgga actggtgata tacaactgac cttatgccag 960  
gttgcgccat tgacagcagc ggtaattgtc accaccctc aaaagttggc gtttattgat 1020  
gttgcaaaag gtgtaaggat gttctcaaaa cttaagggtgc cttgcgttgc tgttgtggag 1080  
aatatgtgcc actttgacgc tgatgggaaa cgttattacc cttttgggaa aggttcagggt 1140  
tctgaggtgg tcaagcaatt cggcatacct cacctctttg acctcccat tagaccaacg 1200  
ttatctgctt cgggggatag cggaactcct gaagtagtgt cggatcctct aagtgcggtt 1260  
gccagaacgt tccaggatct tgggtgatgt gtagtgcaac aatgcgcaa gatacgccag 1320  
caagtatcaa cggccgtgac atacgacaag tatctcaagg caattagagt gaaggtagca 1380  
aactcagacg aagagttctt actgcaccct gcaaccgtca gaagaaatga tagatctgca 1440  
caaagtgtgg atgaatggac tggagagcaa aaagttctat atggcgatgt agcggaagat 1500  
atcgaacctg aggacatacg accaatggga aactacgctg tctcgataac ctggcccgcgac 1560  
gggttttagcc agattgctcc atatgaccag ttggaagaaa ttgaaaggct agtagatgtt 1620  
cctccattgt ctccagtcga agtctagtgc ttgaacaata tgttttcgct ttacgatatc 1680  
tcttgaaaat gaaatttgta tattcatatt aagagcattg ttatgaatct tacaatgatg 1740  
aaaagagggt tactgtaagc tg

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..548

(D) OTHER INFORMATION: / Ceres Seq. ID 1499502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

Arg	Pro	Leu	Val	Phe	Phe	Cys	His	Ser	Leu	Arg	Leu	Ser	Leu	Val	Ala
1				5					10					15	
Met	Pro	Leu	Leu	His	Pro	Gln	Ser	Leu	Arg	His	Pro	Ser	Phe	Glu	Ile
			20						25				30		
Gln	Thr	Gln	Arg	Arg	Ser	Asn	Ser	Thr	Thr	Arg	Leu	Leu	Leu	Ser	His
		35					40					45			
Lys	Phe	Leu	His	Ser	Gln	Ala	Ser	Ile	Ile	Ser	Ile	Ser	Arg	Thr	Arg
	50					55					60				
Ile	Leu	Lys	Arg	Val	Ser	Gln	Asn	Leu	Ser	Val	Ala	Lys	Ala	Ala	Ser
65					70					75					80
Ala	Gln	Ala	Ser	Ser	Ser	Val	Gly	Glu	Ser	Val	Ala	Gln	Thr	Ser	Glu
				85						90				95	
Lys	Asp	Val	Leu	Lys	Ala	Leu	Ser	Gln	Ile	Ile	Asp	Pro	Asp	Phe	Gly
		100						105					110		
Thr	Asp	Ile	Val	Ser	Cys	Gly	Phe	Val	Lys	Asp	Leu	Gly	Ile	Asn	Glu
	115					120						125			
Ala	Leu	Gly	Glu	Val	Ser	Phe	Arg	Leu	Glu	Leu	Thr	Thr	Pro	Ala	Cys
	130					135						140			
Pro	Val	Lys	Asp	Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala
145					150					155					160
Leu	Pro	Trp	Val	Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala
			165						170					175	
Lys	Pro	Ile	Phe	Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser
		180						185					190		
Asn	Ile	Ile	Ala	Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr
	195						200					205			
Val	Ala	Val	Asn	Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val
	210					215					220				
Gly	Ile	Phe	Asp	Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val

225 230 235 240  
Asn Pro Glu Ser Arg Ile Leu Glu Met Asn Pro Glu Lys Lys Thr Ile  
245 250 255  
Ile Pro Thr Glu Tyr Met Gly Val Lys Leu Val Ser Phe Gly Phe Ala  
260 265 270  
Gly Gln Gly Arg Ala Ile Met Arg Gly Pro Met Val Ser Gly Val Ile  
275 280 285  
Asn Gln Leu Leu Thr Thr Thr Glu Trp Gly Glu Leu Asp Tyr Leu Val  
290 295 300  
Ile Asp Met Pro Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Cys Gln  
305 310 315 320  
Val Ala Pro Leu Thr Ala Ala Val Ile Val Thr Thr Pro Gln Lys Leu  
325 330 335  
Ala Phe Ile Asp Val Ala Lys Gly Val Arg Met Phe Ser Lys Leu Lys  
340 345 350  
Val Pro Cys Val Ala Val Val Glu Asn Met Cys His Phe Asp Ala Asp  
355 360 365  
Gly Lys Arg Tyr Tyr Pro Phe Gly Lys Gly Ser Gly Ser Glu Val Val  
370 375 380  
Lys Gln Phe Gly Ile Pro His Leu Phe Asp Leu Pro Ile Arg Pro Thr  
385 390 395 400  
Leu Ser Ala Ser Gly Asp Ser Gly Thr Pro Glu Val Val Ser Asp Pro  
405 410 415  
Leu Ser Asp Val Ala Arg Thr Phe Gln Asp Leu Gly Val Cys Val Val  
420 425 430  
Gln Gln Cys Ala Lys Ile Arg Gln Gln Val Ser Thr Ala Val Thr Tyr  
435 440 445  
Asp Lys Tyr Leu Lys Ala Ile Arg Val Lys Val Pro Asn Ser Asp Glu  
450 455 460  
Glu Phe Leu Leu His Pro Ala Thr Val Arg Arg Asn Asp Arg Ser Ala  
465 470 475 480  
Gln Ser Val Asp Glu Trp Thr Gly Glu Gln Lys Val Leu Tyr Gly Asp  
485 490 495  
Val Ala Glu Asp Ile Glu Pro Glu Asp Ile Arg Pro Met Gly Asn Tyr  
500 505 510  
Ala Val Ser Ile Thr Trp Pro Asp Gly Phe Ser Gln Ile Ala Pro Tyr  
515 520 525  
Asp Gln Leu Glu Glu Ile Glu Arg Leu Val Asp Val Pro Pro Leu Ser  
530 535 540  
Pro Val Glu Val  
545

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..532
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

Met Pro Leu Leu His Pro Gln Ser Leu Arg His Pro Ser Phe Glu Ile  
1 5 10 15  
Gln Thr Gln Arg Arg Ser Asn Ser Thr Arg Leu Leu Leu Ser His  
20 25 30  
Lys Phe Leu His Ser Gln Ala Ser Ile Ile Ser Ile Ser Arg Thr Arg  
35 40 45  
Ile Leu Lys Arg Val Ser Gln Asn Leu Ser Val Ala Lys Ala Ala Ser  
50 55 60

Ala	Gln	Ala	Ser	Ser	Ser	Val	Gly	Glu	Ser	Val	Ala	Gln	Thr	Ser	Glu
65					70					75					80
Lys	Asp	Val	Leu	Lys	Ala	Leu	Ser	Gln	Ile	Ile	Asp	Pro	Asp	Phe	Gly
				85					90					95	
Thr	Asp	Ile	Val	Ser	Cys	Gly	Phe	Val	Lys	Asp	Leu	Gly	Ile	Asn	Glu
			100					105					110		
Ala	Leu	Gly	Glu	Val	Ser	Phe	Arg	Leu	Glu	Leu	Thr	Thr	Pro	Ala	Cys
		115					120					125			
Pro	Val	Lys	Asp	Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala
	130					135					140				
Leu	Pro	Trp	Val	Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala
145					150					155					160
Lys	Pro	Ile	Phe	Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser
				165					170					175	
Asn	Ile	Ile	Ala	Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr
			180					185					190		
Val	Ala	Val	Asn	Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val
		195					200					205			
Gly	Ile	Phe	Asp	Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val
	210					215					220				
Asn	Pro	Glu	Ser	Arg	Ile	Leu	Glu	Met	Asn	Pro	Glu	Lys	Lys	Thr	Ile
225					230					235					240
Ile	Pro	Thr	Glu	Tyr	Met	Gly	Val	Lys	Leu	Val	Ser	Phe	Gly	Phe	Ala
				245					250					255	
Gly	Gln	Gly	Arg	Ala	Ile	Met	Arg	Gly	Pro	Met	Val	Ser	Gly	Val	Ile
			260					265					270		
Asn	Gln	Leu	Leu	Thr	Thr	Thr	Glu	Trp	Gly	Glu	Leu	Asp	Tyr	Leu	Val
		275					280					285			
Ile	Asp	Met	Pro	Pro	Gly	Thr	Gly	Asp	Ile	Gln	Leu	Thr	Leu	Cys	Gln
	290					295					300				
Val	Ala	Pro	Leu	Thr	Ala	Ala	Val	Ile	Val	Thr	Thr	Pro	Gln	Lys	Leu
305					310					315					320
Ala	Phe	Ile	Asp	Val	Ala	Lys	Gly	Val	Arg	Met	Phe	Ser	Lys	Leu	Lys
				325					330					335	
Val	Pro	Cys	Val	Ala	Val	Val	Glu	Asn	Met	Cys	His	Phe	Asp	Ala	Asp
			340					345					350		
Gly	Lys	Arg	Tyr	Tyr	Pro	Phe	Gly	Lys	Gly	Ser	Gly	Ser	Glu	Val	Val
		355					360					365			
Lys	Gln	Phe	Gly	Ile	Pro	His	Leu	Phe	Asp	Leu	Pro	Ile	Arg	Pro	Thr
	370					375					380				
Leu	Ser	Ala	Ser	Gly	Asp	Ser	Gly	Thr	Pro	Glu	Val	Val	Ser	Asp	Pro
385					390					395					400
Leu	Ser	Asp	Val	Ala	Arg	Thr	Phe	Gln	Asp	Leu	Gly	Val	Cys	Val	Val
				405					410					415	
Gln	Gln	Cys	Ala	Lys	Ile	Arg	Gln	Gln	Val	Ser	Thr	Ala	Val	Thr	Tyr
			420					425					430		
Asp	Lys	Tyr	Leu	Lys	Ala	Ile	Arg	Val	Lys	Val	Pro	Asn	Ser	Asp	Glu
		435					440					445			
Glu	Phe	Leu	Leu	His	Pro	Ala	Thr	Val	Arg	Arg	Asn	Asp	Arg	Ser	Ala
	450					455					460				
Gln	Ser	Val	Asp	Glu	Trp	Thr	Gly	Glu	Gln	Lys	Val	Leu	Tyr	Gly	Asp
465					470					475					480
Val	Ala	Glu	Asp	Ile	Glu	Pro	Glu	Asp	Ile	Arg	Pro	Met	Gly	Asn	Tyr
				485					490					495	
Ala	Val	Ser	Ile	Thr	Trp	Pro	Asp	Gly	Phe	Ser	Gln	Ile	Ala	Pro	Tyr
			500					505					510		
Asp	Gln	Leu	Glu	Glu	Ile	Glu	Arg	Leu	Val	Asp	Val	Pro	Pro	Leu	Ser
		515					520					525			
Pro	Val	Glu	Val												
		530													

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1499504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala	Leu	Pro	Trp	Val
1				5				10						15	
Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala	Lys	Pro	Ile	Phe
			20					25					30		
Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser	Asn	Ile	Ile	Ala
			35					40					45		
Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr	Val	Ala	Val	Asn
			50					55				60			
Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val	Gly	Ile	Phe	Asp
65					70					75					80
Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val	Asn	Pro	Glu	Ser
				85					90						95
Arg	Ile	Leu	Glu	Met	Asn	Pro	Glu	Lys	Lys	Thr	Ile	Ile	Pro	Thr	Glu
			100					105						110	
Tyr	Met	Gly	Val	Lys	Leu	Val	Ser	Phe	Gly	Phe	Ala	Gly	Gln	Gly	Arg
			115					120					125		
Ala	Ile	Met	Arg	Gly	Pro	Met	Val	Ser	Gly	Val	Ile	Asn	Gln	Leu	Leu
			130					135					140		
Thr	Thr	Thr	Glu	Trp	Gly	Glu	Leu	Asp	Tyr	Leu	Val	Ile	Asp	Met	Pro
145					150					155					160
Pro	Gly	Thr	Gly	Asp	Ile	Gln	Leu	Thr	Leu	Cys	Gln	Val	Ala	Pro	Leu
				165					170						175
Thr	Ala	Ala	Val	Ile	Val	Thr	Thr	Pro	Gln	Lys	Leu	Ala	Phe	Ile	Asp
			180					185						190	
Val	Ala	Lys	Gly	Val	Arg	Met	Phe	Ser	Lys	Leu	Lys	Val	Pro	Cys	Val
			195				200						205		
Ala	Val	Val	Glu	Asn	Met	Cys	His	Phe	Asp	Ala	Asp	Gly	Lys	Arg	Tyr
			210				215					220			
Tyr	Pro	Phe	Gly	Lys	Gly	Ser	Gly	Ser	Glu	Val	Val	Lys	Gln	Phe	Gly
225					230					235					240
Ile	Pro	His	Leu	Phe	Asp	Leu	Pro	Ile	Arg	Pro	Thr	Leu	Ser	Ala	Ser
				245					250						255
Gly	Asp	Ser	Gly	Thr	Pro	Glu	Val	Val	Ser	Asp	Pro	Leu	Ser	Asp	Val
			260					265						270	
Ala	Arg	Thr	Phe	Gln	Asp	Leu	Gly	Val	Cys	Val	Val	Gln	Gln	Cys	Ala
			275				280						285		
Lys	Ile	Arg	Gln	Gln	Val	Ser	Thr	Ala	Val	Thr	Tyr	Asp	Lys	Tyr	Leu
			290				295					300			
Lys	Ala	Ile	Arg	Val	Lys	Val	Pro	Asn	Ser	Asp	Glu	Glu	Phe	Leu	Leu
305					310					315					320
His	Pro	Ala	Thr	Val	Arg	Arg	Asn	Asp	Arg	Ser	Ala	Gln	Ser	Val	Asp
				325					330						335
Glu	Trp	Thr	Gly	Glu	Gln	Lys	Val	Leu	Tyr	Gly	Asp	Val	Ala	Glu	Asp
			340					345						350	
Ile	Glu	Pro	Glu	Asp	Ile	Arg	Pro	Met	Gly	Asn	Tyr	Ala	Val	Ser	Ile
			355				360					365			
Thr	Trp	Pro	Asp	Gly	Phe	Ser	Gln	Ile	Ala	Pro	Tyr	Asp	Gln	Leu	Glu
			370				375					380			
Glu	Ile	Glu	Arg	Leu	Val	Asp	Val	Pro	Pro	Leu	Ser	Pro	Val	Glu	Val
385					390					395					400

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

```
aagcatctct ccctcatatt cacctaaaaa tcagggttaat aaaaaagaat aatgatgttt      60
tcgggtgacgg ttgcgacacct tgtttgtctt attggctaca ttaccgatc atttaagcct      120
ccaccaccgc gaatctgcgg ccatacctaac ggtcctccgg ttacttctcc gagaatcaag      180
ctcagtgatg gaagatatct tgcttataga gaatctgggg ttgatagaga caatgctaac      240
tacaagatca ttgtcgttca tggcttcaac agctccaaag acaactgaatt ttccatccct      300
aaggatgtaa ttgaggagct tgggatatac tttgtgttct acgatagagc aggatatgga      360
gaaagtgatc cacacccatc acgcactgtt aagagtgaag cacacgacat tcaagaactc      420
gccgataaac tcaagatcgg accaaagttc tacgttcttg gtatatcact cgggtgcttac      480
tcggtttata gttgcctcaa atacattccc cacagactag ctggagcagt cttaatgggt      540
ccattttgtg actattgggt gactaaagt cctcaagaaa aattgagtaa agcgttggag      600
ctaattgcaa agaaagacca atggacgtt aaagtggctc attatgttcc gtggttggtt      660
tattggtggt tgacccaaaa actatttccg tcttcgagta tgatcacggg gaacaatgcg      720
ttatgcagcg acaaagattt ggtcgtcata aagaagaaaa tggagaatcc acgccctggc      780
ttggaaaaag ttagacaaca aggtgaccat gaatgtcttc accgggacat gatagccgga      840
ttcgcgacat gggaattcga cccgactgaa ttagaaaaatc cgtttgcgga aggcgaagga      900
tcggtccacg tttggcaagg gatggaagac agaatcattc catacgaaat taatcgatat      960
atatcagaga agcttccatg gattaagtac catgaggtct taggttatgg acatcttcta     1020
aacgccgagg aggagaaatg caaagacatt atcaaggcac ttcttgtaaa ctgatgatca     1080
tctctacaca agatgccaca aaaaatatag catatttaat agattttatt ttttatttat     1140
ggattataat attatagcat attataagtt tgtaagtaag atgaaaacca cttgaaagtc     1200
attaattttac t
```

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

```
Met Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr
1      5      10      15
Ile Tyr Arg Ser Phe Lys Pro Pro Pro Pro Arg Ile Cys Gly His Pro
20     25     30
Asn Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg
35     40     45
Tyr Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr
50     55     60
Lys Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe
65     70     75     80
Ser Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe
85     90     95
Tyr Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr
100    105    110
```

Val Lys Ser Glu Ala His Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys  
115 120 125  
Ile Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser  
130 135 140  
Val Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val  
145 150 155 160  
Leu Met Val Pro Phe Val Asn Tyr Trp Trp Thr Lys Val Pro Gln Glu  
165 170 175  
Lys Leu Ser Lys Ala Leu Glu Leu Met Pro Lys Lys Asp Gln Trp Thr  
180 185 190  
Phe Lys Val Ala His Tyr Val Pro Trp Leu Leu Tyr Trp Trp Leu Thr  
195 200 205  
Gln Lys Leu Phe Pro Ser Ser Ser Met Ile Thr Gly Asn Asn Ala Leu  
210 215 220  
Cys Ser Asp Lys Asp Leu Val Val Ile Lys Lys Lys Met Glu Asn Pro  
225 230 235 240  
Arg Pro Gly Leu Glu Lys Val Arg Gln Gln Gly Asp His Glu Cys Leu  
245 250 255  
His Arg Asp Met Ile Ala Gly Phe Ala Thr Trp Glu Phe Asp Pro Thr  
260 265 270  
Glu Leu Glu Asn Pro Phe Ala Glu Gly Glu Gly Ser Val His Val Trp  
275 280 285  
Gln Gly Met Glu Asp Arg Ile Ile Pro Tyr Glu Ile Asn Arg Tyr Ile  
290 295 300  
Ser Glu Lys Leu Pro Trp Ile Lys Tyr His Glu Val Leu Gly Tyr Gly  
305 310 315 320  
His Leu Leu Asn Ala Glu Glu Glu Lys Cys Lys Asp Ile Ile Lys Ala  
325 330 335  
Leu Leu Val Asn  
340

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr Ile  
1 5 10 15  
Tyr Arg Ser Phe Lys Pro Pro Pro Pro Arg Ile Cys Gly His Pro Asn  
20 25 30  
Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg Tyr  
35 40 45  
Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr Lys  
50 55 60  
Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe Ser  
65 70 75 80  
Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe Tyr  
85 90 95  
Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr Val  
100 105 110  
Lys Ser Glu Ala His Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys Ile  
115 120 125  
Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser Val  
130 135 140  
Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val Leu



145		150		155		160									
Met	Val	Pro	Phe	Val	Asn	Tyr	Trp	Trp	Thr	Lys	Val	Pro	Gln	Glu	Lys
				165					170					175	
Leu	Ser	Lys	Ala	Leu	Glu	Leu	Met	Pro	Lys	Lys	Asp	Gln	Trp	Thr	Phe
			180					185					190		
Lys	Val	Ala	His	Tyr	Val	Pro	Trp	Leu	Leu	Tyr	Trp	Trp	Leu	Thr	Gln
		195					200					205			
Lys	Leu	Phe	Pro	Ser	Ser	Ser	Met	Ile	Thr	Gly	Asn	Asn	Ala	Leu	Cys
	210					215					220				
Ser	Asp	Lys	Asp	Leu	Val	Val	Ile	Lys	Lys	Lys	Met	Glu	Asn	Pro	Arg
225					230						235				240
Pro	Gly	Leu	Glu	Lys	Val	Arg	Gln	Gln	Gly	Asp	His	Glu	Cys	Leu	His
			245						250					255	
Arg	Asp	Met	Ile	Ala	Gly	Phe	Ala	Thr	Trp	Glu	Phe	Asp	Pro	Thr	Glu
			260					265					270		
Leu	Glu	Asn	Pro	Phe	Ala	Glu	Gly	Glu	Gly	Ser	Val	His	Val	Trp	Gln
		275					280					285			
Gly	Met	Glu	Asp	Arg	Ile	Ile	Pro	Tyr	Glu	Ile	Asn	Arg	Tyr	Ile	Ser
	290					295					300				
Glu	Lys	Leu	Pro	Trp	Ile	Lys	Tyr	His	Glu	Val	Leu	Gly	Tyr	Gly	His
305					310					315					320
Leu	Leu	Asn	Ala	Glu	Glu	Lys	Cys	Lys	Asp	Ile	Ile	Lys	Ala	Leu	
			325					330					335		

Leu Val Asn

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1499512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

Met	Val	Pro	Phe	Val	Asn	Tyr	Trp	Trp	Thr	Lys	Val	Pro	Gln	Glu	Lys
1				5					10					15	
Leu	Ser	Lys	Ala	Leu	Glu	Leu	Met	Pro	Lys	Lys	Asp	Gln	Trp	Thr	Phe
			20					25					30		
Lys	Val	Ala	His	Tyr	Val	Pro	Trp	Leu	Leu	Tyr	Trp	Trp	Leu	Thr	Gln
		35				40					45				
Lys	Leu	Phe	Pro	Ser	Ser	Ser	Met	Ile	Thr	Gly	Asn	Asn	Ala	Leu	Cys
	50					55					60				
Ser	Asp	Lys	Asp	Leu	Val	Val	Ile	Lys	Lys	Lys	Met	Glu	Asn	Pro	Arg
65					70					75					80
Pro	Gly	Leu	Glu	Lys	Val	Arg	Gln	Gln	Gly	Asp	His	Glu	Cys	Leu	His
			85						90					95	
Arg	Asp	Met	Ile	Ala	Gly	Phe	Ala	Thr	Trp	Glu	Phe	Asp	Pro	Thr	Glu
		100						105					110		
Leu	Glu	Asn	Pro	Phe	Ala	Glu	Gly	Glu	Gly	Ser	Val	His	Val	Trp	Gln
		115					120					125			
Gly	Met	Glu	Asp	Arg	Ile	Ile	Pro	Tyr	Glu	Ile	Asn	Arg	Tyr	Ile	Ser
	130					135					140				
Glu	Lys	Leu	Pro	Trp	Ile	Lys	Tyr	His	Glu	Val	Leu	Gly	Tyr	Gly	His
145					150					155					160
Leu	Leu	Asn	Ala	Glu	Glu	Glu	Lys	Cys	Lys	Asp	Ile	Ile	Lys	Ala	Leu
			165						170					175	

Leu Val Asn

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

```
atctacgcat gaaaatatga ttctgtcttt tttttgttg tctatctttc aatacttttaa      60
aaagtgtatt tctagaggcg atttgtcatt tcccgaatag gaatttgagt aaaaaaaca      120
ctctgttttt tatttccact aatatcaaatt cggcgaatat agttcccacc attcttatct      180
ccttgctgct actcgggaatt ttttaaataa taggatcgct ttaataatat aatctctata      240
atztatagtt ccttttccaa tattggcgct tccgttgaag ctttcacaaa atctcaaatt      300
tgtttgagga ctctcaaatt tctccttctc tcgacaatga tttcgtctct gatttgtttt      360
gcttcgatca aagcaatgga gcagaacttg atgattacac acagtttggg gtaaatttgc      420
agactgatca agaggatacc tttccagatt ttgtgtcata tgggtgtgaat ttgcagcagg      480
agccagatga agtcttttag attggagctt ctcaattgga tttgtcctcg tataatggag      540
ttttgtcgct agagccagaa caggtggggc aacaagattg tgaagttgtg caggaagaag      600
aagtagagat caattctggt tcatctggtg gagctgttaa ggaagaacag gaacatttag      660
atgacgattg ctccagaaag cgggcaagga ctggatcgct tagcagagga ggaggaacta      720
aagcgtgtcg tgaaagggtt aggagggaga agctaaatga gaggtttatg gatttgagct      780
cggttttgga gcctgggagg actcctaaga ctgataaacc ggctatactc gatgatgcaa      840
tccgtatatt gaatcaactt agagatgaag ctcttaagct tgaagaaact aaccagaagc      900
ttttagagga gatcaagagt ctcaaggcgg agaagaacga gctgagggag gaaaagctgg      960
tgttgaaggc ggataaagag aagacagaac aacagttaaa gtctatgacg gctccatctt     1020
cagggttcat acctcatatt ccagctgcat ttaaccacaa caaatggct gtttatccaa     1080
gttacggtta catgccaatg tggcattata tgcctcaatc cgttcgtgac acatctcgtg     1140
atcaagaact caggcctcct gctgcttaaa ctctcaattg tttttttttg gt
```

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```
Met Tyr Pro Ser Leu Asp Asn Asp Phe Val Ser Asp Leu Phe Cys Phe
1          5          10          15
Asp Gln Ser Asn Gly Ala Glu Leu Asp Asp Tyr Thr Gln Phe Gly Val
20          25          30
Asn Leu Gln Thr Asp Gln Glu Asp Thr Phe Pro Asp Phe Val Ser Tyr
35          40          45
Gly Val Asn Leu Gln Gln Glu Pro Asp Glu Val Phe Ser Ile Gly Ala
50          55          60
Ser Gln Leu Asp Leu Ser Ser Tyr Asn Gly Val Leu Ser Leu Glu Pro
65          70          75          80
Glu Gln Val Gly Gln Gln Asp Cys Glu Val Val Gln Glu Glu Glu Val
85          90          95
Glu Ile Asn Ser Gly Ser Ser Gly Gly Ala Val Lys Glu Glu Gln Glu
100         105         110
His Leu Asp Asp Asp Cys Ser Arg Lys Arg Ala Arg Thr Gly Ser Cys
115         120         125
Ser Arg Gly Gly Gly Thr Lys Ala Cys Arg Glu Arg Leu Arg Arg Glu
```

130	135	140
Lys Leu Asn Glu Arg Phe Met Asp Leu Ser Ser Val Leu Glu Pro Gly		
145	150	155
Arg Thr Pro Lys Thr Asp Lys Pro Ala Ile Leu Asp Asp Ala Ile Arg		160
	165	170
Ile Leu Asn Gln Leu Arg Asp Glu Ala Leu Lys Leu Glu Glu Thr Asn		175
	180	185
Gln Lys Leu Leu Glu Glu Ile Lys Ser Leu Lys Ala Glu Lys Asn Glu		190
	195	200
Leu Arg Glu Glu Lys Leu Val Leu Lys Ala Asp Lys Glu Lys Thr Glu		205
	210	215
Gln Gln Leu Lys Ser Met Thr Ala Pro Ser Ser Gly Phe Ile Pro His		220
225	230	235
Ile Pro Ala Ala Phe Asn His Asn Lys Met Ala Val Tyr Pro Ser Tyr		240
	245	250
Gly Tyr Met Pro Met Trp His Tyr Met Pro Gln Ser Val Arg Asp Thr		255
	260	265
Ser Arg Asp Gln Glu Leu Arg Pro Pro Ala Ala		270
	275	280

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

attctaaacc acacaggcaa gcatgtgggc tgtgcctttg tagagtttgg tttctgctaac	60
gaagcaaaga tgtcgtttga aacgaaaaac ggcgaatatt tgaacgattg caagattttt	120
cttgaagtgg ctaagatggc tccataccct ccaccaagt attgcattga tcacaagggt	180
tggtacgaag actaccttcg acgagaaatc cttctgatag aagaaaatga ggcagaggaa	240
ggacttgatg acactcccg ctttgttgag gaatttgccg taagaaaaaa gacgctcttt	300
gttgccaatc tctcaccag aactaaaata tcacatatca tcaagttttt taaagatgtt	360
gcagaagttg ttcgtgttcg acttattgta aaccacaggg gtgagcatgt gggctgtggc	420
tttgttgagt ttgcttctgt taacgaagca cagaaggcgc tgcaaaagaa gaatggtgaa	480
aatttgcgca gtcgtgagat ttttcttgac gtggctgagt tagctccata ccctctccga	540
cccaagtaca accatgcaga gaaacttttg cacgaacgag aaagtcttct gaagaaacag	600
aaggaatatg agatgttgag cgagaggacc gaattctgcg gtccttttag gttttcggat	660
tcgagcaaaa acaaaatctc cgcaatcgag agaaactctg agatcggaat caatggagtc	720
cacaatatcg ttgaaggta acaaaggaaa aggcaaagga tcaaaggag cttcctcttc	780
cgatgacaaa tccaagtttg atgtcggtta ggaatggacc aattgggtcat tgaagaaggc	840
tcccaaacct catctcttcc agctccttag ccctgtctga tccatccaat ttcacatca	900
acctaaatca atcgaatcgg tcttctctcg gtttggttcc ttcatatctt tacgcgtgtt	1020
cttagattcg ccgaatcttc ttttatgctt ttttcattag ctagtttttg aatactttct	1080
ctatggtact gtattgaata acttttagatt atgatataat gtgaaatcga attttatgtt	1140
ttgaaaatct gggaattgct ttaaagattg aagtttggtg gaatgtcttg t	

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1499520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

Ile Leu Asn His Thr Gly Lys His Val Gly Cys Ala Phe Val Glu Phe  
1 5 10 15  
Gly Ser Ala Asn Glu Ala Lys Met Ser Leu Glu Thr Lys Asn Gly Glu  
20 25 30  
Tyr Leu Asn Asp Cys Lys Ile Phe Leu Glu Val Ala Lys Met Ala Pro  
35 40 45  
Tyr Pro Pro Pro Lys Tyr Cys Ile Asp His Lys Val Trp Tyr Glu Asp  
50 55 60  
Tyr Leu Arg Arg Glu Ile Leu Leu Ile Glu Glu Asn Glu Ala Glu Glu  
65 70 75 80  
Gly Leu Asp Asp Thr Pro Ala Leu Val Glu Glu Phe Ala Val Arg Lys  
85 90 95  
Lys Thr Leu Phe Val Ala Asn Leu Ser Pro Arg Thr Lys Ile Ser His  
100 105 110  
Ile Ile Lys Phe Phe Lys Asp Val Ala Glu Val Val Arg Val Arg Leu  
115 120 125  
Ile Val Asn His Arg Gly Glu His Val Gly Cys Gly Phe Val Glu Phe  
130 135 140  
Ala Ser Val Asn Glu Ala Gln Lys Ala Leu Gln Lys Lys Asn Gly Glu  
145 150 155 160  
Asn Leu Arg Ser Arg Glu Ile Phe Leu Asp Val Ala Glu Leu Ala Pro  
165 170 175  
Tyr Pro Leu Arg Pro Lys Tyr Asn His Ala Glu Lys Leu Trp His Glu  
180 185 190  
Arg Glu Ser Leu Leu Lys Lys Gln Lys Glu Tyr Glu Met Leu Ser Glu  
195 200 205  
Arg Thr Glu Phe Cys Gly Pro Leu Gly Phe Ser Asp Ser Ser Lys Asn  
210 215 220  
Lys Ile Ser Ala Ile Glu Arg Asn Ser Glu Ile Gly Ile Asn Gly Val  
225 230 235 240  
His Asn Ile Val Glu Gly Gln Gln Arg Lys Arg Gln Arg Ile Lys Gly  
245 250 255  
Ser Phe Leu Phe Arg  
260

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1499521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

Met Ser Leu Glu Thr Lys Asn Gly Glu Tyr Leu Asn Asp Cys Lys Ile  
1 5 10 15  
Phe Leu Glu Val Ala Lys Met Ala Pro Tyr Pro Pro Pro Lys Tyr Cys  
20 25 30  
Ile Asp His Lys Val Trp Tyr Glu Asp Tyr Leu Arg Arg Glu Ile Leu  
35 40 45  
Leu Ile Glu Glu Asn Glu Ala Glu Glu Gly Leu Asp Asp Thr Pro Ala  
50 55 60  
Leu Val Glu Glu Phe Ala Val Arg Lys Lys Thr Leu Phe Val Ala Asn  
65 70 75 80  
Leu Ser Pro Arg Thr Lys Ile Ser His Ile Ile Lys Phe Phe Lys Asp  
85 90 95  
Val Ala Glu Val Val Arg Val Arg Leu Ile Val Asn His Arg Gly Glu

	100		105		110
His Val Gly	Cys Gly Phe Val	Glu Phe Ala Ser Val	Asn Glu Ala Gln		
115		120		125	
Lys Ala Leu	Gln Lys Lys Asn Gly	Glu Asn Leu Arg Ser	Arg Glu Ile		
130		135		140	
Phe Leu Asp	Val Ala Glu Leu Ala	Pro Tyr Pro Leu	Arg Pro Lys Tyr		
145		150		155	
Asn His Ala	Glu Lys Leu Trp His	Glu Arg Glu Ser	Leu Leu Lys Lys		
	165		170		175
Gln Lys Glu	Tyr Glu Met Leu Ser	Glu Arg Thr Glu	Phe Cys Gly Pro		
	180		185		190
Leu Gly Phe	Ser Asp Ser Ser Lys	Asn Lys Ile Ser	Ala Ile Glu Arg		
	195		200		205
Asn Ser Glu	Ile Gly Ile Asn Gly	Val His Asn Ile	Val Glu Gly Gln		
	210		215		220
Gln Arg Lys	Arg Gln Arg Ile Lys	Gly Ser Phe Leu	Phe Arg		
225		230		235	

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1499522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Met Ala Pro	Tyr Pro Pro	Lys Tyr Cys Ile	Asp His Lys Val	Trp	
1		5		10	15
Tyr Glu Asp	Tyr Leu Arg	Arg Glu Ile Leu	Leu Ile Glu Glu	Asn Glu	
	20		25		30
Ala Glu Glu	Gly Leu Asp	Asp Thr Pro Ala	Leu Val Glu Glu	Phe Ala	
	35		40		45
Val Arg Lys	Lys Thr Leu Phe	Val Ala Asn Leu	Ser Pro Arg Thr	Lys	
	50		55		60
Ile Ser His	Ile Ile Lys Phe	Phe Lys Asp Val	Ala Glu Val Val	Arg	
	65		70		75
Val Arg Leu	Ile Val Asn His	Arg Gly Glu His	Val Gly Cys Gly	Phe	
	85		90		95
Val Glu Phe	Ala Ser Val Asn	Glu Ala Gln Lys	Ala Leu Gln Lys	Lys	
	100		105		110
Asn Gly Glu	Asn Leu Arg Ser	Arg Glu Ile Phe	Leu Asp Val Ala	Glu	
	115		120		125
Leu Ala Pro	Tyr Pro Leu Arg	Pro Lys Tyr Asn	His Ala Glu Lys	Leu	
	130		135		140
Trp His Glu	Arg Glu Ser Leu	Leu Lys Lys Gln	Lys Glu Tyr Glu	Met	
	145		150		155
Leu Ser Glu	Arg Thr Glu Phe	Cys Gly Pro Leu	Gly Phe Ser Asp	Ser	
	165		170		175
Ser Lys Asn	Lys Ile Ser Ala	Ile Glu Arg Asn	Ser Glu Ile Gly	Ile	
	180		185		190
Asn Gly Val	His Asn Ile Val	Glu Gly Gln Gln	Arg Lys Arg Gln	Arg	
	195		200		205
Ile Lys Gly	Ser Phe Leu Phe	Arg			
	210		215		

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1673 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1673  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

ataatttgtc	attgttcttg	ggcggaccaa	taaaagcctc	tottttgaat	ccccacaca	60
gatctatcgc	ctcttcttcc	ctcctgtctg	ccagaatttt	tgtttcccgt	tgataaaggg	120
tttatctttg	gtggatgatt	agtgaactt	tttaaggaga	tattagtcca	catgttttag	180
ttaaaaatgg	cagcttcaag	cggctctggt	ttggaagctg	aggaggggga	aataagtata	240
gacatggaag	aagacatgga	tctaacagaa	gatgattcca	gaaatgtgtc	tggccagttt	300
tcaggacaag	catcgatcgt	ggaggttggg	gatgctgttg	atgtgagagt	cgaaccctg	360
aaagtagatg	ttagttctaa	atctggtgtt	aaaagagcca	gaacaatctc	tctggaacag	420
caaccttcag	tccatgttac	ttataaacac	ttaacaagag	atagtaagca	gaagctggaa	480
agtttattac	agcaatgggc	agaatgggag	gcagaacaaa	attccttgtc	cgaggatcaa	540
gaacaagtac	tagaagctgg	tgatgagaca	tactttcctg	ctttgcgtgt	gggattgcag	600
aagacatcat	ctgtatcatt	ttggtttgac	taccaaactg	gtcacagtcc	ttcgaagaag	660
tctgttccag	tggaaagtag	cactactcct	ctttataacc	gtggatttac	aattggttta	720
gattcagggt	caaataacgt	ggaaggaggc	ttggagatta	ttgatgatcc	tccacgttgc	780
ttcaactgtg	gcgcatacag	tcattctatt	agagaatgtc	caaggccttt	tgatcgatca	840
gcagttagta	atgctcggag	gcaacataaa	agaaaaagaa	atcagactcc	tggatcccgt	900
ctaccatcca	gatattatca	gagccttcaa	cgtggaaaat	atgatggctt	gaagcctggc	960
tcacttgatg	cagagacgcg	taagcttctc	ggtctaaagg	aactcgatcc	tcctccatgg	1020
cttaacagaa	tgcgagagat	tggatatcca	ccaggatatt	ttgctgtaga	agaagacgat	1080
gatgatcact	cgagaataac	tatatttggg	gaggaagaga	ctaaagaaga	ggaagaagtt	1140
aagactgaag	aaggtgaaat	cttggaaaaa	gcaagccctc	aagagccaag	aaagataatg	1200
acagttggat	ttcccgggat	taacgcaccc	attccagaaa	acgcagattc	gtggctatgg	1260
gaacagagga	atagtaacac	aggacatact	aattatcata	atcaccttcg	accacaatat	1320
gagatgggcc	ctctaggtat	tcaactgtct	tcaagctttc	ctccaatgca	tggcattaga	1380
tatgatcata	ggttcgggtt	atgaccaata	agcccgggat	ccgaaagagt	taagatccat	1440
tttagtttta	gcagcagaag	atagattcat	tagtgaatgt	gggatgtatg	ataaccatta	1500
gttaaagagt	taaccacaag	ccaactacgg	ttaaaacatt	caggcctaag	ccaaagtagt	1560
ctatgcttaa	ggcagaatcg	aactttttacg	tcttttggtcg	taaaactgga	atcgtgatta	1620
tacacgtttg	gtgttgtaac	atgtccatca	atgtacaaga	tttttgtttt	gtt	

(2) INFORMATION FOR SEQ ID NO:1061:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 405 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..405  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

Met	Ala	Ala	Ser	Ser	Gly	Ser	Gly	Leu	Glu	Ala	Glu	Glu	Gly	Glu	Ile
1					5			10						15	
Ser	Ile	Asp	Met	Glu	Glu	Asp	Met	Asp	Leu	Thr	Glu	Asp	Asp	Phe	Arg
			20					25						30	
Asn	Val	Ser	Gly	Gln	Phe	Ser	Gly	Gln	Ala	Ser	Ile	Val	Glu	Val	Gly
			35					40						45	
Asp	Ala	Val	Asp	Val	Arg	Val	Glu	Thr	Val	Lys	Val	Asp	Val	Ser	Ser
			50					55						60	
Lys	Ser	Gly	Val	Lys	Arg	Ala	Arg	Thr	Ile	Ser	Leu	Glu	Gln	Gln	Pro
			65					70						75	80
Ser	Val	His	Val	Thr	Tyr	Lys	His	Leu	Thr	Arg	Asp	Ser	Lys	Gln	Lys
								85						90	95
Leu	Glu	Ser	Leu	Leu	Gln	Gln	Trp	Ser	Glu	Trp	Glu	Ala	Glu	Gln	Asn

(X1) SEQUENCE DESCRIPTION OF <b>PROTEIN</b>															
Met	Glu	Glu	Asp	Met	Asp	Leu	Thr	Glu	Asp	Asp	Phe	Arg	Asn	Val	Ser
1				5					10					15	
Gly	Gln	Phe	Ser	Gly	Gln	Ala	Ser	Ile	Val	Glu	Val	Gly	Asp	Ala	Val
			20					25					30		
Asp	Val	Arg	Val	Glu	Thr	Val	Lys	Val	Asp	Val	Ser	Ser	Lys	Ser	Gly
		35					40					45			
Val	Lys	Arg	Ala	Arg	Thr	Ile	Ser	Leu	Glu	Gln	Gln	Pro	Ser	Val	His
	50					55					60				
Val	Thr	Tyr	Lys	His	Leu	Thr	Arg	Asp	Ser	Lys	Gln	Lys	Leu	Glu	Ser
65					70					75				80	

Leu	Leu	Gln	Gln	Trp	Ser	Glu	Trp	Glu	Ala	Glu	Gln	Asn	Ser	Leu	Ser		
				85					90					95			
Glu	Asp	Gln	Glu	Gln	Val	Leu	Glu	Ala	Gly	Asp	Glu	Thr	Tyr	Phe	Pro		
			100					105					110				
Ala	Leu	Arg	Val	Gly	Leu	Gln	Lys	Thr	Ser	Ser	Val	Ser	Phe	Trp	Phe		
		115					120						125				
Asp	Tyr	Gln	Thr	Gly	His	Ser	Ser	Ser	Lys	Lys	Ser	Val	Pro	Val	Glu		
	130					135					140						
Ser	Ser	Thr	Thr	Pro	Leu	Tyr	Asn	Arg	Gly	Phe	Thr	Ile	Gly	Leu	Asp		
	145				150					155				160			
Ser	Gly	Ser	Asn	Asn	Val	Glu	Gly	Gly	Leu	Glu	Ile	Ile	Asp	Asp	Pro		
			165					170					175				
Pro	Arg	Cys	Phe	Asn	Cys	Gly	Ala	Tyr	Ser	His	Ser	Ile	Arg	Glu	Cys		
			180					185					190				
Pro	Arg	Pro	Phe	Asp	Arg	Ser	Ala	Val	Ser	Asn	Ala	Arg	Arg	Gln	His		
		195					200					205					
Lys	Arg	Lys	Arg	Asn	Gln	Thr	Pro	Gly	Ser	Arg	Leu	Pro	Ser	Arg	Tyr		
	210				215						220						
Tyr	Gln	Ser	Leu	Gln	Arg	Gly	Lys	Tyr	Asp	Gly	Leu	Lys	Pro	Gly	Ser		
	225				230					235				240			
Leu	Asp	Ala	Glu	Thr	Arg	Lys	Leu	Leu	Gly	Leu	Lys	Glu	Leu	Asp	Pro		
			245					250					255				
Pro	Pro	Trp	Leu	Asn	Arg	Met	Arg	Glu	Ile	Gly	Tyr	Pro	Pro	Gly	Tyr		
			260					265					270				
Phe	Ala	Val	Glu	Glu	Asp	Asp	Asp	Asp	His	Ser	Arg	Ile	Thr	Ile	Phe		
		275					280					285					
Gly	Glu	Glu	Glu	Thr	Lys	Glu	Glu	Glu	Glu	Val	Lys	Thr	Glu	Glu	Gly		
	290				295					300							
Glu	Ile	Leu	Glu	Lys	Ala	Ser	Pro	Gln	Glu	Pro	Arg	Lys	Ile	Met	Thr		
	305				310					315				320			
Val	Gly	Phe	Pro	Gly	Ile	Asn	Ala	Pro	Ile	Pro	Glu	Asn	Ala	Asp	Ser		
			325					330					335				
Trp	Leu	Trp	Glu	Gln	Arg	Asn	Ser	Asn	Thr	Gly	His	Thr	Asn	Tyr	His		
			340					345					350				
Asn	His	Leu	Arg	Pro	Gln	Tyr	Glu	Met	Gly	Pro	Leu	Gly	Ile	Gln	Leu		
		355				360						365					
Ser	Ser	Ser	Phe	Pro	Pro	Met	His	Gly	Ile	Arg	Tyr	Asp	His	Arg	Phe		
	370				375						380						
Gly	Leu																
	385																

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1499526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met	Asp	Leu	Thr	Glu	Asp	Asp	Phe	Arg	Asn	Val	Ser	Gly	Gln	Phe	Ser		
1				5					10					15			
Gly	Gln	Ala	Ser	Ile	Val	Glu	Val	Gly	Asp	Ala	Val	Asp	Val	Arg	Val		
		20						25					30				
Glu	Thr	Val	Lys	Val	Asp	Val	Ser	Ser	Lys	Ser	Gly	Val	Lys	Arg	Ala		
		35				40					45						
Arg	Thr	Ile	Ser	Leu	Glu	Gln	Gln	Pro	Ser	Val	His	Val	Thr	Tyr	Lys		
	50				55					60							
His	Leu	Thr	Arg	Asp	Ser	Lys	Gln	Lys	Leu	Glu	Ser	Leu	Leu	Gln	Gln		



65					70					75					80
Trp	Ser	Glu	Trp	Glu	Ala	Glu	Gln	Asn	Ser	Leu	Ser	Glu	Asp	Gln	Glu
				85					90					95	
Gln	Val	Leu	Glu	Ala	Gly	Asp	Glu	Thr	Tyr	Phe	Pro	Ala	Leu	Arg	Val
			100					105					110		
Gly	Leu	Gln	Lys	Thr	Ser	Ser	Val	Ser	Phe	Trp	Phe	Asp	Tyr	Gln	Thr
		115					120					125			
Gly	His	Ser	Ser	Ser	Lys	Lys	Ser	Val	Pro	Val	Glu	Ser	Ser	Thr	Thr
	130					135					140				
Pro	Leu	Tyr	Asn	Arg	Gly	Phe	Thr	Ile	Gly	Leu	Asp	Ser	Gly	Ser	Asn
145					150					155					160
Asn	Val	Glu	Gly	Gly	Leu	Glu	Ile	Ile	Asp	Asp	Pro	Pro	Arg	Cys	Phe
			165						170					175	
Asn	Cys	Gly	Ala	Tyr	Ser	His	Ser	Ile	Arg	Glu	Cys	Pro	Arg	Pro	Phe
			180					185					190		
Asp	Arg	Ser	Ala	Val	Ser	Asn	Ala	Arg	Arg	Gln	His	Lys	Arg	Lys	Arg
	195					200						205			
Asn	Gln	Thr	Pro	Gly	Ser	Arg	Leu	Pro	Ser	Arg	Tyr	Tyr	Gln	Ser	Leu
	210					215					220				
Gln	Arg	Gly	Lys	Tyr	Asp	Gly	Leu	Lys	Pro	Gly	Ser	Leu	Asp	Ala	Glu
225					230					235					240
Thr	Arg	Lys	Leu	Leu	Gly	Leu	Lys	Glu	Leu	Asp	Pro	Pro	Pro	Trp	Leu
			245						250					255	
Asn	Arg	Met	Arg	Glu	Ile	Gly	Tyr	Pro	Pro	Gly	Tyr	Phe	Ala	Val	Glu
			260					265					270		
Glu	Asp	Asp	Asp	Asp	His	Ser	Arg	Ile	Thr	Ile	Phe	Gly	Glu	Glu	Glu
	275						280					285			
Thr	Lys	Glu	Glu	Glu	Glu	Val	Lys	Thr	Glu	Glu	Gly	Glu	Ile	Leu	Glu
	290					295					300				
Lys	Ala	Ser	Pro	Gln	Glu	Pro	Arg	Lys	Ile	Met	Thr	Val	Gly	Phe	Pro
	305				310					315					320
Gly	Ile	Asn	Ala	Pro	Ile	Pro	Glu	Asn	Ala	Asp	Ser	Trp	Leu	Trp	Glu
			325					330						335	
Gln	Arg	Asn	Ser	Asn	Thr	Gly	His	Thr	Asn	Tyr	His	Asn	His	Leu	Arg
			340					345					350		
Pro	Gln	Tyr	Glu	Met	Gly	Pro	Leu	Gly	Ile	Gln	Leu	Ser	Ser	Ser	Phe
	355					360					365				
Pro	Pro	Met	His	Gly	Ile	Arg	Tyr	Asp	His	Arg	Phe	Gly	Leu		
	370				375					380					

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1043
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

gaaatttcct	ctcttcttct	tttgcttgag	ctttaggttt	tgagagcaaa	gaaaaacgaa	60
gacgcgtcaa	agagcttttg	tgagagaggt	ctgcttgctt	gctacaatgg	gttacgcca	120
gctagttatt	ggtccagcag	gcagtggaaa	gtcaacttat	tgctcgtctt	tgatgaaca	180
ttgtgaaact	atcggtcgaa	caatgcatgt	tgtaacctt	gatcctgctg	cggagatctt	240
caactatcct	gtggctatgg	atatcagaga	acttatttct	ttggaagatg	tgatggagga	300
tctaaagctt	ggctctaattg	gtgcccttat	gtattgcatg	gagtatcttg	aggatagctt	360
acatgattgg	gtggatgaag	aattggagaa	ctacagggat	gacgattacc	ttatctttga	420
ttgtccaggc	cagatagagc	tgtttacaca	tgttcctgtg	ctcaagaact	ttgtggagca	480
tttgaagcag	aagaacttca	acgtctgtgt	tgtttatctg	cttgattcac	agttcatcac	540
agatgtaacc	aagtttatca	gtggttgcat	gtcatctctc	gctgcaatga	tccagcttga	600

```
attaccacat gtcaacatcc tctcaaaaat ggacctcttg caggacaaaa gcaacattga      660
tgattacttg aatccggagc ctcgcacatt gctagcagag ttaaacaaaa ggatgggtcc      720
tcaatatgca aaactaaaca aagccttgat tgagatgggtg ggagagtatg ggatgggtgaa      780
tttcataccc attaacttga gaaaagaaaa gagcattcaa tatgttctgt cacaaatcga      840
cgtctgtatt cagtttggag aagatgctga tgtgaacatc aaagatgatg acgatttttag      900
tgacgatggt cctgacctat aattgttata ttcggtttct acaacttttg ttaaaagtct      960
aaacaagctt ggtctcattg ttctgtcag ttaccaatgg cgtttgtgag aacttttgtt     1020
gaatatcaaa agccttcaat gtg
```

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1499528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```
Met Gly Tyr Ala Gln Leu Val Ile Gly Pro Ala Gly Ser Gly Lys Ser
1      5      10      15
Thr Tyr Cys Ser Ser Leu Tyr Glu His Cys Glu Thr Ile Gly Arg Thr
20     25     30
Met His Val Val Asn Leu Asp Pro Ala Ala Glu Ile Phe Asn Tyr Pro
35     40     45
Val Ala Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu
50     55     60
Asp Leu Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr
65     70     75     80
Leu Glu Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr
85     90     95
Arg Asp Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu
100    105    110
Phe Thr His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln
115    120    125
Lys Asn Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile
130    135    140
Thr Asp Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala
145    150    155    160
Met Ile Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp
165    170    175
Leu Leu Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro
180    185    190
Arg Thr Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala
195    200    205
Lys Leu Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val
210    215    220
Asn Phe Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val
225    230    235    240
Leu Ser Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val
245    250    255
Asn Ile Lys Asp Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
260    265    270
```

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1499529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

```
Met His Val Val Asn Leu Asp Pro Ala Ala Glu Ile Phe Asn Tyr Pro
1          5          10          15
Val Ala Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu
20          25          30
Asp Leu Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr
35          40          45
Leu Glu Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr
50          55          60
Arg Asp Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu
65          70          75          80
Phe Thr His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln
85          90          95
Lys Asn Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile
100          105          110
Thr Asp Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala
115          120          125
Met Ile Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp
130          135          140
Leu Leu Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro
145          150          155          160
Arg Thr Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala
165          170          175
Lys Leu Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val
180          185          190
Asn Phe Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val
195          200          205
Leu Ser Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val
210          215          220
Asn Ile Lys Asp Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
225          230          235
```

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1499530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

```
Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu Asp Leu
1          5          10          15
Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr Leu Glu
20          25          30
Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr Arg Asp
35          40          45
Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu Phe Thr
50          55          60
His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln Lys Asn
65          70          75          80
Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile Thr Asp
85          90          95
Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala Met Ile
100          105          110
```

Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp Leu Leu  
115 120 125  
Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro Arg Thr  
130 135 140  
Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala Lys Leu  
145 150 155 160  
Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val Asn Phe  
165 170 175  
Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val Leu Ser  
180 185 190  
Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val Asn Ile  
195 200 205  
Lys Asp Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

aaaatttagt	tcctttctca	tttatccact	gctcttaatc	caacttcaat	atctctctat	60
cctcacata	tttgttctgt	ttctmcttca	actttcaact	gataaaagttt	aaacctttat	120
gctctttact	ctctgatctc	aaaagggtt	tggttagttc	nmctcaaac	catggrgatt	180
tgcttaagt	ctmagattaa	agctgtgagt	ccaggtaagc	caggtgcaag	tccgaagtat	240
atgagctcag	aggctaata	ttcactggga	agtaaaagct	cttctgtgtc	aatcagaaca	300
aacccaagaa	ctgaaggaga	gatcttgcaa	tctcctaata	tcaaaaagttt	cacttttgct	360
gagcttaaag	cagcanctag	gnattttaga	ccagatagtg	ttcttggtga	aggtgggttt	420
ggttctgttt	tcaaaggttg	gatt				

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

Met Xaa	Ile Cys	Leu Ser	Ala Xaa	Ile Lys	Ala Val	Ser Pro	Gly Lys	
1	5			10			15	
Pro Gly	Ala Ser	Pro Lys	Tyr Met	Ser Ser	Glu Ala	Asn Asp	Ser Leu	
	20		25			30		
Gly Ser	Lys Ser	Ser Ser	Val Ser	Ile Arg	Thr Asn	Pro Arg	Thr Glu	
	35		40			45		
Gly Glu	Ile Leu	Gln Ser	Pro Asn	Leu Lys	Ser Phe	Thr Phe	Ala Glu	
	50		55		60			
Leu Lys	Ala Ala	Xaa Arg	Xaa Phe	Arg Pro	Asp Ser	Val Leu	Gly Glu	
65	70		75			80		
Gly Gly	Phe Gly	Ser Val	Phe Lys	Gly Trp	Ile			
	85		90					

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..68  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499540  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:  
Met Ser Ser Glu Ala Asn Asp Ser Leu Gly Ser Lys Ser Ser Ser Val  
1 5 10 15  
Ser Ile Arg Thr Asn Pro Arg Thr Glu Gly Glu Ile Leu Gln Ser Pro  
20 25 30  
Asn Leu Lys Ser Phe Thr Phe Ala Glu Leu Lys Ala Ala Xaa Arg Xaa  
35 40 45  
Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val Phe  
50 55 60  
Lys Gly Trp Ile  
65

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

Met Ile His Trp Glu Val Lys Ala Leu Leu Cys Gln Ser Glu Gln Thr  
1 5 10 15  
Gln Glu Leu Lys Glu Arg Ser Cys Asn Leu Leu Ile Ser Lys Val Ser  
20 25 30  
Leu Leu Leu Ser Leu Lys Gln Xaa Leu Xaa Ile Leu Asp Gln Ile Val  
35 40 45  
Phe Leu Val Lys Val Val Leu Val Leu Phe Ser Lys Val Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1396  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

agaaccaa at cctcggcggc gattgaagaa acctttccga tggatctgct caggggaagag 60  
attctgaaga aacgtaagag tctagctgag gaatctggtg gtaagaagtt cttcaagcgg 120  
tctgagatcg agcagaagaa aatccagaag cttcgagagg aagaacgacg cgagcacgag 180  
cttaaggctc agcggagagc cgccgcccgc gcttccggtg gagatggaaa atcatccggc 240  
tctgctcctg gttcttctaa cgcagctacg tctgcgtctt ccaaatacctc tgcatacggac 300  
gctgctgcta tcgcccattc aaaagcccta accgacgaaa acctaatctt cccgaggcag 360  
gaagtgattc gtcgtttgag attccttaag cagccgatga ctctcttcgg agaagatgat 420  
caatcgcggc tcgatacgact caagtacgtt ttgaaggaag gattgttcga ggttgatagt 480  
gatatgactg aaggacagac gaatgatttc ttgcgtgaca tcgcagagct taagaagagg 540  
cagaagagtg gtatgatggg agataggaag aggaagagta gagatgagag aggaagagac 600

```

gaaggtgata gaggtgaaac aagggaatat gaacttagtg gtgggtgaatc gagtgatgtt      660
gatgctgata aagatatgaa acgtttgaaa gctaactttg aggatctatg cgatgaggat      720
aagatccttg tgttttataa gaagctgttg attgaatgga aacaggagct tgatgcgatg      780
gagaacactg agaggagaac tgcaaaaagg aaacagatgg tagccacttt taagcagtgt      840
gctaggtatc tagttcctct cttcaactta tgcaggaaga aggggtttacc agctgacatt      900
cgtcaagctt taatggtgat ggtaaccac tgcataaagc gagactacct tgctgcaatg      960
gaccactaca tcaaactagc tatcggaac gcgccatggc ctattggagt gactatgggt      1020
ggtattcacg aacgttcagc tcgagagaag atttacacca acagtgttgc tcacatcatg      1080
aacgatgaaa ccactcgcaa gtatcttcag tcagttaaaa gactgatgac tttctgtcaa      1140
agacgttatc caactatgcc ttctaaagcc gttgagttca atagcttagc caacggaagc      1200
gacttacagt ctttgctagc cgaagagaga ttctttgggt gtaatcgtga acaggtctca      1260
gaggagagac tccggctcat gccttctcag agcgaaagct agtcttactg tgtttcttgc      1320
tttgttgtgt ttttattttt gtatcaaaac gttgactctg tattatcgtc tattttaaac      1380
gttgacctga ttgtcg

```

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..433
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

```

Arg Thr Lys Ser Ser Ala Ala Ile Glu Glu Thr Phe Pro Met Asp Leu
1          5          10          15
Leu Arg Glu Glu Ile Leu Lys Lys Arg Lys Ser Leu Ala Glu Ser
20          25          30
Gly Gly Lys Lys Phe Phe Lys Arg Ser Glu Ile Glu Gln Lys Lys Ile
35          40          45
Gln Lys Leu Arg Glu Glu Glu Arg Arg Glu His Glu Leu Lys Ala Gln
50          55          60
Arg Arg Ala Ala Ala Ala Ala Ser Gly Gly Asp Gly Lys Ser Ser Gly
65          70          75          80
Ser Ala Pro Gly Ser Ser Asn Ala Ala Thr Ser Ala Ser Ser Lys Ser
85          90          95
Ser Ala Ser Asp Ala Ala Ala Ile Ala Asp Ser Lys Ala Leu Thr Asp
100          105          110
Glu Asn Leu Ile Leu Pro Arg Gln Glu Val Ile Arg Arg Leu Arg Phe
115          120          125
Leu Lys Gln Pro Met Thr Leu Phe Gly Glu Asp Asp Gln Ser Arg Leu
130          135          140
Asp Arg Leu Lys Tyr Val Leu Lys Glu Gly Leu Phe Glu Val Asp Ser
145          150          155          160
Asp Met Thr Glu Gly Gln Thr Asn Asp Phe Leu Arg Asp Ile Ala Glu
165          170          175
Leu Lys Lys Arg Gln Lys Ser Gly Met Met Gly Asp Arg Lys Arg Lys
180          185          190
Ser Arg Asp Glu Arg Gly Arg Asp Glu Gly Asp Arg Gly Glu Thr Arg
195          200          205
Glu Tyr Glu Leu Ser Gly Gly Glu Ser Ser Asp Val Asp Ala Asp Lys
210          215          220
Asp Met Lys Arg Leu Lys Ala Asn Phe Glu Asp Leu Cys Asp Glu Asp
225          230          235          240
Lys Ile Leu Val Phe Tyr Lys Lys Leu Leu Ile Glu Trp Lys Gln Glu
245          250          255
Leu Asp Ala Met Glu Asn Thr Glu Arg Arg Thr Ala Lys Gly Lys Gln
260          265          270
Met Val Ala Thr Phe Lys Gln Cys Ala Arg Tyr Leu Val Pro Leu Phe

```

275	280	285
Asn Leu Cys Arg Lys Lys Gly Leu Pro Ala Asp Ile Arg Gln Ala Leu		
290	295	300
Met Val Met Val Asn His Cys Ile Lys Arg Asp Tyr Leu Ala Ala Met		
305	310	315
Asp His Tyr Ile Lys Leu Ala Ile Gly Asn Ala Pro Trp Pro Ile Gly		
320	325	330
Val Thr Met Val Gly Ile His Glu Arg Ser Ala Arg Glu Lys Ile Tyr		
335	340	345
Thr Asn Ser Val Ala His Ile Met Asn Asp Glu Thr Thr Arg Lys Tyr		
350	355	360
Leu Gln Ser Val Lys Arg Leu Met Thr Phe Cys Gln Arg Arg Tyr Pro		
365	370	375
Thr Met Pro Ser Lys Ala Val Glu Phe Asn Ser Leu Ala Asn Gly Ser		
380	385	390
Asp Leu Gln Ser Leu Leu Ala Glu Glu Arg Phe Phe Gly Gly Asn Arg		
395	400	405
Glu Gln Val Ser Glu Glu Arg Leu Arg Leu Met Pro Ser Gln Ser Glu		
410	415	420
	425	430
Ser		

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1499544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Asp Leu Leu Arg Glu Glu Ile Leu Lys Lys Arg Lys Ser Leu Ala		
1	5	10
Glu Glu Ser Gly Gly Lys Lys Phe Phe Lys Arg Ser Glu Ile Glu Gln		
15	20	25
Lys Lys Ile Gln Lys Leu Arg Glu Glu Arg Arg Glu His Glu Leu		
30	35	40
Lys Ala Gln Arg Arg Ala Ala Ala Ala Ala Ser Gly Gly Asp Gly Lys		
45	50	55
Ser Ser Gly Ser Ala Pro Gly Ser Ser Asn Ala Ala Thr Ser Ala Ser		
60	65	70
Ser Lys Ser Ser Ala Ser Asp Ala Ala Ala Ile Ala Asp Ser Lys Ala		
75	80	85
Leu Thr Asp Glu Asn Leu Ile Leu Pro Arg Gln Glu Val Ile Arg Arg		
90	95	100
Leu Arg Phe Leu Lys Gln Pro Met Thr Leu Phe Gly Glu Asp Asp Gln		
105	110	115
Ser Arg Leu Asp Arg Leu Lys Tyr Val Leu Lys Glu Gly Leu Phe Glu		
120	125	130
Val Asp Ser Asp Met Thr Glu Gly Gln Thr Asn Asp Phe Leu Arg Asp		
135	140	145
Ile Ala Glu Leu Lys Lys Arg Gln Lys Ser Gly Met Met Gly Asp Arg		
150	155	160
Lys Arg Lys Ser Arg Asp Glu Arg Gly Arg Asp Glu Gly Asp Arg Gly		
165	170	175
Glu Thr Arg Glu Tyr Glu Leu Ser Gly Gly Glu Ser Ser Asp Val Asp		
180	185	190
Ala Asp Lys Asp Met Lys Arg Leu Lys Ala Asn Phe Glu Asp Leu Cys		
195	200	205
210	215	220

```

Asp Glu Asp Lys Ile Leu Val Phe Tyr Lys Lys Leu Leu Ile Glu Trp
225                230                235                240
Lys Gln Glu Leu Asp Ala Met Glu Asn Thr Glu Arg Arg Thr Ala Lys
                245                250                255
Gly Lys Gln Met Val Ala Thr Phe Lys Gln Cys Ala Arg Tyr Leu Val
                260                265                270
Pro Leu Phe Asn Leu Cys Arg Lys Lys Gly Leu Pro Ala Asp Ile Arg
                275                280                285
Gln Ala Leu Met Val Met Val Asn His Cys Ile Lys Arg Asp Tyr Leu
290                295                300
Ala Ala Met Asp His Tyr Ile Lys Leu Ala Ile Gly Asn Ala Pro Trp
305                310                315                320
Pro Ile Gly Val Thr Met Val Gly Ile His Glu Arg Ser Ala Arg Glu
                325                330                335
Lys Ile Tyr Thr Asn Ser Val Ala His Ile Met Asn Asp Glu Thr Thr
                340                345                350
Arg Lys Tyr Leu Gln Ser Val Lys Arg Leu Met Thr Phe Cys Gln Arg
                355                360                365
Arg Tyr Pro Thr Met Pro Ser Lys Ala Val Glu Phe Asn Ser Leu Ala
370                375                380
Asn Gly Ser Asp Leu Gln Ser Leu Leu Ala Glu Glu Arg Phe Phe Gly
385                390                395                400
Gly Asn Arg Glu Gln Val Ser Glu Glu Arg Leu Arg Leu Met Pro Ser
                405                410                415
Gln Ser Glu Ser
                420

```

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

```

Met Thr Leu Phe 5 Glu Asp Asp Gln Ser Arg Leu Asp Arg Leu Lys
1                10                15
Tyr Val Leu Lys Glu Gly Leu Phe Glu Val Asp Ser Asp Met Thr Glu
                20                25                30
Gly Gln Thr Asn Asp Phe Leu Arg Asp Ile Ala Glu Leu Lys Lys Arg
                35                40                45
Gln Lys Ser Gly Met Met Gly Asp Arg Lys Arg Lys Ser Arg Asp Glu
50                55                60
Arg Gly Arg Asp Glu Gly Asp Arg Gly Glu Thr Arg Glu Tyr Glu Leu
65                70                75                80
Ser Gly Gly Glu Ser Ser Asp Val Asp Ala Asp Lys Asp Met Lys Arg
                85                90                95
Leu Lys Ala Asn Phe Glu Asp Leu Cys Asp Glu Asp Lys Ile Leu Val
                100                105                110
Phe Tyr Lys Lys Leu Leu Ile Glu Trp Lys Gln Glu Leu Asp Ala Met
115                120                125
Glu Asn Thr Glu Arg Arg Thr Ala Lys Gly Lys Gln Met Val Ala Thr
130                135                140
Phe Lys Gln Cys Ala Arg Tyr Leu Val Pro Leu Phe Asn Leu Cys Arg
145                150                155                160
Lys Lys Gly Leu Pro Ala Asp Ile Arg Gln Ala Leu Met Val Met Val
                165                170                175
Asn His Cys Ile Lys Arg Asp Tyr Leu Ala Ala Met Asp His Tyr Ile

```



(2) INFORMATION FOR SEQ ID NO:1076:

(A) LENGTH: 527 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1499547

acgaaacang	naggggaggt	gagaggacta	gaggagtctg	agcctcggag	gagggagagg	60
gcgaagagta	gggggaacca	aatcttgtag	gggaaacgta	gagttctttc	gtggaggaag	120
cgggtgcaac	tggaggaggg	tagaggtagc	tcaatagatc	tactgctgtc	gggggagtta	180
atgcaaagct	gagttgctgc	acgttggtt	tcttcagaga	tggcttcagc	tgggtgtagcc	240
ccatctgggt	acaaaaacag	cagcagcact	agcattgggt	ccgagaagtt	gcaagatcag	300
atgaacgagc	taaagattag	agatgataag	gaagttgaag	caaccataat	taattgggaaa	360
gggactgaaa	ctgggcacat	aattgtcacc	actactggtg	gcaagaatgg	ttaaccaaaaa	420
cagacagtga	gctacattggc	tgagcgcat	gtaggtcaag	gttcttttgg	gattgtcttc	480
caqgctaagt	gtttggagac	gggtgagact	gttgccataa	agaaggt		

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1499548

[illegible]

100

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

```
Met Asn Glu Leu Lys Ile Arg Asp Asp Lys Glu Val Glu Ala Thr Ile
1           5           10           15
Ile Asn Gly Lys Gly Thr Glu Thr Gly His Ile Ile Val Thr Thr Thr
          20           25           30
Gly Gly Lys Asn Gly Gln Pro Lys Gln Thr Val Ser Tyr Met Ala Glu
          35           40           45
Arg Ile Val Gly Gln Gly Ser Phe Gly Ile Val Phe Gln Ala Lys Cys
          50           55           60
Leu Glu Thr Gly Glu Thr Val Ala Ile Lys Lys
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

```
aaagctcccc cacaccctgc ctgatccctc ccaataagct cccagctcc acgccggaacg      60
cagcagcagc agcagtagag atggccgccc tcgccgctc ctccacggcc gccttcgccg      120
ccaagccgcg cctcccacgc gcgcgcctca ccgtggcctg ctccgccacc ggcgncgacg      180
gcaacggcag cagcagcagt gtgtcgctcg catcctccgt gaagacgttc tcggccgcgc      240
tggtctgtgc gtcggtgctt ctctcctcgg ccgcsacctc cmctscctccc gcggccgctg      300
acatcgcggg gctgaccccg tgcaaggagt ccaaggcggt cgccaagcgc gagaagaact      360
cgatcaagaa gstcaccgcg tcgctcaaga agtacgcg
```

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

```
Ser Ser Arg Thr Pro Cys Leu Ile Pro Pro Asn Lys Leu Pro Ser Ser
1           5           10           15
Thr Pro Asp Ala Ala Ala Ala Val Glu Met Ala Ala Leu Ala Ala
          20           25           30
Ser Ser Thr Ala Ala Phe Ala Ala Lys Pro Arg Leu Pro Arg Ala Arg
          35           40           45
Leu Thr Val Ala Cys Ser Ala Thr Gly Xaa Asp Gly Asn Gly Ser Ser
```

50 55 60  
Ser Ser Val Ser Leu Ala Ser Ser Val Lys Thr Phe Ser Ala Ala Leu  
65 70 75 80  
Ala Leu Ser Ser Val Leu Leu Ser Ser Ala Xaa Thr Ser Xaa Xaa Pro  
85 90 95  
Ala Ala Ala Asp Ile Ala Gly Leu Thr Pro Cys Lys Glu Ser Lys Ala  
100 105 110  
Phe Ala Lys Arg Glu Lys Asn Ser Ile Lys Lys Xaa Thr Ala Ser Leu  
115 120 125  
Lys Lys Tyr Ala  
130

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

Met Ala Ala Leu Ala Ala Ser Ser Thr Ala Ala Phe Ala Ala Lys Pro  
1 5 10 15  
Arg Leu Pro Arg Ala Arg Leu Thr Val Ala Cys Ser Ala Thr Gly Xaa  
20 25 30  
Asp Gly Asn Gly Ser Ser Ser Ser Val Ser Leu Ala Ser Ser Val Lys  
35 40 45  
Thr Phe Ser Ala Ala Leu Ala Leu Ser Ser Val Leu Leu Ser Ser Ala  
50 55 60  
Xaa Thr Ser Xaa Xaa Pro Ala Ala Ala Asp Ile Ala Gly Leu Thr Pro  
65 70 75 80  
Cys Lys Glu Ser Lys Ala Phe Ala Lys Arg Glu Lys Asn Ser Ile Lys  
85 90 95  
Lys Xaa Thr Ala Ser Leu Lys Lys Tyr Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

atcctcaagt catcagctag ctagccttcc ctacagcaac tgcatacata caacacttcc 60  
atctgcccgc tegtcttcga tcaattccca agtcaaataa tataacagca atggtggttc 120  
ccgtgatcga cttctccaag ctggacggcg ctgagagggc cgaaaccctg gcgcagatcg 180  
ccaatggctg cgaggagtgg ggattcttcc agctcgtgaa ccacggcatc ccgctggagc 240  
tgctcgagcg cgtaagaag gtgtgctccg acagctaccg cctccgggag gccgggttca 300  
aggcgctcga gccgggtgcgc acgctggagg cgctcgtcga cgcggasrcg ccggkttgaa 360  
gtggtggcgc cgggtggacga cctggactgg gaggacatct tctacattca tgacggatgc 420  
cagtdgccgt ccgaccgc

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499568  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:  
Met Val Val Pro Val Ile Asp Phe Ser Lys Leu Asp Gly Ala Glu Arg  
1 5 10 15  
Ala Glu Thr Leu Ala Gln Ile Ala Asn Gly Cys Glu Glu Trp Gly Phe  
20 25 30  
Phe Gln Leu Val Asn His Gly Ile Pro Leu Glu Leu Leu Glu Arg Val  
35 40 45  
Lys Lys Val Cys Ser Asp Ser Tyr Arg Leu Arg Glu Ala Gly Phe Lys  
50 55 60  
Ala Ser Glu Pro Val Arg Thr Leu Glu Ala Leu Val Asp Ala Xaa Xaa  
65 70 75 80  
Pro Xaa

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..471  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

accaaacaga tcaaatacaga gatggcaagt cgtagtagct ctgcagaagg tgcaggcagg 60  
acgttgccgtg tcaatctcaa gttgatcacc gtgctgagca tcgatggcgg cggcatcaga 120  
gggatcatcc cggccaccat cctgcgcttc ctggaagcga actccaggaa ctggacgggc 180  
cagacgctcg tatcgcggaac tacttcgacg tcgtcgccgg cagcagcacc ggcggtctcc 240  
tgacggcgat gctcacggcc ccggacacga acgaacggcc gctgttcgcc gccaaaggacc 300  
tggcgcgggt ctacatccag cactcgccca aaatcttccg gcagaagaat gctatggggt 360  
ccaagctcgt cggcaagctg aggatggctt gtgggcccaa gtacgacggc aagtacctcc 420  
atgcgcavtc cgacggcttc ttgtaatat gaggctggac aggacactga c

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..80  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

Thr Lys Gln Ile Lys Ser Glu Met Ala Ser Arg Ser Ser Ser Ala Glu  
1 5 10 15  
Gly Ala Gly Arg Thr Leu Pro Val Asn Leu Lys Leu Ile Thr Val Leu  
20 25 30  
Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu  
35 40 45  
Ala Phe Leu Glu Ala Asn Ser Arg Asn Trp Thr Gly Gln Thr Leu Val  
50 55 60  
Ser Arg Thr Thr Ser Thr Ser Ser Pro Ala Arg Ala Pro Ala Val Ser

65

70

75

80

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

```
Met Ala Ser Arg Ser Ser Ser Ala Glu Gly Ala Gly Arg Thr Leu Pro
1          5          10          15
Val Asn Leu Lys Leu Ile Thr Val Leu Ser Ile Asp Gly Gly Gly Ile
          20          25          30
Arg Gly Ile Ile Pro Ala Thr Ile Leu Ala Phe Leu Glu Ala Asn Ser
          35          40          45
Arg Asn Trp Thr Gly Gln Thr Leu Val Ser Arg Thr Thr Ser Thr Ser
          50          55          60
Ser Pro Ala Arg Ala Pro Ala Val Ser
65          70
```

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

```
Met Ala Ala Ala Ser Glu Gly Ser Ser Arg Pro Pro Ser Ser Pro Ser
1          5          10          15
Trp Lys Arg Thr Pro Gly Thr Gly Arg Ala Arg Arg Ser Tyr Arg Gly
          20          25          30
Leu Leu Arg Arg Arg Arg Arg His Glu His Arg Arg Ser Pro Asp Gly
          35          40          45
Asp Ala His Gly Pro Gly His Glu Arg Thr Ala Ala Val Arg Arg Gln
          50          55          60
Gly Pro Gly Ala Val Leu His Pro Ala Leu Ala Gln Asn Leu Pro Ala
65          70          75          80
Glu Glu Cys Tyr Gly Val Gln Ala Arg Arg Gln Ala Glu Asp Gly Leu
          85          90          95
Trp Ala Gln Val Arg Arg Gln Val Pro Pro Cys Ala Xaa Arg Arg Leu
          100          105          110
Leu Gly Asn Met Arg Leu Asp Arg Thr Leu
          115          120
```

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1499591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

aactcgggtgc	gaaaccacac	cacccatcgc	caccaccaat	caatccatca	cgttagctgc	60
acctgcgcct	ctccttgavg	tcgcgcasca	gcaatggcgt	gctccaaagc	ngtgctgctc	120
gcmgcgctcc	tagccgtcgc	aggagcgctc	tcctccgctg	cggtgtggga	ggactacgac	180
caccacatgt	accacaagtg	ctacaggtcc	tgcattgagga	agtgcgacga	cgacgatgcc	240
gatgatgcct	tgaagaatag	catcagcccc	gttggtcacct	ctgtgtccga	tgatcacgac	300
catgacgacg	atcacgacca	ccacgatgat	cacaaccacg	accacgacga	ccaccatgat	360
gatcacgacc	acgaccacca	tcacgatgat	cacgaccacg	accatgatga	tcacgaccac	420
gaccataatg	acaaccacgg	cgaacaccat	gacgacgacg	atgaggatga	cgattac	

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1499592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met	Ala	Cys	Ser	Lys	Xaa	Val	Leu	Leu	Xaa	Ala	Leu	Leu	Ala	Val	Ala	
1				5					10					15		
Gly	Ala	Leu	Ser	Ser	Ala	Ala	Val	Trp	Glu	Asp	Tyr	Asp	His	His	Met	
			20					25					30			
Tyr	His	Lys	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	Asp	
		35					40					45				
Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Val	Thr	Ser	Val	
	50					55					60					
Ser	Asp	Asp	His	Asp	His	Asp	Asp	Asp	His	Asp	His	His	Asp	Asp	His	
65				70					75				80			
Asn	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His	His	
			85					90					95			
His	Asp	Asp	His	Asp	His	Asp	His	Asp	His	Asp	His	Asp	His	Asn		
		100						105					110			
Asp	Asn	His	Gly	Glu	His	His	Asp	Asp	Asp	Glu	Asp	Asp	Asp	Tyr		
		115					120						125			

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1499593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

Met	Tyr	His	Lys	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	
1			5					10					15			
Asp	Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Val	Thr	Ser	
			20					25					30			
Val	Ser	Asp	Asp	His	Asp	His	Asp	Asp	Asp	His	Asp	His	His	Asp	Asp	
		35					40					45				
His	Asn	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His	

50 55 60  
His His Asp Asp His Asp His Asp Asp Asp His Asp His Asp His  
65 70 75 80  
Asn Asp Asn His Gly Glu His His Asp Asp Asp Asp Glu Asp Asp Asp  
85 90 95  
Tyr

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

Met Arg Lys Cys Asp Asp Asp Asp Ala Asp Asp Ala Leu Lys Asn Ser  
1 5 10 15  
Ile Ser Pro Val Val Thr Ser Val Ser Asp Asp His Asp His Asp Asp  
20 25 30  
Asp His Asp His His Asp Asp His Asn His Asp His Asp Asp His His  
35 40 45  
Asp Asp His Asp His Asp His His His Asp Asp His Asp His Asp His  
50 55 60  
Asp Asp His Asp His Asp His Asn Asp Asn His Gly Glu His His Asp  
65 70 75 80  
Asp Asp Asp Glu Asp Asp Asp Tyr  
85

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

tctccttttcg gargargcgg accargtaag cagcagcagg aaccctagca ccgccgcacg 60  
cccagccatg ggtatcgacc tcgttgccgg tgggaggaac aagaagacca agcgcacagc 120  
gccgaagtcc gacgatgttt atctcaccgg gatggargtc gccgagatcg acggcgcccc 180  
gaggatgggc ccgacgttcg gcgccatgat gatctccggc cagaaggcgg cgcacctr gc 240  
gctgaaggca ctggngcagg cccaacgccg tggacgggac catccccgar gtgtcgccgg 300  
cgctrckmga rgagttcgtg attdrtcca aggacgacga ggtcgtg

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

Leu Leu Ser Xaa Xaa Ala Asp Xaa Val Ser Ser Ser Arg Asn Pro Ser  
1 5 10 15  
Thr Ala Ala Ser Pro Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg  
20 25 30  
Asn Lys Lys Thr Lys Arg Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu  
35 40 45  
Thr Gly Met Xaa Val Ala Glu Ile Asp Gly Ala Pro Arg Met Gly Pro  
50 55 60  
Thr Phe Gly Ala Met Met Ile Ser Gly Gln Lys Ala Ala His Xaa Ala  
65 70 75 80  
Leu Lys Ala Leu Xaa Gln Ala Gln Arg Arg Gly Arg Asp His Pro Arg  
85 90 95  
Xaa Val Ala Gly Ala Xaa Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg  
100 105 110  
Arg Gly Arg  
115

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg  
1 5 10 15  
Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu Thr Gly Met Xaa Val Ala  
20 25 30  
Glu Ile Asp Gly Ala Pro Arg Met Gly Pro Thr Phe Gly Ala Met Met  
35 40 45  
Ile Ser Gly Gln Lys Ala Ala His Xaa Ala Leu Lys Ala Leu Xaa Gln  
50 55 60  
Ala Gln Arg Arg Gly Arg Asp His Pro Arg Xaa Val Ala Gly Ala Xaa  
65 70 75 80  
Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg Arg Gly Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

Met Xaa Val Ala Glu Ile Asp Gly Ala Pro Arg Met Gly Pro Thr Phe  
1 5 10 15  
Gly Ala Met Met Ile Ser Gly Gln Lys Ala Ala His Xaa Ala Leu Lys  
20 25 30  
Ala Leu Xaa Gln Ala Gln Arg Arg Gly Arg Asp His Pro Arg Xaa Val  
35 40 45  
Ala Gly Ala Xaa Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg Arg Gly  
50 55 60  
Arg



65

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

ctctaaaagt ggtctgttct gcaggttact ccctgtgact aagtaccgca ggctttccagt	60
ggctcgatagc tcaggcaaac tggttgggat cattacaaga gggaacgtcg tccaagccgc	120
cctcgaaatc aagaaaaagg ttgaaggac actctgagat gactacctcc aggtatcctt	180
tttctgcca catggggggc ttaggacttg gacacatctc tagttggcaa ctgatcaatc	240
aaagcgactg tcagagttag cgatgaaagt cgctatgttt atgaagattt gcccgagaa	300
gcacaggtgt atgtgtagt tttgttatat atgctgatgc agtccttgct ggccaaaaca	360
caggttaccg attgttcttg tttcctgggc ttctttggac accaaattct taacctaggt	420
cttgtttggg tgcacacgta tctagttcaa cttacttgta ttgaggttca ttgaagtgga	480
aaatcaacta gttttcgcac ttc	

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

Ser	Lys	Ser	Gly	Leu	Phe	Cys	Arg	Leu	Leu	Pro	Val	Thr	Lys	Tyr	Arg
1				5					10					15	
Arg	Leu	Pro	Val	Val	Asp	Ser	Ser	Gly	Lys	Leu	Val	Gly	Ile	Ile	Thr
			20					25					30		
Arg	Gly	Asn	Val	Val	Gln	Ala	Ala	Leu	Glu	Ile	Lys	Lys	Lys	Val	Glu
		35					40					45			
Gly	Thr	Leu													
		50													

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

Met	Leu	Met	Gln	Ser	Leu	Leu	Ala	Lys	Thr	Gln	Val	Thr	Asp	Cys	Ser
1				5					10					15	
Gly	Phe	Leu	Gly	Phe	Phe	Gly	His	Gln	Ile	Leu	Asn	Leu	Gly	Leu	Val
			20				25						30		
Trp	Val	His	Thr	Tyr	Leu	Val	Gln	Leu	Thr	Cys	Ile	Glu	Val	His	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 45 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..45  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499630  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:  
Met Gln Ser Leu Leu Ala Lys Thr Gln Val Thr Asp Cys Ser Gly Phe  
1                  5                  10                  15  
Leu Gly Phe Phe Gly His Gln Ile Leu Asn Leu Gly Leu Val Trp Val  
                  20                  25                  30  
His Thr Tyr Leu Val Gln Leu Thr Cys Ile Glu Val His  
                  35                  40                  45  
(2) INFORMATION FOR SEQ ID NO:1100:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 476 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..476  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499649  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:  
aattactgtg cctttatctt caaccctaac catccattac catattccta agctatcatg                  60  
gtgcaccgga cttccatagc cgatgtgcat gtgatgtgca tggatctaag cccaaagaaa                  120  
cccaacaagg ccagcgccas sancggcgga gctactacga ctgggtcccc gccgatctgc                  180  
ccatgtctgg cgttgcctcc attgggtgcc ccaagctctg cctcaccgcc ggaggtcttg                  240  
ccctaccagc ctactccgac tctgccaaga tcgcctacgt cctccaaggc aaaggtatat                  300  
tcggcggtgt tctcccgagg gcgaccaagg agaaggtcat ctccgtcaag gaaggcgacg                  360  
cgctggcgct ccccttcggc gtcgtcacct ggtggcacia caacgccgac gccgctatct                  420  
ccgacctcgt ggtgctcttc ctggcgaca cctccacggg ccacaagccg ggccag  
(2) INFORMATION FOR SEQ ID NO:1101:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 158 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..158  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499650  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:  
Leu Leu Cys Leu Tyr Leu Gln Pro Lys Pro Ser Ile Thr Ile Phe Leu  
1                  5                  10                  15  
Ser Tyr His Gly Ala Pro Asp Phe His Ser Arg Cys Ala Cys Asp Val  
                  20                  25                  30  
His Gly Ser Lys Pro Lys Glu Thr Gln Gln Gly Gln Arg Xaa Xaa Arg  
                  35                  40                  45  
Arg Ser Tyr Tyr Asp Trp Ser Pro Ala Asp Leu Pro Met Leu Gly Val  
                  50                  55                  60  
Ala Ser Ile Gly Ala Ala Lys Leu Cys Leu Thr Ala Gly Gly Leu Ala  
                  65                  70                  75                  80  
Leu Pro Ser Tyr Ser Asp Ser Ala Lys Ile Ala Tyr Val Leu Gln Gly  
                  85                  90                  95

Lys Gly Ile Phe Gly Val Val Leu Pro Glu Ala Thr Lys Glu Lys Val  
100 105 110  
Ile Ser Val Lys Glu Gly Asp Ala Leu Ala Leu Pro Phe Gly Val Val  
115 120 125  
Thr Trp Trp His Asn Asn Ala Asp Ala Ala Ile Ser Asp Leu Val Val  
130 135 140  
Leu Phe Leu Gly Asp Thr Ser Thr Gly His Lys Pro Gly Gln  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1499651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

Met Val His Arg Thr Ser Ile Ala Asp Val His Val Met Cys Met Asp  
1 5 10 15  
Leu Ser Pro Lys Lys Pro Asn Lys Ala Ser Ala Xaa Xaa Gly Gly Ala  
20 25 30  
Thr Thr Thr Gly Pro Pro Pro Ile Cys Pro Cys Ser Ala Leu Pro Pro  
35 40 45  
Leu Val Pro Pro Ser Ser Ala Ser Pro Pro Glu Val Leu Pro Tyr Pro  
50 55 60  
Ala Thr Pro Thr Leu Pro Arg Ser Pro Thr Ser Lys Ala Lys Val  
65 70 75 80  
Tyr Ser Ala Trp Phe Ser Arg Arg Arg Pro Arg Arg Arg Ser Ser Pro  
85 90 95  
Ser Arg Lys Ala Thr Arg Trp Arg Ser Pro Ser Ala Ser Ser Pro Gly  
100 105 110  
Gly Thr Thr Thr Pro Thr Pro Leu Ser Pro Thr Ser Trp Cys Ser Ser  
115 120 125  
Ser Ala Thr Pro Pro Arg Ala Thr Ser Arg Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1499652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

Met Cys Met Asp Leu Ser Pro Lys Lys Pro Asn Lys Ala Ser Ala Xaa  
1 5 10 15  
Xaa Gly Gly Ala Thr Thr Thr Gly Pro Pro Pro Ile Cys Pro Cys Ser  
20 25 30  
Ala Leu Pro Pro Leu Val Pro Pro Ser Ser Ala Ser Pro Pro Glu Val  
35 40 45  
Leu Pro Tyr Pro Ala Thr Pro Thr Leu Pro Arg Ser Pro Thr Ser Ser  
50 55 60  
Lys Ala Lys Val Tyr Ser Ala Trp Phe Ser Arg Arg Arg Pro Arg Arg  
65 70 75 80  
Arg Ser Ser Pro Ser Arg Lys Ala Thr Arg Trp Arg Ser Pro Ser Ala

85 90 95  
Ser Ser Pro Gly Gly Thr Thr Thr Pro Thr Pro Leu Ser Pro Thr Ser  
100 105 110  
Trp Cys Ser Ser Ser Ala Thr Pro Pro Arg Ala Thr Ser Arg Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

ctactaaccg cgtctcctct ccagcgcccg ccgtcgccgc cgcctcctc ttgggtccgc	60
cgtcgcgtcg ggtcatcatg gtgaggggtca gtgtgctcaa cgatgcgctc aagtccatgt	120
acaatgcaga gaagaggggc aagaggcagg tcatgatcag gccgtcgtcc aagggtgatca	180
tcaagttcct gacgggtcaag acctgggctt ctttgccaat ttccctgggca tcttcatctt	240
tgtcttggtt attgcgtacc acttcgtgat ggcagaccgc aagtacgaag gaaactgatg	300
tcctctagtg caaagatcct attatctgca ggccgaaata gggctatact gttagctaat	360
gctagtgaga tcgcttgaca ctttgagtgc atatcatgga agctggacat gcagttcctg	420
gcattttggt ttgcccattg ttttaatctg ctgaattagt aaatcctgga gaatcc	

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

Thr Asn Arg Val Ser Ser Pro Ala Pro Ala Val Ala Ala Leu Leu	
1 5 10 15	
Leu Val Pro Pro Ser Val Glu Val Ile Met Val Arg Val Ser Val Leu	
20 25 30	
Asn Asp Ala Leu Lys Ser Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg	
35 40 45	
Gln Val Met Ile Arg Pro Ser Lys Val Ile Ile Lys Phe Leu Thr	
50 55 60	
Val Lys Thr Trp Ala Ser Leu Pro Ile Ser Trp Ala Ser Ser Ser Leu	
65 70 75 80	
Ser Trp Leu Leu Arg Thr Thr Ser	
85	

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn  
1 5 10 15  
Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys  
20 25 30  
Val Ile Ile Lys Phe Leu Thr Val Lys Thr Trp Ala Ser Leu Pro Ile  
35 40 45  
Ser Trp Ala Ser Ser Ser Leu Ser Trp Leu Leu Arg Thr Thr Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1499658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro  
1 5 10 15  
Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Lys Thr Trp Ala Ser  
20 25 30  
Leu Pro Ile Ser Trp Ala Ser Ser Ser Leu Ser Trp Leu Leu Arg Thr  
35 40 45  
Thr Ser  
50

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1499667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

agaggatttc	tattgtagaa	atgcagttag	gccatttagg	ttttgcctct	ttttttttca	60
gactcggatt	ggtctgccgt	ccttgtgctc	cgccggcaat	ggcgtccacc	gccgtcaagc	120
tcacgcacat	cgcagtcaac	ttcacagatg	gcatgttcaa	gggcatctac	cacggcaagc	180
agtgccacgc	cgccgacatc	ccggccgtac	ttgcgcgcgc	gtgggctgca	ggcgtcgacc	240
gcatcattgt	caccggaggc	tccctgaaag	agtccagaga	ggcattgcag	atcgccgaga	300
ccgacgggag	actgttctgc	actgtgggag	tgcacccaac	aagatgcggg	gaattcgagg	360
agagtggaga	tcccgaragt	cattttcagg	cactgctggc	tctagcgaag	gagggtttag	420
ataaaggcaa	ggtcgttrct	gttggtgaat	gtggtttga	ttatgacaga	cttcagttct	480
gtccsggcag	atatgcaaaa	gaagtacttc	gagg			

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1499668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

Glu Asp Phe Tyr Cys Arg Asn Ala Val Arg Pro Ile Arg Phe Cys Leu  
1 5 10 15  
Phe Phe Phe Gln Thr Arg Ile Gly Leu Pro Ser Leu Cys Ser Ala Gly  
20 25 30  
Asn Gly Val His Arg Arg Gln Ala His Arg His Arg Ser Gln Leu His  
35 40 45  
Arg Trp His Val Gln Gly His Leu Pro Arg Gln Ala Val Pro Arg Arg  
50 55 60  
Arg His Pro Gly Arg Thr Cys Ala Arg Val Gly Cys Arg Arg Arg Pro  
65 70 75 80  
His His Cys His Arg Arg Leu Pro Glu Arg Val Gln Arg Gly Ile Ala  
85 90 95  
Asp Arg Arg Asp Arg Arg Glu Thr Val Leu His Cys Gly Ser Ala Pro  
100 105 110  
Asn Lys Met Arg Gly Ile Arg Gly Glu Trp Arg Ser Arg Xaa Ser Phe  
115 120 125  
Ser Gly Thr Ala Gly Ser Ser Glu Gly Gly Phe Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1499669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

Arg Ile Ser Ile Val Glu Met Gln Leu Gly Pro Leu Gly Phe Ala Ser  
1 5 10 15  
Phe Phe Phe Arg Leu Gly Leu Val Cys Arg Pro Cys Ala Pro Pro Ala  
20 25 30  
Met Ala Ser Thr Ala Val Lys Leu Ile Asp Ile Ala Val Asn Phe Thr  
35 40 45  
Asp Gly Met Phe Lys Gly Ile Tyr His Gly Lys Gln Cys His Ala Ala  
50 55 60  
Asp Ile Pro Ala Val Leu Ala Arg Ala Trp Ala Ala Gly Val Asp Arg  
65 70 75 80  
Ile Ile Val Thr Gly Gly Ser Leu Lys Glu Ser Arg Glu Ala Leu Gln  
85 90 95  
Ile Ala Glu Thr Asp Gly Arg Leu Phe Cys Thr Val Gly Val His Pro  
100 105 110  
Thr Arg Cys Gly Glu Phe Glu Ser Gly Asp Pro Xaa Gly His Phe  
115 120 125  
Gln Ala Leu Leu Ala Leu Ala Lys Glu Gly Leu Asp Lys Gly Lys Val  
130 135 140  
Val Xaa Val Gly Glu Cys Gly Leu Asp Tyr Asp Arg Leu Gln Phe Cys  
145 150 155 160  
Xaa Gly Arg Tyr Ala Lys Glu Val Leu Arg  
165 170

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1499670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

Met	Gln	Leu	Gly	Pro	Leu	Gly	Phe	Ala	Ser	Phe	Phe	Phe	Arg	Leu	Gly
1				5					10					15	
Leu	Val	Cys	Arg	Pro	Cys	Ala	Pro	Pro	Ala	Met	Ala	Ser	Thr	Ala	Val
			20					25					30		
Lys	Leu	Ile	Asp	Ile	Ala	Val	Asn	Phe	Thr	Asp	Gly	Met	Phe	Lys	Gly
		35					40					45			
Ile	Tyr	His	Gly	Lys	Gln	Cys	His	Ala	Ala	Asp	Ile	Pro	Ala	Val	Leu
	50					55					60				
Ala	Arg	Ala	Trp	Ala	Ala	Gly	Val	Asp	Arg	Ile	Ile	Val	Thr	Gly	Gly
65					70				75					80	
Ser	Leu	Lys	Glu	Ser	Arg	Glu	Ala	Leu	Gln	Ile	Ala	Glu	Thr	Asp	Gly
				85					90					95	
Arg	Leu	Phe	Cys	Thr	Val	Gly	Val	His	Pro	Thr	Arg	Cys	Gly	Glu	Phe
			100					105					110		
Glu	Glu	Ser	Gly	Asp	Pro	Xaa	Gly	His	Phe	Gln	Ala	Leu	Leu	Ala	Leu
		115					120					125			
Ala	Lys	Glu	Gly	Leu	Asp	Lys	Gly	Lys	Val	Val	Xaa	Val	Gly	Glu	Cys
	130					135					140				
Gly	Leu	Asp	Tyr	Asp	Arg	Leu	Gln	Phe	Cys	Xaa	Gly	Arg	Tyr	Ala	Lys
145					150					155					160
Glu	Val	Leu	Arg												

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..540

(D) OTHER INFORMATION: / Ceres Seq. ID 1499671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

atagaagaag	agcaggcagg	agctataagt	accccgcccc	cttcaccct	ctccttcac	60
ctccctccct	tgctgcctca	tccattccag	agctgcgaag	acagacagac	agagagaaaag	120
agggatcgac	ggagcaaggc	ggggccgtgt	ccggtcacac	acgagcgagc	cctctcggcc	180
gcgcgtttgt	gaatggtgaa	cvgcgagcgg	cgggcggacg	cggagtgcac	gcgggcgtcg	240
ctgctgggga	ggtatgagat	cgggcggacc	ctcggcgagg	gcaacttcgg	caaggtgaag	300
tacgcgcgcc	acatcgccag	cgggggccac	ttcgccatca	agatcctcga	ccgcagcaag	360
atcctctccc	tccgcatcga	cgaccagatc	aggagggaga	tcgggacgct	caagctgctc	420
aagcacccca	atgtcgctcc	cttgccagag	gttgctgcca	gtaaaacgaa	gatctacatg	480
gtgcttgagt	ttgtcaacgg	cggcgagctc	ttcgacaaga	tcgctatcaa	ggggaaactg	540

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1499672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

Ile	Glu	Glu	Glu	Gln	Ala	Gly	Ala	Ile	Ser	Thr	Pro	Pro	Ser	Thr
1				5					10				15	

Leu Ser Phe His Leu Pro Pro Leu Leu Pro His Pro Phe Gln Ser Cys  
20 25 30  
Glu Asp Arg Gln Thr Glu Arg Lys Arg Asp Arg Arg Ser Lys Ala Gly  
35 40 45  
Pro Cys Pro Val Thr His Glu Arg Ala Leu Ser Ala Ala Arg Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1499673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Arg Arg Arg Ala Gly Arg Ser Tyr Lys Tyr Pro Ala Pro Phe His Pro  
1 5 10 15  
Leu Leu Pro Pro Ser Leu Ala Ala Ser Ser Ile Pro Glu Leu Arg  
20 25 30  
Arg Gln Thr Asp Arg Glu Lys Glu Gly Ser Thr Glu Gln Gly Gly Ala  
35 40 45  
Val Ser Gly His Thr Arg Ala Ser Pro Leu Gly Arg Ala Phe Val Asn  
50 55 60  
Gly Glu Xaa Arg Ala Ala Gly Gly Arg Gly Val His Ala Gly Val Ala  
65 70 75 80  
Ala Gly Glu Val

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1499674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

Met Val Asn Xaa Glu Arg Arg Ala Asp Ala Glu Cys Thr Arg Ala Ser  
1 5 10 15  
Leu Leu Gly Arg Tyr Glu Ile Gly Arg Thr Leu Gly Glu Gly Asn Phe  
20 25 30  
Gly Lys Val Lys Tyr Ala Arg His Ile Ala Ser Gly Xaa His Phe Ala  
35 40 45  
Ile Lys Ile Leu Asp Arg Ser Lys Ile Leu Ser Leu Arg Ile Asp Asp  
50 55 60  
Gln Ile Arg Arg Glu Ile Gly Thr Leu Lys Leu Leu Lys His Pro Asn  
65 70 75 80  
Val Val Arg Leu His Glu Val Ala Ala Ser Lys Thr Lys Ile Tyr Met  
85 90 95  
Val Leu Glu Phe Val Asn Gly Gly Glu Leu Phe Asp Lys Ile Ala Ile  
100 105 110  
Lys Gly Lys Leu  
115

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..478  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499675  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:  
aaaaaccaca acacaagaac gggaagcgtg catgcacacg cacgagcacg aacctgagct 60  
gtagegccct ctcgctcgct ccccgcgcg c atggccagc gtascccagg tcccatgcaa 120  
accagccatg cctcacggcg gccgatccct acagctacag gccccgtgcc cgtggccgtg 180  
cttctcgccg ccgcccgcgt cggcctcctc gcgctgctgc cgtcgctggc cgaggccgtg 240  
tgaggaggtgc cgcacctctt cctcctcggc gccgtcatct ccttcggcgt cttcacgcag 300  
aggaacagcg acgcccagcg ccgcccgaag gacagctcac aggcgtggag cgcggtgtgc 360  
caccgccgatg cccccctcgt cgtgatcgcg gatcacacgg cgccgagcga cgacgacgac 420  
aacgacgact acgggctgga actggaagaa ggcgcacgag agacgccgct ttcgttgc  
(2) INFORMATION FOR SEQ ID NO:1117:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 158 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..158  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499676  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:  
Lys Pro Gln His Lys Asn Gly Lys Arg Ala Cys Thr Arg Thr Ser Thr  
1 5 10 15  
Asn Leu Ser Cys Ser Ala Leu Ser Leu Ala Pro Arg Ala Gln Trp Pro  
20 25 30  
Ala Xaa Pro Arg Ser His Ala Asn Gln Pro Cys Leu Thr Ala Ala Asp  
35 40 45  
Pro Tyr Ser Tyr Arg Pro Arg Ala Arg Gly Arg Ala Ser Arg Arg Arg  
50 55 60  
Arg Arg Arg Pro Pro Arg Ala Ala Ala Val Ala Gly Arg Gly Arg Val  
65 70 75 80  
Gly Gly Ala Ala Pro Leu Pro Pro Arg Arg Arg His Leu Leu Arg Arg  
85 90 95  
Leu His Ala Glu Glu Gln Arg Arg Arg Arg Pro Arg Gln Gly Gln Leu  
100 105 110  
Thr Gly Val Glu Arg Gly Val Pro Pro Arg Cys Pro Pro Arg Arg Asp  
115 120 125  
Arg Gly Ser His Gly Ala Glu Arg Arg Arg Arg Gln Arg Arg Leu Arg  
130 135 140  
Ala Gly Thr Gly Arg Arg Arg Thr Arg Asp Ala Ala Phe Val  
145 150 155  
(2) INFORMATION FOR SEQ ID NO:1118:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 97 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..97  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499677  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

Met Ala Ser Val Xaa Gln Val Pro Cys Lys Pro Ala Met Pro His Gly  
1 5 10 15  
Gly Arg Ser Leu Gln Leu Gln Ala Pro Cys Pro Trp Pro Cys Phe Ser  
20 25 30  
Pro Pro Pro Pro Ser Ala Ser Ser Arg Cys Cys Arg Arg Trp Pro Arg  
35 40 45  
Pro Cys Gly Arg Cys Arg Thr Ser Ser Ser Ser Ala Pro Ser Ser Pro  
50 55 60  
Ser Ala Ser Ser Arg Arg Gly Thr Ala Thr Pro Thr Ala Ala Pro Arg  
65 70 75 80  
Thr Ala His Arg Arg Gly Ala Arg Cys Ala Thr Pro Met Pro Pro Ser  
85 90 95  
Ser

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

Met Gln Thr Ser His Ala Ser Arg Arg Pro Ile Pro Thr Ala Thr Gly  
1 5 10 15  
Pro Val Pro Val Ala Val Leu Leu Ala Ala Ala Val Gly Leu Leu  
20 25 30  
Ala Leu Leu Pro Ser Leu Ala Glu Ala Val Trp Glu Val Pro His Leu  
35 40 45  
Phe Leu Leu Gly Ala Val Ile Ser Phe Gly Val Phe Thr Gln Arg Asn  
50 55 60  
Ser Asp Ala Asp Gly Arg Ala Lys Asp Ser Ser Gln Ala Trp Ser Ala  
65 70 75 80  
Val Cys His Pro Asp Ala Pro Leu Val Val Ile Ala Asp His Thr Ala  
85 90 95  
Pro Ser Asp Asp Asp Asn Asp Asp Tyr Gly Leu Glu Leu Glu Glu  
100 105 110  
Gly Ala Arg Glu Thr Pro Leu Ser Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

aggcagagca ctgcacgcca ccttatctct aaccggagat caaagaagta gccgttaacg	60
atggcttccg acgagctcgc aaaggccgtc gagcccagga agaagggcaa cgtcaagtat	120
gcctccatat gtgccatcct ggccctccatg gcctctgtca tccttggcta tgacattggg	180
gtgatgagtg gagcggccat gtacatcaag aaggacctga atatcacgga cgtkcagctg	240
gagatcctga tcgggatcct cagtctctac tcgctgttcg gatccttcgc tggcgcgcg	300
acgtccgaca ggatcgggcg ccgcttgacc gtcgtgttcg ccgctgtcat cttcttcgtg	360
ggctcgttgc tcatgggttt cgccgtcaac tacggcatgc tcatggcggg ccgcttcgtg	420

480

(2) INFORMATION FOR SEQ ID NO:1121:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 147 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..147
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499687
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1122:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 118 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..118
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499688
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

[illegible]

115

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

```
Met Ser Gly Ala Ala Met Tyr Ile Lys Lys Asp Leu Asn Ile Thr Asp
1           5           10           15
Xaa Gln Leu Glu Ile Leu Ile Gly Ile Leu Ser Leu Tyr Ser Leu Phe
20           25           30
Gly Ser Phe Ala Gly Ala Arg Thr Ser Asp Arg Ile Gly Arg Arg Leu
35           40           45
Thr Val Val Phe Ala Ala Val Ile Phe Phe Val Gly Ser Leu Leu Met
50           55           60
Gly Phe Ala Val Asn Tyr Gly Met Leu Met Ala Gly Arg Phe Val Ala
65           70           75           80
Gly Val Gly Val Gly Tyr Gly Gly Met Ile Xaa Pro Val Tyr Thr Ala
85           90           95
Glu Ile Ser Pro Xaa Xaa Pro Val Ala Ser
100          105
```

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..861
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

```
aagcaagcga asatcgccag attggtatat cgatcgattg awcrghnnnn gavgaangrg      60
aggacggrgg gcagatggcg gcgtagccggg gcttcttcga gtgcctgctc aggctgctca      120
acttcaccc caccgtcgcc ggccctcgcta tggttgggta cgggatctac ctgctcgtcg      180
agtggatgaa gatatccgan gacggcator gcggggcttc gacggcgbag gtgctcgtct      240
ctdgccggcc gttgttgagg gctgtcattc tcggtgacag ctctctcgac aatctaccca      300
aagcatgggt tattttattt tttattgggt ttggcaccat cgtcatcttg gtgtctctgt      360
ttggctgcat tggagcaggg acaagaaaca cctgctgttt gtgtttctat gctttcttgg      420
tcatattggt gatccttgct gaagctgcag ctgctgcatt cattttcttt gaccatggct      480
ggaaagatgt aattccagtg gacaaaacac ataactttga tgttatgtat gactttctga      540
aggaaaactg ggagattgca agatgggtcg ctctgggctg tgttggtttt gaggcagtgc      600
tcttgctggt agctctggct gtcagggcaa tgaacaaacc tgctgagtat gacagtgatg      660
acgaaattat agcaattggc cgaagcccta ccatccggca gccactgatc catacccaaa      720
atgttcctgc cactggtggt cctgtcccaa cacttgatca acgtgcaagt agaaatgatg      780
cctggagcca aaggatgcga gagaagtatg gtctggacac gagccagttc acatacaacc      840
cttcagaccc aagcaggtac c
```

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1499691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

Met	Ala	Ala	Cys	Arg	Gly	Phe	Phe	Glu	Cys	Leu	Leu	Arg	Leu	Leu	Asn
1			5					10						15	
Phe	Ile	Leu	Thr	Val	Ala	Gly	Leu	Ala	Met	Val	Gly	Tyr	Gly	Ile	Tyr
		20						25					30		
Leu	Leu	Val	Glu	Trp	Met	Lys	Ile	Ser	Xaa	Asp	Gly	Ile	Xaa	Gly	Ala
		35					40					45			
Ser	Thr	Ala	Xaa	Val	Leu	Val	Ser	Xaa	Arg	Pro	Leu	Leu	Gly	Ala	Val
	50					55					60				
Ile	Leu	Gly	Asp	Ser	Phe	Leu	Asp	Asn	Leu	Pro	Lys	Ala	Trp	Phe	Ile
65					70				75					80	
Tyr	Leu	Phe	Ile	Gly	Val	Gly	Thr	Ile	Val	Ile	Leu	Val	Ser	Leu	Phe
			85					90						95	
Gly	Cys	Ile	Gly	Ala	Gly	Thr	Arg	Asn	Thr	Cys	Cys	Leu	Cys	Phe	Tyr
		100						105						110	
Ala	Phe	Leu	Val	Ile	Leu	Leu	Ile	Leu	Ala	Glu	Ala	Ala	Ala	Ala	Ala
		115					120					125			
Phe	Ile	Phe	Phe	Asp	His	Gly	Trp	Lys	Asp	Val	Ile	Pro	Val	Asp	Lys
	130					135					140				
Thr	His	Asn	Phe	Asp	Val	Met	Tyr	Asp	Phe	Leu	Lys	Glu	Asn	Trp	Glu
145					150				155					160	
Ile	Ala	Arg	Trp	Val	Ala	Leu	Gly	Val	Val	Val	Phe	Glu	Ala	Val	Leu
			165					170						175	
Leu	Leu	Leu	Ala	Leu	Ala	Val	Arg	Ala	Met	Asn	Lys	Pro	Ala	Glu	Tyr
		180						185					190		
Asp	Ser	Asp	Asp	Glu	Ile	Ile	Ala	Ile	Gly	Arg	Ser	Pro	Thr	Ile	Arg
		195					200					205			
Gln	Pro	Leu	Ile	His	Thr	Gln	Asn	Val	Pro	Ala	Thr	Gly	Val	Pro	Val
	210					215						220			
Pro	Thr	Leu	Asp	Gln	Arg	Ala	Ser	Arg	Asn	Asp	Ala	Trp	Ser	Gln	Arg
225				230					235					240	
Met	Arg	Glu	Lys	Tyr	Gly	Leu	Asp	Thr	Ser	Gln	Phe	Thr	Tyr	Asn	Pro
			245					250						255	
Ser	Asp	Pro	Ser	Arg	Tyr										
			260												

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1499692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

Met	Val	Gly	Tyr	Gly	Ile	Tyr	Leu	Leu	Val	Glu	Trp	Met	Lys	Ile	Ser
1			5						10					15	
Xaa	Asp	Gly	Ile	Xaa	Gly	Ala	Ser	Thr	Ala	Xaa	Val	Leu	Val	Ser	Xaa
		20						25					30		
Arg	Pro	Leu	Leu	Gly	Ala	Val	Ile	Leu	Gly	Asp	Ser	Phe	Leu	Asp	Asn
		35					40					45			
Leu	Pro	Lys	Ala	Trp	Phe	Ile	Tyr	Leu	Phe	Ile	Gly	Val	Gly	Thr	Ile
	50					55					60				
Val	Ile	Leu	Val	Ser	Leu	Phe	Gly	Cys	Ile	Gly	Ala	Gly	Thr	Arg	Asn
65					70				75					80	

Thr Cys Cys Leu Cys Phe Tyr Ala Phe Leu Val Ile Leu Leu Ile Leu  
85 90 95  
Ala Glu Ala Ala Ala Ala Phe Ile Phe Phe Asp His Gly Trp Lys  
100 105 110  
Asp Val Ile Pro Val Asp Lys Thr His Asn Phe Asp Val Met Tyr Asp  
115 120 125  
Phe Leu Lys Glu Asn Trp Glu Ile Ala Arg Trp Val Ala Leu Gly Val  
130 135 140  
Val Val Phe Glu Ala Val Leu Leu Leu Leu Ala Leu Ala Val Arg Ala  
145 150 155 160  
Met Asn Lys Pro Ala Glu Tyr Asp Ser Asp Asp Glu Ile Ile Ala Ile  
165 170 175  
Gly Arg Ser Pro Thr Ile Arg Gln Pro Leu Ile His Thr Gln Asn Val  
180 185 190  
Pro Ala Thr Gly Val Pro Val Pro Thr Leu Asp Gln Arg Ala Ser Arg  
195 200 205  
Asn Asp Ala Trp Ser Gln Arg Met Arg Glu Lys Tyr Gly Leu Asp Thr  
210 215 220  
Ser Gln Phe Thr Tyr Asn Pro Ser Asp Pro Ser Arg Tyr  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1499693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

Met Lys Ile Ser Xaa Asp Gly Ile Xaa Gly Ala Ser Thr Ala Xaa Val  
1 5 10 15  
Leu Val Ser Xaa Arg Pro Leu Leu Gly Ala Val Ile Leu Gly Asp Ser  
20 25 30  
Phe Leu Asp Asn Leu Pro Lys Ala Trp Phe Ile Tyr Leu Phe Ile Gly  
35 40 45  
Val Gly Thr Ile Val Ile Leu Val Ser Leu Phe Gly Cys Ile Gly Ala  
50 55 60  
Gly Thr Arg Asn Thr Cys Cys Leu Cys Phe Tyr Ala Phe Leu Val Ile  
65 70 75 80  
Leu Leu Ile Leu Ala Glu Ala Ala Ala Ala Phe Ile Phe Phe Asp  
85 90 95  
His Gly Trp Lys Asp Val Ile Pro Val Asp Lys Thr His Asn Phe Asp  
100 105 110  
Val Met Tyr Asp Phe Leu Lys Glu Asn Trp Glu Ile Ala Arg Trp Val  
115 120 125  
Ala Leu Gly Val Val Val Phe Glu Ala Val Leu Leu Leu Leu Ala Leu  
130 135 140  
Ala Val Arg Ala Met Asn Lys Pro Ala Glu Tyr Asp Ser Asp Asp Glu  
145 150 155 160  
Ile Ile Ala Ile Gly Arg Ser Pro Thr Ile Arg Gln Pro Leu Ile His  
165 170 175  
Thr Gln Asn Val Pro Ala Thr Gly Val Pro Val Pro Thr Leu Asp Gln  
180 185 190  
Arg Ala Ser Arg Asn Asp Ala Trp Ser Gln Arg Met Arg Glu Lys Tyr  
195 200 205  
Gly Leu Asp Thr Ser Gln Phe Thr Tyr Asn Pro Ser Asp Pro Ser Arg  
210 215 220  
Tyr

225

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

aatatcatgc	gcaggggctg	aaagctgaaa	ctgctcaaga	cgccaccgtc	ttcctccgcg	60
atcttcagtt	ctctgtctct	ccctctctct	ttcctctagc	tcccaaccaa	gccaagagta	120
cgctgtcaag	cgcgccgcs	g	tggtgtgtgt	cagtaggcta	cagggctcgg	180
tcattgagctt	gacgagcatg	atggaggcgc	ggctgcccgc	ggggttccgg	ttccacccga	240
gggacgacga	gctcgtgctc	gactacctct	gccgcaagct	ctccggcaaa	ggcggcgggc	300
gasgtacggc	ggcatcgcat	ggtcgacgtc	gacctcaaca	agtgcgagcc	gtgggatctt	360
ccagacgagg	cgtrcrtggg	cggccgcgag	tggtacttct	tcagcctgca	cgaccgcaag	420
tacgccacgg	ggcag					

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

Tyr	His	Ala	Gln	Gly	Leu	Lys	Ala	Glu	Thr	Ala	Gln	Asp	Ala	Thr	Val	
1				5					10					15		
Phe	Leu	Arg	Asp	Leu	Gln	Phe	Ser	Val	Ser	Pro	Ser	Leu	Phe	Pro	Leu	
		20						25					30			
Ala	Pro	Asn	Gln	Ala	Lys	Ser	Thr	Ser	Ser	Ser	Ala	Pro	Xaa	Xaa	Cys	
		35					40					45				
Val	Ser	Val	Gly	Tyr	Arg	Ala	Arg	Arg	Asn	Ala	Val	Met	Ser	Leu	Ile	
	50					55					60					
Ser	Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	Arg	Phe	His	Pro	Arg	
65			70						75				80			
Asp	Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys	Leu	Ser	Gly	Lys	
		85						90					95			
Gly	Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg	Arg	Arg	Pro	Gln	
		100						105				110				
Gln	Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa	Xaa	Gly	Arg	Pro	
	115					120					125					
Arg	Val	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val	Arg	His	Gly	Ala	
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..84  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

Met	Ser	Leu	Ile	Ser	Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	Arg
1			5						10					15	
Phe	His	Pro	Arg	Asp	Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys
			20					25					30		
Leu	Ser	Gly	Lys	Gly	Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg
		35					40					45			
Arg	Arg	Pro	Gln	Gln	Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa
	50					55				60					
Xaa	Gly	Arg	Pro	Arg	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val	
65					70				75					80	
Arg	His	Gly	Ala												

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	His	Pro	Arg	Asp
1			5					10				15	
Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys	Leu	Ser	Gly
			20					25				30	
Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg	Arg	Arg	Pro
		35					40					45	
Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa	Xaa	Gly	Arg
	50					55				60			
Val	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val	Arg	His	Gly
65					70				75				

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1156  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

atttttcgctc	aaaagaatca	gtaaaaacta	aacattttga	ctatataccta	cttgaatcaa	60
ttcttcggct	gattttgaag	ttttgtgaca	ttcagatatt	ctagggtttt	gtggtaaagt	120
gaatcgaatc	acgaaggcaa	cgcgatacaa	gtgattgacc	aagtaacaac	catgacccat	180
ctgtctgacc	cgaatccgaa	aaccaaaccg	ggtatgatgc	tcatgaaaca	agaagacggg	240
tatttgcagc	cggatgaagac	taaaccggct	ccgaagagac	cgacttctaa	agaccgtcac	300
acgaaagtag	aaggacgagc	tcggaggatc	cgaatgccgc	cgggttgccg	tgctcgggtc	360
tttcaattga	cccgatgaact	tggtcacaaa	tccgacggag	aaacgatacg	gtgggttattg	420
gaacgagctg	aaccggcgat	aattgaagca	accggaaccg	gaactgtacc	ggctattgct	480
gtatcgggta	acggaacttt	aaaaatcccc	acgagctctc	cagtgttgaa	tgacggcggc	540
cgtgacgggtg	acgggtgacct	aatgaagaaa	cggaggaaga	gaaactgtac	gagcgatttc	600
gtagacgtta	atgacagctg	tcatagctcc	gttacttctg	ggtttagctcc	gataacggcg	660



```
tcaaactacg gcggttaatat cctgaacggt aatacacagg ggtttgtgcc gttttggcct 720
atgggtatgg gtactgcgta tgttactggt gggccggatc aaatgggcca aatgtgggct 780
attcctaccg ttgctacagc tccgtttctc aatgttggtg ctagaccggt gtctagttat 840
gtctcaaacg cttcagacgc tgaggcggag atggaaacga gcggtggcgg aacgacgcaa 900
ccgctgaggg atttttcgtt ggagatttat gataagagag agcttcagtt tttgggtggc 960
tcagggaact catctccgtc ttcatgtcat gagacttaag gaattttaac tcttagttct 1020
agtttctttt tagtttttag taagttagtgc tcctgattta ggtaagtaa gatttgtaaa 1080
agaattggga gcacaatttc aattttatgt ttctgtcaaa cattttggta attaataaaa 1140
ctatcctatc attttt
```

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1499721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

```
Met Glu Ser Asn His Glu Gly Asn Ala Ile Gln Val Ile Asp Gln Val
1      5      10      15
Thr Thr Met Thr His Leu Ser Asp Pro Asn Pro Lys Thr Lys Pro Gly
20      25      30
Met Met Leu Met Lys Gln Glu Asp Gly Tyr Leu Gln Pro Val Lys Thr
35      40      45
Lys Pro Ala Pro Lys Arg Pro Thr Ser Lys Asp Arg His Thr Lys Val
50      55      60
Glu Gly Arg Gly Arg Arg Ile Arg Met Pro Ala Gly Cys Ala Ala Arg
65      70      75      80
Val Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr
85      90      95
Ile Arg Trp Leu Leu Glu Arg Ala Glu Pro Ala Ile Ile Glu Ala Thr
100      105      110
Gly Thr Gly Thr Val Pro Ala Ile Ala Val Ser Val Asn Gly Thr Leu
115      120      125
Lys Ile Pro Thr Ser Ser Pro Val Leu Asn Asp Gly Gly Arg Asp Gly
130      135      140
Asp Gly Asp Leu Met Lys Lys Arg Arg Lys Arg Asn Cys Thr Ser Asp
145      150      155      160
Phe Val Asp Val Asn Asp Ser Cys His Ser Ser Val Thr Ser Gly Leu
165      170      175
Ala Pro Ile Thr Ala Ser Asn Tyr Gly Val Asn Ile Leu Asn Val Asn
180      185      190
Thr Gln Gly Phe Val Pro Phe Trp Pro Met Gly Met Gly Thr Ala Tyr
195      200      205
Val Thr Gly Gly Pro Asp Gln Met Gly Gln Met Trp Ala Ile Pro Thr
210      215      220
Val Ala Thr Ala Pro Phe Leu Asn Val Gly Ala Arg Pro Val Ser Ser
225      230      235      240
Tyr Val Ser Asn Ala Ser Asp Ala Glu Ala Glu Met Glu Thr Ser Gly
245      250      255
Gly Gly Thr Thr Gln Pro Leu Arg Asp Phe Ser Leu Glu Ile Tyr Asp
260      265      270
Lys Arg Glu Leu Gln Phe Leu Gly Gly Ser Gly Asn Ser Ser Pro Ser
275      280      285
Ser Cys His Glu Thr
290
```

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..275  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499722  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met	Thr	His	Leu	Ser	Asp	Pro	Asn	Pro	Lys	Thr	Lys	Pro	Gly	Met	Met
1			5					10						15	
Leu	Met	Lys	Gln	Glu	Asp	Gly	Tyr	Leu	Gln	Pro	Val	Lys	Thr	Lys	Pro
			20					25						30	
Ala	Pro	Lys	Arg	Pro	Thr	Ser	Lys	Asp	Arg	His	Thr	Lys	Val	Glu	Gly
			35					40						45	
Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Gly	Cys	Ala	Ala	Arg	Val	Phe
			50					55						60	
Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp	Gly	Glu	Thr	Ile	Arg
65								70						75	
Trp	Leu	Leu	Glu	Arg	Ala	Glu	Pro	Ala	Ile	Ile	Glu	Ala	Thr	Gly	Thr
			85					90						95	
Gly	Thr	Val	Pro	Ala	Ile	Ala	Val	Ser	Val	Asn	Gly	Thr	Leu	Lys	Ile
			100					105						110	
Pro	Thr	Ser	Ser	Pro	Val	Leu	Asn	Asp	Gly	Gly	Arg	Asp	Gly	Asp	Gly
			115					120						125	
Asp	Leu	Met	Lys	Lys	Arg	Arg	Lys	Arg	Asn	Cys	Thr	Ser	Asp	Phe	Val
			130					135						140	
Asp	Val	Asn	Asp	Ser	Cys	His	Ser	Ser	Val	Thr	Ser	Gly	Leu	Ala	Pro
145								150						155	
Ile	Thr	Ala	Ser	Asn	Tyr	Gly	Val	Asn	Ile	Leu	Asn	Val	Asn	Thr	Gln
			165					170						175	
Gly	Phe	Val	Pro	Phe	Trp	Pro	Met	Gly	Met	Gly	Thr	Ala	Tyr	Val	Thr
			180					185						190	
Gly	Gly	Pro	Asp	Gln	Met	Gly	Gln	Met	Trp	Ala	Ile	Pro	Thr	Val	Ala
			195					200						205	
Thr	Ala	Pro	Phe	Leu	Asn	Val	Gly	Ala	Arg	Pro	Val	Ser	Ser	Tyr	Val
			210					215						220	
Ser	Asn	Ala	Ser	Asp	Ala	Glu	Ala	Glu	Met	Glu	Thr	Ser	Gly	Gly	Gly
225								230						235	
Thr	Thr	Gln	Pro	Leu	Arg	Asp	Phe	Ser	Leu	Glu	Ile	Tyr	Asp	Lys	Arg
			245					250						255	
Glu	Leu	Gln	Phe	Leu	Gly	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Ser	Ser	Cys
			260					265						270	
His	Glu	Thr													
			275												

(2) INFORMATION FOR SEQ ID NO:1135:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..261  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499723  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

Met	Met	Leu	Met	Lys	Gln	Glu	Asp	Gly	Tyr	Leu	Gln	Pro	Val	Lys	Thr
1				5						10				15	
Lys	Pro	Ala	Pro	Lys	Arg	Pro	Thr	Ser	Lys	Asp	Arg	His	Thr	Lys	Val

(X1) Sequence alignment of the 1000 bp						
cattaacggt	gttgcagagt	aaagctggaa	aatagagagt	tcgatgaact	cttgttacta	60
taatggaggc	tcaggagttt	gaaaaccgag	agatttcccc	cggttcgagg	ttcctgattg	120
agaatcagat	cagaagtagc	tcaatatggt	gacaactacc	accgatgagg	aaatagactt	180
gtcctgcgac	ggaggtgtca	cggagcctca	aaaagttgct	ataatcttcg	cgttttgtgg	240
tgtaggatac	caaggaatgc	aaaagaatcc	cggcgcgaaa	accattgaag	gcgagctcga	300
agaagctttg	tttcatgccg	gagctgtacc	ggagtccatt	agaggcaagc	caaaaactata	360
cgatttcgca	cgatctgcac	ggacagataa	aggagttagt	gctgtggac	aagtagtttc	420
aggtcgcttt	atcgttgatc	cacttggatt	cgtaaatcgt	ctcaattcaa	atctccctaa	480
tcagattaga	atcttctggt	acaagcatgt	aacgccgtcg	tttagctcca	agaagttttg	540
cgatcgaaga	aggatatgtt	atctgcttcc	agtgtttgct	cttgatccaa	tctcgcacgc	600
tgatagagaa	acagtaatgg	ctagtttggg	tccgggagag	gaatatgtta	agtgccttga	660
gtgctcagag	agaggtcgta	agattcctcc	aggctcttg	ggtaaattga	aaggtaccaa	720
ctttgggact	aaatcattgg	atcttcagtc	agacatttcg	tcgaacaact	ctagtgcatt	780
aagaagtgc	atcaagattg	aagctttgag	ttctaattta	gctggcttat	gctcagtaga	840
tgttgaagta	ggtaggatac	aagaagacag	ttgtaaatg	aatacaaat	catcagagac	900
taaggtaaag	agcaagtttt	gttatggtga	aaaggaaaag	gaagggttca	gtagaatact	960
aagttggtat	gttggtatcat	ataatttcca	taacttcact	acaagaacaa	aagcagatga	1020
tccgactgcg	aatcgtcaaa	tcattctcct	cactgctaatt	actgtgatta	atcttgatgg	1080

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gattgacttt atcaagtgtg aagtcttagg caaaagcttt atgcttcatc agattcggaa 1140
gatgatgggt cttgctgttg caatcatgcg gaattgtgct tctgaatcac ttatccaaag 1200
tgctttcagc aaggatgtga atataactgt accaatggcg ccagaagttg gactttatct 1260
ggacgaatgc ttcttcacat cttataacag aaactttgaa gacagtcacg aagaagtgtc 1320
catggaagca tacaagaag aagctgaagc attcaaattg aagcatatct attctcatat 1380
cggcgctaca gagcgaaaat acggaaatat ggctcttttg ttacattcct tgaactatag 1440
aaactatcca gacctaaact ttggcagctg tggacaaaac acagaccaag ttcttgttca 1500
taagaaaatt gatgaaagag caagtcatag tctctaagca aaatgatgga agcttagttt 1560
gaagattttg acattgtttt tgttattgtt ggttaatccc accatttttg taacttttta 1620
atcaaattag tatatttttg tgttgtaagg tgacactaat gaattgattt gttatcctcc 1680
```

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1499729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

```
Met Leu Thr Thr Thr Thr Asp Glu Glu Ile Asp Leu Ser Cys Asp Gly
1          5          10          15
Gly Val Thr Glu Pro Gln Lys Val Ala Ile Ile Phe Ala Phe Cys Gly
20          25          30
Val Gly Tyr Gln Gly Met Gln Lys Asn Pro Gly Ala Lys Thr Ile Glu
35          40          45
Gly Glu Leu Glu Glu Ala Leu Phe His Ala Gly Ala Val Pro Glu Ser
50          55          60
Ile Arg Gly Lys Pro Lys Leu Tyr Asp Phe Ala Arg Ser Ala Arg Thr
65          70          75          80
Asp Lys Gly Val Ser Ala Val Gly Gln Val Val Ser Gly Arg Phe Ile
85          90          95
Val Asp Pro Leu Gly Phe Val Asn Arg Leu Asn Ser Asn Leu Pro Asn
100         105         110
Gln Ile Arg Ile Phe Gly Tyr Lys His Val Thr Pro Ser Phe Ser Ser
115         120         125
Lys Lys Phe Cys Asp Arg Arg Arg Tyr Val Tyr Leu Leu Pro Val Phe
130         135         140
Ala Leu Asp Pro Ile Ser His Arg Asp Arg Glu Thr Val Met Ala Ser
145         150         155         160
Leu Gly Pro Gly Glu Glu Tyr Val Lys Cys Phe Glu Cys Ser Glu Arg
165         170         175
Gly Arg Lys Ile Pro Pro Gly Leu Val Gly Lys Trp Lys Gly Thr Asn
180         185         190
Phe Gly Thr Lys Ser Leu Asp Phe Gln Ser Asp Ile Ser Ser Asn Asn
195         200         205
Ser Ser Ala Leu Arg Ser Asp Ile Lys Ile Glu Ala Leu Ser Ser Asn
210         215         220
Leu Ala Gly Leu Cys Ser Val Asp Val Glu Val Gly Arg Ile Gln Glu
225         230         235         240
Asp Ser Cys Lys Leu Asn Thr Asn Ser Ser Glu Thr Lys Val Lys Ser
245         250         255
Lys Phe Cys Tyr Gly Glu Lys Glu Lys Glu Arg Phe Ser Arg Ile Leu
260         265         270
Ser Cys Tyr Val Gly Ser Tyr Asn Phe His Asn Phe Thr Thr Arg Thr
275         280         285
Lys Ala Asp Asp Pro Thr Ala Asn Arg Gln Ile Ile Ser Phe Thr Ala
290         295         300
```

Asn Thr Val Ile Asn Leu Asp Gly Ile Asp Phe Ile Lys Cys Glu Val  
305 310 315 320  
Leu Gly Lys Ser Phe Met Leu His Gln Ile Arg Lys Met Met Gly Leu  
325 330 335  
Ala Val Ala Ile Met Arg Asn Cys Ala Ser Glu Ser Leu Ile Gln Ser  
340 345 350  
Ala Phe Ser Lys Asp Val Asn Ile Thr Val Pro Met Ala Pro Glu Val  
355 360 365  
Gly Leu Tyr Leu Asp Glu Cys Phe Phe Thr Ser Tyr Asn Arg Asn Phe  
370 375 380  
Glu Asp Ser His Glu Glu Val Ser Met Glu Ala Tyr Lys Glu Glu Ala  
385 390 395 400  
Glu Ala Phe Lys Leu Lys His Ile Tyr Ser His Ile Gly Ala Thr Glu  
405 410 415  
Arg Lys Tyr Gly Asn Met Ala Leu Trp Leu His Ser Leu Asn Tyr Arg  
420 425 430  
Asn Tyr Pro Asp Leu Asn Phe Gly Ser Cys Gly Gln Asn Thr Asp Gln  
435 440 445  
Val Leu Val His Lys Lys Ile Asp Glu Arg Ala Ser His Ser Leu  
450 455 460

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

Met Gln Lys Asn Pro Gly Ala Lys Thr Ile Glu Gly Glu Leu Glu Glu  
1 5 10 15  
Ala Leu Phe His Ala Gly Ala Val Pro Glu Ser Ile Arg Gly Lys Pro  
20 25 30  
Lys Leu Tyr Asp Phe Ala Arg Ser Ala Arg Thr Asp Lys Gly Val Ser  
35 40 45  
Ala Val Gly Gln Val Val Ser Gly Arg Phe Ile Val Asp Pro Leu Gly  
50 55 60  
Phe Val Asn Arg Leu Asn Ser Asn Leu Pro Asn Gln Ile Arg Ile Phe  
65 70 75 80  
Gly Tyr Lys His Val Thr Pro Ser Phe Ser Ser Lys Lys Phe Cys Asp  
85 90 95  
Arg Arg Arg Tyr Val Tyr Leu Leu Pro Val Phe Ala Leu Asp Pro Ile  
100 105 110  
Ser His Arg Asp Arg Glu Thr Val Met Ala Ser Leu Gly Pro Gly Glu  
115 120 125  
Glu Tyr Val Lys Cys Phe Glu Cys Ser Glu Arg Gly Arg Lys Ile Pro  
130 135 140  
Pro Gly Leu Val Gly Lys Trp Lys Gly Thr Asn Phe Gly Thr Lys Ser  
145 150 155 160  
Leu Asp Phe Gln Ser Asp Ile Ser Ser Asn Asn Ser Ser Ala Leu Arg  
165 170 175  
Ser Asp Ile Lys Ile Glu Ala Leu Ser Ser Asn Leu Ala Gly Leu Cys  
180 185 190  
Ser Val Asp Val Glu Val Gly Arg Ile Gln Glu Asp Ser Cys Lys Leu  
195 200 205  
Asn Thr Asn Ser Ser Glu Thr Lys Val Lys Ser Lys Phe Cys Tyr Gly  
210 215 220  
Glu Lys Glu Lys Glu Arg Phe Ser Arg Ile Leu Ser Cys Tyr Val Gly

225					230					235				240	
Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr	Thr	Arg	Thr	Lys	Ala	Asp	Asp	Pro
				245					250					255	
Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser	Phe	Thr	Ala	Asn	Thr	Val	Ile	Asn
			260					265					270		
Leu	Asp	Gly	Ile	Asp	Phe	Ile	Lys	Cys	Glu	Val	Leu	Gly	Lys	Ser	Phe
		275					280					285			
Met	Leu	His	Gln	Ile	Arg	Lys	Met	Met	Gly	Leu	Ala	Val	Ala	Ile	Met
	290					295				300					
Arg	Asn	Cys	Ala	Ser	Glu	Ser	Leu	Ile	Gln	Ser	Ala	Phe	Ser	Lys	Asp
305					310					315					320
Val	Asn	Ile	Thr	Val	Pro	Met	Ala	Pro	Glu	Val	Gly	Leu	Tyr	Leu	Asp
			325						330					335	
Glu	Cys	Phe	Phe	Thr	Ser	Tyr	Asn	Arg	Asn	Phe	Glu	Asp	Ser	His	Glu
			340					345					350		
Glu	Val	Ser	Met	Glu	Ala	Tyr	Lys	Glu	Glu	Ala	Glu	Ala	Phe	Lys	Leu
		355					360					365			
Lys	His	Ile	Tyr	Ser	His	Ile	Gly	Ala	Thr	Glu	Arg	Lys	Tyr	Gly	Asn
	370					375					380				
Met	Ala	Leu	Trp	Leu	His	Ser	Leu	Asn	Tyr	Arg	Asn	Tyr	Pro	Asp	Leu
385					390					395					400
Asn	Phe	Gly	Ser	Cys	Gly	Gln	Asn	Thr	Asp	Gln	Val	Leu	Val	His	Lys
				405					410					415	
Lys	Ile	Asp	Glu	Arg	Ala	Ser	His	Ser	Leu						
			420					425							

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1499731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

Met	Ala	Ser	Leu	Gly	Pro	Gly	Glu	Glu	Tyr	Val	Lys	Cys	Phe	Glu	Cys
1			5				10							15	
Ser	Glu	Arg	Gly	Arg	Lys	Ile	Pro	Pro	Gly	Leu	Val	Gly	Lys	Trp	Lys
			20				25						30		
Gly	Thr	Asn	Phe	Gly	Thr	Lys	Ser	Leu	Asp	Phe	Gln	Ser	Asp	Ile	Ser
		35				40					45				
Ser	Asn	Asn	Ser	Ser	Ala	Leu	Arg	Ser	Asp	Ile	Lys	Ile	Glu	Ala	Leu
	50					55					60				
Ser	Ser	Asn	Leu	Ala	Gly	Leu	Cys	Ser	Val	Asp	Val	Glu	Val	Gly	Arg
65					70					75					80
Ile	Gln	Glu	Asp	Ser	Cys	Lys	Leu	Asn	Thr	Asn	Ser	Ser	Glu	Thr	Lys
			85						90					95	
Val	Lys	Ser	Lys	Phe	Cys	Tyr	Gly	Glu	Lys	Glu	Lys	Glu	Arg	Phe	Ser
			100					105					110		
Arg	Ile	Leu	Ser	Cys	Tyr	Val	Gly	Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr
		115					120					125			
Thr	Arg	Thr	Lys	Ala	Asp	Asp	Pro	Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser
	130					135						140			
Phe	Thr	Ala	Asn	Thr	Val	Ile	Asn	Leu	Asp	Gly	Ile	Asp	Phe	Ile	Lys
145					150					155					160
Cys	Glu	Val	Leu	Gly	Lys	Ser	Phe	Met	Leu	His	Gln	Ile	Arg	Lys	Met
			165						170					175	
Met	Gly	Leu	Ala	Val	Ala	Ile	Met	Arg	Asn	Cys	Ala	Ser	Glu	Ser	Leu
			180					185						190	

Ile Gln Ser Ala Phe Ser Lys Asp Val Asn Ile Thr Val Pro Met Ala  
195 200 205  
Pro Glu Val Gly Leu Tyr Leu Asp Glu Cys Phe Phe Thr Ser Tyr Asn  
210 215 220  
Arg Asn Phe Glu Asp Ser His Glu Glu Val Ser Met Glu Ala Tyr Lys  
225 230 235 240  
Glu Glu Ala Glu Ala Phe Lys Leu Lys His Ile Tyr Ser His Ile Gly  
245 250 255  
Ala Thr Glu Arg Lys Tyr Gly Asn Met Ala Leu Trp Leu His Ser Leu  
260 265 270  
Asn Tyr Arg Asn Tyr Pro Asp Leu Asn Phe Gly Ser Cys Gly Gln Asn  
275 280 285  
Thr Asp Gln Val Leu Val His Lys Lys Ile Asp Glu Arg Ala Ser His  
290 295 300  
Ser Leu  
305

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1402

(D) OTHER INFORMATION: / Ceres Seq. ID 1499732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

gggatgtttg	tgaccttttg	tctcttcttc	tctaaaattc	tctttctccc	aaaaactaaa	60
aaaacaaaaa	aaacaaaaaa	tgtacgcaat	gaaagaagaa	gactgtcttc	aaacatttca	120
caacttacaa	gactatcaag	accagtttca	tcttcatcat	catccacaaa	ttctcccctg	180
gtcgtcgaca	tctttacctt	cttttgacct	actccatttc	ccatctaacc	cgaccctgta	240
ttctgaccgg	gttactact	tcaacagaag	agcttcttct	tcctcttctt	cttttgacta	300
taacgacggg	tttgtctctc	ctcctccttc	catggatcat	cctcagaacc	atctaaggat	360
tttatccgaa	gctcttggac	ccatcatgcg	tcgtggctcg	tcctttgggt	tcgatgggtga	420
gatcatggga	aaattgagtg	cacaagaagt	catggatgct	aaggctttag	ctgcttcaaa	480
gagtcatagt	gaagctgaga	gaagaagacg	agagagaatc	aacactcatc	ttgctaagct	540
gcgtagtata	ttaccaaaca	caaccaaacc	ggacaaaagt	tctttgctag	cggaagtgat	600
ccaacacatg	aaggagctaa	aacgacaaac	atcacagatc	accgacacgt	atcaagtccc	660
aacagagtgc	gatgatctga	ccgtagattc	gtcttacaac	gacgaggaag	gaaacttggt	720
gataagagca	tccttttgct	gccaaagacg	gactgacctc	atgcatgacg	tcataaatgc	780
cttaaagtct	cttctgtctc	gaactctcaa	agctgagatc	gcaaccgtag	gtggtagagt	840
caagaacatc	ttgttcttga	gccgagaata	cgatgatgaa	gaagatcatg	attcatatcg	900
tagaaacttc	gatgggtgatg	acgtggagga	ttatgatgaa	gagaggatga	tgaataatcg	960
tgtgagttcg	atagaagaag	cgtaaaggcg	ggttatagag	aagtgtgttc	ataataatga	1020
tgaaagtaac	gataacaata	acttgagaaa	atcatcttca	gggggtatta	agaggcaaaag	1080
gactagtaag	atgggtgaatc	gatgttataa	ttagttaatt	aagtcaagtc	tttattaact	1140
aggggttagtt	aattagactt	gcaaaatggg	atgttgattat	gggttggtga	tattagtatt	1200
attttcggtg	tttttagtag	ttgggattgg	gtttattctt	ctatgttttt	ttaatctatg	1260
aagaaccctt	tgtttagggg	tttatagtga	tgagtttggt	ttatatatgg	tagttaagac	1320
attttatcgt	cttaattaat	ataggaaatg	tatagagctt	gggtttgtat	taatttatca	1380
agaagttttt	tttatcatat	tc				

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1499733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

```
Met Tyr Ala Met Lys Glu Glu Asp Cys Leu Gln Thr Phe His Asn Leu
1      5      10      15
Gln Asp Tyr Gln Asp Gln Phe His Leu His His His Pro Gln Ile Leu
20      25      30
Pro Trp Ser Ser Thr Ser Leu Pro Ser Phe Asp Pro Leu His Phe Pro
35      40      45
Ser Asn Pro Thr Arg Tyr Ser Asp Pro Val His Tyr Phe Asn Arg Arg
50      55      60
Ala Ser Ser Ser Ser Ser Ser Phe Asp Tyr Asn Asp Gly Phe Val Ser
65      70      75      80
Pro Pro Pro Ser Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser
85      90      95
Glu Ala Leu Gly Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp
100      105      110
Gly Glu Ile Met Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys
115      120      125
Ala Leu Ala Ala Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg
130      135      140
Glu Arg Ile Asn Thr His Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn
145      150      155      160
Thr Thr Lys Thr Asp Lys Ala Ser Leu Leu Ala Glu Val Ile Gln His
165      170      175
Met Lys Glu Leu Lys Arg Gln Thr Ser Gln Ile Thr Asp Thr Tyr Gln
180      185      190
Val Pro Thr Glu Cys Asp Asp Leu Thr Val Asp Ser Ser Tyr Asn Asp
195      200      205
Glu Glu Gly Asn Leu Val Ile Arg Ala Ser Phe Cys Cys Gln Asp Arg
210      215      220
Thr Asp Leu Met His Asp Val Ile Asn Ala Leu Lys Ser Leu Arg Leu
225      230      235      240
Arg Thr Leu Lys Ala Glu Ile Ala Thr Val Gly Gly Arg Val Lys Asn
245      250      255
Ile Leu Phe Leu Ser Arg Glu Tyr Asp Asp Glu Glu Asp His Asp Ser
260      265      270
Tyr Arg Arg Asn Phe Asp Gly Asp Asp Val Glu Asp Tyr Asp Glu Glu
275      280      285
Arg Met Met Asn Asn Arg Val Ser Ser Ile Glu Glu Ala Leu Lys Ala
290      295      300
Val Ile Glu Lys Cys Val His Asn Asn Asp Glu Ser Asn Asp Asn Asn
305      310      315      320
Asn Leu Glu Lys Ser Ser Ser Gly Gly Ile Lys Arg Gln Arg Thr Ser
325      330      335
Lys Met Val Asn Arg Cys Tyr Asn
340
```

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1499734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

```
Met Lys Glu Glu Asp Cys Leu Gln Thr Phe His Asn Leu Gln Asp Tyr
1      5      10      15
```



Gln Asp Gln Phe His Leu His His His Pro Gln Ile Leu Pro Trp Ser  
20 25 30  
Ser Thr Ser Leu Pro Ser Phe Asp Pro Leu His Phe Pro Ser Asn Pro  
35 40 45  
Thr Arg Tyr Ser Asp Pro Val His Tyr Phe Asn Arg Arg Ala Ser Ser  
50 55 60  
Ser Ser Ser Ser Phe Asp Tyr Asn Asp Gly Phe Val Ser Pro Pro Pro  
65 70 75 80  
Ser Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser Glu Ala Leu  
85 90 95  
Gly Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp Gly Glu Ile  
100 105 110  
Met Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys Ala Leu Ala  
115 120 125  
Ala Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile  
130 135 140  
Asn Thr His Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn Thr Thr Lys  
145 150 155 160  
Thr Asp Lys Ala Ser Leu Leu Ala Glu Val Ile Gln His Met Lys Glu  
165 170 175  
Leu Lys Arg Gln Thr Ser Gln Ile Thr Asp Thr Tyr Gln Val Pro Thr  
180 185 190  
Glu Cys Asp Asp Leu Thr Val Asp Ser Ser Tyr Asn Asp Glu Glu Gly  
195 200 205  
Asn Leu Val Ile Arg Ala Ser Phe Cys Cys Gln Asp Arg Thr Asp Leu  
210 215 220  
Met His Asp Val Ile Asn Ala Leu Lys Ser Leu Arg Leu Arg Thr Leu  
225 230 235 240  
Lys Ala Glu Ile Ala Thr Val Gly Gly Arg Val Lys Asn Ile Leu Phe  
245 250 255  
Leu Ser Arg Glu Tyr Asp Asp Glu Glu Asp His Asp Ser Tyr Arg Arg  
260 265 270  
Asn Phe Asp Gly Asp Asp Val Glu Asp Tyr Asp Glu Glu Arg Met Met  
275 280 285  
Asn Asn Arg Val Ser Ser Ile Glu Glu Ala Leu Lys Ala Val Ile Glu  
290 295 300  
Lys Cys Val His Asn Asn Asp Glu Ser Asn Asp Asn Asn Asn Leu Glu  
305 310 315 320  
Lys Ser Ser Ser Gly Ile Lys Arg Gln Arg Thr Ser Lys Met Val  
325 330 335  
Asn Arg Cys Tyr Asn  
340

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260

(D) OTHER INFORMATION: / Ceres Seq. ID 1499735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser Glu Ala Leu Gly  
1 5 10 15  
Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp Gly Glu Ile Met  
20 25 30  
Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys Ala Leu Ala Ala  
35 40 45  
Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn

50	55	60
Thr His Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn Thr Thr Lys Thr		
65	70	75
Asp Lys Ala Ser Leu Ala Glu Val Ile Gln His Met Lys Glu Leu		
	85	90
Lys Arg Gln Thr Ser Gln Ile Thr Asp Thr Tyr Gln Val Pro Thr Glu		
	100	105
Cys Asp Asp Leu Thr Val Asp Ser Ser Tyr Asn Asp Glu Glu Gly Asn		
	115	120
Leu Val Ile Arg Ala Ser Phe Cys Cys Gln Asp Arg Thr Asp Leu Met		
	130	135
His Asp Val Ile Asn Ala Leu Lys Ser Leu Arg Leu Arg Thr Leu Lys		
145	150	155
Ala Glu Ile Ala Thr Val Gly Gly Arg Val Lys Asn Ile Leu Phe Leu		
	165	170
Ser Arg Glu Tyr Asp Asp Glu Glu Asp His Asp Ser Tyr Arg Arg Asn		
	180	185
Phe Asp Gly Asp Asp Val Glu Asp Tyr Asp Glu Glu Arg Met Met Asn		
	195	200
Asn Arg Val Ser Ser Ile Glu Glu Ala Leu Lys Ala Val Ile Glu Lys		
	210	215
Cys Val His Asn Asn Asp Glu Ser Asn Asp Asn Asn Leu Glu Lys		
225	230	235
Ser Ser Ser Gly Gly Ile Lys Arg Gln Arg Thr Ser Lys Met Val Asn		
	245	250
Arg Cys Tyr Asn		
	260	

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

aaattcccag	acgtgggtgga	gtgaacaacc	aaaaaaacaa	catgattgat	tgattctgaa	60
attcacttta	attttcaaga	gagagtttct	gaggatcttg	atatcagaat	ctgtcatgag	120
agaagcagga	gaagagaaaag	tggcgtggaa	gtactttacc	agagatgttg	tgccgtttgc	180
tgcgatgttt	gcggtggagt	gtgccactgt	tgggtcaaac	acgctgttta	aggctgctac	240
tttaagagga	ttgagcttct	atgtctttgt	cttctactct	tatatgttt	caacacttct	300
ccttcttcca	ctttctgtaa	tctttggaag	gtcaagaaga	ttaccagcag	ctaagtctcc	360
tcttttcttc	aagattttct	tacttgggct	tggttgattg	ctggttgtaa	aggtattgca	420
tacagttccc	caactcttgc	atctgctatc	agcaatctca	caccggcttt	cacattcaca	480
ctcgctgtta	tcttcaggat	ggagcaagta	aggttaagga	gctctgcgac	ycaggctaaa	540
atcattgggtg	caatactatc	tatatctggt	gctctggtag	ttgtgctgta	taaaggccca	600
caagttctcg	cctctgcata	ttttacaact	gtattaccta	ccgttacact	tcaccagcat	660
ttgacctcaa	tagagtcaag	ctggataatc	ggagggtctc	tgcttgcttc	acagtatttt	720
cttatatccg	tctgactcgt	gtcatggagg	tttaccctga	agagataacc	gtagtcttct	780
tctacaattt	atttgcaaca	ctaattctcag	taccagtatg	tctttttgcg	gagagcaact	840
tgacttcttg	ggtgcttaaa	ccagacattt	ccctcgctgc	aatcatatac	tcgggagctc	900
tcgtttcatt	attcagecgc	cttaccacaa	catgggggtc	gcactctgaag	ggtccggtat	960
acatatccct	gttcaggcca	ttgtctattg	cgattgcagt	cgccatgggt	gctatatctc	1020
tcggcgatgc	acttcacctt	gggagtgtca	ttggatcaay	gatattgtgc	mttggtattc	1080
acactgtgat	ttggggcaaa	gcaagagagg	atacaatcaa	aactgtagct	ggttctgagc	1140
agtcaccttt	gctgcttaca	catatcatag	aagatggagc	ctttccatta	agctaggatt	1200
gatgcaagtg	aaatcccttat	actattttatt	aataaatatg	gatccctaaa	agaggtgtac	1260
catatatgtt	tatatatgtc	tatagttaca	tataagatat	ctgttctttt	tttcttgttt	1320

tattttgatg ttacatatga atgagaatta tgaatctata agaaatattt ggtcctttt

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

Met	Arg	Glu	Ala	Gly	Glu	Glu	Lys	Val	Ala	Trp	Lys	Tyr	Phe	Thr	Arg
1				5					10					15	
Asp	Val	Val	Pro	Phe	Ala	Ala	Met	Phe	Ala	Val	Glu	Cys	Ala	Thr	Val
			20					25					30		
Gly	Ser	Asn	Thr	Leu	Phe	Lys	Ala	Ala	Thr	Leu	Arg	Gly	Leu	Ser	Phe
		35				40					45				
Tyr	Val	Phe	Val	Phe	Tyr	Ser	Tyr	Ile	Val	Ser	Thr	Leu	Leu	Leu	Leu
	50				55					60					
Pro	Leu	Ser	Val	Ile	Phe	Gly	Arg	Ser	Arg	Arg	Leu	Pro	Ala	Ala	Lys
65				70				75					80		
Ser	Pro	Leu	Phe	Phe	Lys	Ile	Phe	Leu	Leu	Gly	Leu	Val	Gly	Leu	Leu
			85					90					95		
Val	Val	Lys	Val	Leu	His	Thr	Val	Pro	Gln	Leu	Leu	His	Leu	Leu	Ser
		100				105						110			
Ala	Ile	Ser	His	Arg	Leu	Ser	His	Ser	His	Ser	Leu	Leu	Ser	Ser	Gly
		115				120						125			
Trp	Ser	Lys													
		130													

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

Met	Phe	Ala	Val	Glu	Cys	Ala	Thr	Val	Gly	Ser	Asn	Thr	Leu	Phe	Lys
1				5					10					15	
Ala	Ala	Thr	Leu	Arg	Gly	Leu	Ser	Phe	Tyr	Val	Phe	Val	Phe	Tyr	Ser
			20					25					30		
Tyr	Ile	Val	Ser	Thr	Leu	Leu	Leu	Leu	Pro	Leu	Ser	Val	Ile	Phe	Gly
	35				40						45				
Arg	Ser	Arg	Arg	Leu	Pro	Ala	Ala	Lys	Ser	Pro	Leu	Phe	Phe	Lys	Ile
	50				55					60					
Phe	Leu	Leu	Gly	Leu	Val	Gly	Leu	Leu	Val	Val	Lys	Val	Leu	His	Thr
65				70				75					80		
Val	Pro	Gln	Leu	Leu	His	Leu	Leu	Ser	Ala	Ile	Ser	His	Arg	Leu	Ser
			85					90					95		
His	Ser	His	Ser	Leu	Leu	Ser	Ser	Gly	Trp	Ser	Lys				
		100				105									

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..150  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499743  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  
Met Glu Val Tyr Pro Glu Glu Ile Thr Val Val Phe Phe Tyr Asn Leu  
1                    5                    10                    15  
Phe Ala Thr Leu Ile Ser Val Pro Val Cys Leu Phe Ala Glu Ser Asn  
                    20                    25                    30  
Leu Thr Ser Trp Val Leu Lys Pro Asp Ile Ser Leu Ala Ala Ile Ile  
                    35                    40                    45  
Tyr Ser Gly Val Phe Val Ser Leu Phe Ser Ala Leu Thr His Thr Trp  
                    50                    55                    60  
Gly Leu His Leu Lys Gly Pro Val Tyr Ile Ser Leu Phe Arg Pro Leu  
65                    70                    75                    80  
Ser Ile Ala Ile Ala Val Ala Met Gly Ala Ile Phe Leu Gly Asp Ala  
                    85                    90                    95  
Leu His Leu Gly Ser Val Ile Gly Ser Xaa Ile Leu Cys Xaa Gly Phe  
                    100                    105                    110  
Tyr Thr Val Ile Trp Gly Lys Ala Arg Glu Asp Thr Ile Lys Thr Val  
                    115                    120                    125  
Ala Gly Ser Glu Gln Ser Pro Leu Leu Leu Thr His Ile Ile Glu Asp  
130                    135                    140  
Gly Ala Phe Pro Leu Ser  
145                    150

(2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 685 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..685  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

attcaatctc	acaacaacca	atctacacac	aaaacaataa	caacaacaac	aacaacaaca	60
acaacaaaca	acaacaaaca	acaacaaaat	gtttacaaaa	tcaatccttt	taccttttct	120
tctggtaatc	atcttcgtct	cagcatctca	agctagtcgt	caactctggg	atagtgggaat	180
cagcgagatg	tttggttcca	aatccgggtt	tcatcatgga	ttttccgggt	tttcgggggtc	240
ctctggagggt	gctggagggtg	ctggaggatc	attcggagat	atgatgaatg	ctggagggtgc	300
acatacatgc	tcggcgcaag	gagcttgtag	cggtaagaag	ctgacatgtc	ccgaggagtgc	360
ctacaaatca	accaacgtta	acaaggatgg	ttataaaaagc	accagccgca	gtggaggatg	420
ttcatttgac	tgtacgacca	agtgtgccgc	gacttggtca	aattaacatg	ttaatttgca	480
catatatatt	atatgttcgt	atagtatggt	gttatgttat	gttatagcat	tatatagtct	540
atatatatgt	caatataata	aaaccggcaa	gggtatatggg	aggtttgtgt	ctccctttgt	600
aattttgtat	ggatcttgat	tagaagcttt	ctatgaatct	atgtacataa	tatgattttg	660
aataaaaagaa	aatttagtgt	ttctc				

(2) INFORMATION FOR SEQ ID NO:1149:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 125 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1499749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

```
Met Phe Thr Lys Ser Ile Leu Leu Pro Phe Leu Leu Val Ile Ile Phe
1           5           10           15
Val Ser Ala Ser Gln Ala Ser Arg Gln Leu Trp Asp Ser Gly Ile Ser
20           25           30
Glu Met Phe Gly Ser Lys Ser Gly Phe His His Gly Phe Ser Gly Phe
35           40           45
Ser Gly Ser Ser Gly Gly Ala Gly Gly Ala Gly Ser Phe Gly Asp
50           55           60
Met Met Asn Ala Gly Gly Ala His Thr Cys Ser Ala Gln Gly Ala Cys
65           70           75           80
Ser Gly Lys Lys Leu Thr Cys Pro Glu Glu Cys Tyr Lys Ser Thr Asn
85           90           95
Val Asn Lys Asp Gly Tyr Lys Ser Thr Ser Arg Ser Gly Gly Cys Ser
100          105          110
Phe Asp Cys Thr Thr Lys Cys Ala Ala Thr Cys Ser Asn
115          120          125
```

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1499750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

```
Met Phe Gly Ser Lys Ser Gly Phe His His Gly Phe Ser Gly Phe Ser
1           5           10           15
Gly Ser Ser Gly Gly Ala Gly Gly Ala Gly Gly Ser Phe Gly Asp Met
20           25           30
Met Asn Ala Gly Gly Ala His Thr Cys Ser Ala Gln Gly Ala Cys Ser
35           40           45
Gly Lys Lys Leu Thr Cys Pro Glu Glu Cys Tyr Lys Ser Thr Asn Val
50           55           60
Asn Lys Asp Gly Tyr Lys Ser Thr Ser Arg Ser Gly Gly Cys Ser Phe
65           70           75           80
Asp Cys Thr Thr Lys Cys Ala Ala Thr Cys Ser Asn
85           90
```

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1499751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

```
actttctctt gatcactcac tgcatacaaca atggccagag agaagattgt ggtggctggt      60
ggtaccacaa agagctggaa actactcttg gggctgagaa tatttgcatt catggctact      120
ttagctgcag ccattgtaat gtcactaaac aaagagacaa agaccttggt tgtggccacc      180
attggtactg ttcctattaa agccacttta accgctaagt ttcagcacac accggctttt      240
gtgttctttg ttatagctaa tgtaatgggt agcttcocaca atttgttgat gattgctctt      300
cagattttca gcccgaact ggagtacaaa ggtctccgtc tcctctctat cgctattctc      360
```

```
gacatgctaa acgcaacact agtatctgcg gctgcaaacg cggcggtggt cgtggcgagag 420
ctaggggaaga acgggaacaa gcacgccaag tggaacaaag tctgcgacag gtttgccact 480
tactgtgatac acggcgagcagg agcaatcatc gcagcattcg scggagtcac tctaattgctc 540
ctgggtgtccg ccgtctccat ttcccgcctc ttaatcaatt ctaaaaaactt ctccaccacc 600
gccaccacaaa cctccgctcgt ctaaaacatc gtggccaaaa attcagcaac atgtgtgtga 660
ccattttata gatgtgtgg cttactttgt gtgtttgtct ctcaagtcac tagcaaattg 720
tgtaatgcac tcctttgttc t
```

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

```
Met Ala Arg Glu Lys Ile Val Val Ala Gly Thr Thr Lys Ser Trp
1      5      10      15
Lys Leu Leu Leu Gly Leu Arg Ile Phe Ala Phe Met Ala Thr Leu Ala
20     25     30
Ala Ala Ile Val Met Ser Leu Asn Lys Glu Thr Lys Thr Leu Val Val
35     40     45
Ala Thr Ile Gly Thr Val Pro Ile Lys Ala Thr Leu Thr Ala Lys Phe
50     55     60
Gln His Thr Pro Ala Phe Val Phe Phe Val Ile Ala Asn Val Met Val
65     70     75     80
Ser Phe His Asn Leu Met Ile Ala Leu Gln Ile Phe Ser Pro Lys
85     90     95
Leu Glu Tyr Lys Gly Leu Arg Leu Leu Ser Ile Ala Ile Leu Asp Met
100    105    110
Leu Asn Ala Thr Leu Val Ser Ala Ala Ala Asn Ala Ala Val Phe Val
115    120    125
Ala Glu Leu Gly Lys Asn Gly Asn Lys His Ala Lys Trp Asn Lys Val
130    135    140
Cys Asp Arg Phe Ala Thr Tyr Cys Asp His Gly Ala Gly Ala Ile Ile
145    150    155    160
Ala Ala Phe Xaa Gly Val Ile Leu Met Leu Leu Val Ser Ala Val Ser
165    170    175
Ile Ser Arg Leu Leu Ile Asn Ser Lys Asn Phe Ser Thr Thr Ala Thr
180    185    190
Thr Thr Ser Val Val
195
```

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

```
Met Ala Thr Leu Ala Ala Ala Ile Val Met Ser Leu Asn Lys Glu Thr
1      5      10      15
Lys Thr Leu Val Val Ala Thr Ile Gly Thr Val Pro Ile Lys Ala Thr
20     25     30
```

Leu Thr Ala Lys Phe Gln His Thr Pro Ala Phe Val Phe Phe Val Ile  
35 40 45  
Ala Asn Val Met Val Ser Phe His Asn Leu Leu Met Ile Ala Leu Gln  
50 55 60  
Ile Phe Ser Pro Lys Leu Glu Tyr Lys Gly Leu Arg Leu Leu Ser Ile  
65 70 75 80  
Ala Ile Leu Asp Met Leu Asn Ala Thr Leu Val Ser Ala Ala Ala Asn  
85 90 95  
Ala Ala Val Phe Val Ala Glu Leu Gly Lys Asn Gly Asn Lys His Ala  
100 105 110  
Lys Trp Asn Lys Val Cys Asp Arg Phe Ala Thr Tyr Cys Asp His Gly  
115 120 125  
Ala Gly Ala Ile Ile Ala Ala Phe Xaa Gly Val Ile Leu Met Leu Leu  
130 135 140  
Val Ser Ala Val Ser Ile Ser Arg Leu Leu Ile Asn Ser Lys Asn Phe  
145 150 155 160  
Ser Thr Thr Ala Thr Thr Thr Ser Val Val  
165 170

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

Met Ser Leu Asn Lys Glu Thr Lys Thr Leu Val Val Ala Thr Ile Gly  
1 5 10 15  
Thr Val Pro Ile Lys Ala Thr Leu Thr Ala Lys Phe Gln His Thr Pro  
20 25 30  
Ala Phe Val Phe Phe Val Ile Ala Asn Val Met Val Ser Phe His Asn  
35 40 45  
Leu Leu Met Ile Ala Leu Gln Ile Phe Ser Pro Lys Leu Glu Tyr Lys  
50 55 60  
Gly Leu Arg Leu Leu Ser Ile Ala Ile Leu Asp Met Leu Asn Ala Thr  
65 70 75 80  
Leu Val Ser Ala Ala Ala Asn Ala Ala Val Phe Val Ala Glu Leu Gly  
85 90 95  
Lys Asn Gly Asn Lys His Ala Lys Trp Asn Lys Val Cys Asp Arg Phe  
100 105 110  
Ala Thr Tyr Cys Asp His Gly Ala Gly Ala Ile Ile Ala Ala Phe Xaa  
115 120 125  
Gly Val Ile Leu Met Leu Leu Val Ser Ala Val Ser Ile Ser Arg Leu  
130 135 140  
Leu Ile Asn Ser Lys Asn Phe Ser Thr Thr Ala Thr Thr Thr Ser Val  
145 150 155 160  
Val

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1499755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

acaacttccc	cattttctgc	ttctttttgt	tcaactccaa	tcacacaatt	cacaacccat	60
tgagaaacca	ataaaataac	ctcaatcaaa	aaaaaaaaa	aaaaaagatg	aaaatctcaa	120
tttagtaaag	gagaaaaaag	ccatttcgaa	taacttgaaa	aggttttggt	tttgacagaag	180
aaaatgaagg	agaaggcgga	gagtgggtga	ggagttaggat	acgtgagagc	agatcagata	240
gatttaaaga	gtctggacga	gcaattgcag	agacacttaa	gtaaagcatg	gacgatggag	300
aagaggaaga	gtttgagtga	tgggtgaagat	aacgtcaata	acacccgaca	taaccagaac	360
aacttcggac	atcgacagct	tgtgttttcag	aggccgcttc	cttggtggtg	gatatagcaa	420
caacaacaac	agcagcaaga	acgacataat	taggtcgacc	gaggttgaga	agtcgaggag	480
agagtgggag	attgatcctt	ctaagcttat	aatcaaaagt	gtgattgcta	gagggtacttt	540
tggtagcggt	caccgtggaa	tctacgatgg	tcaagatgtc	gccgtaaaac	tactagactg	600
gggagaagag	gggcacaggt	cagacgcaga	gatagcttcg	cttagagctg	ctttcactca	660
agaagtt						

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1499756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

Met	Lys	Glu	Lys	Ala	Glu	Ser	Gly	Gly	Gly	Val	Gly	Tyr	Val	Arg	Ala
1			5					10						15	
Asp	Gln	Ile	Asp	Leu	Lys	Ser	Leu	Asp	Glu	Gln	Leu	Gln	Arg	His	Leu
		20					25					30			
Ser	Lys	Ala	Trp	Thr	Met	Glu	Lys	Arg	Lys	Ser	Leu	Ser	Asp	Gly	Glu
		35					40					45			
Asp	Asn	Val	Asn	Asn	Thr	Arg	His	Asn	Gln	Asn	Asn	Phe	Gly	His	Arg
		50					55					60			
Gln	Leu	Val	Phe	Gln	Arg	Pro	Leu	Pro	Trp	Trp	Trp	Ile			
65				70					75						

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1499757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

Met	Val	Lys	Ile	Thr	Ser	Ile	Thr	Pro	Asp	Ile	Thr	Arg	Thr	Thr	Ser
1			5					10						15	
Asp	Ile	Asp	Ser	Leu	Cys	Phe	Arg	Gly	Arg	Phe	Leu	Gly	Gly	Gly	Tyr
		20						25				30			
Ser	Asn	Asn	Asn	Asn	Ser	Ser	Lys	Asn	Asp	Ile	Ile	Arg	Ser	Thr	Glu
		35					40					45			
Val	Glu	Lys	Ser	Arg	Arg	Glu	Trp	Glu	Ile	Asp	Pro	Ser	Lys	Leu	Ile
		50					55				60				
Ile	Lys	Ser	Val	Ile	Ala	Arg	Gly	Thr	Phe	Gly	Thr	Val	His	Arg	Gly
65				70					75					80	
Ile	Tyr	Asp	Gly	Gln	Asp	Val	Ala	Val	Lys	Leu	Leu	Asp	Trp	Gly	Glu
			85						90					95	



Glu Gly His Arg Ser Asp Ala Glu Ile Ala Ser Leu Arg Ala Ala Phe  
100 105 110  
Thr Gln Glu Val  
115

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

tttttttcgt cgagcagccg cgcttttttg cgcaggaagg ataaagagag acgccatggg	60
aagaagacct gcgaggtgtt accgtcagat caagggttaag ccatacccaa agtctcgcta	120
ctgtcgtggg gtgccagatc caaaaatcag gatctacgat gttggtatga agaggaaggg	180
tggtgatgag ttcccatggc gtctctcttt atccttcttc ggcc	

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

Phe Phe Arg Arg Ala Ala Ala Leu Phe Gly Arg Gly Arg Ile Lys Arg	
1 5 10 15	
Asp Ala Met Gly Arg Arg Pro Ala Arg Cys Tyr Arg Gln Ile Lys Gly	
20 25 30	
Lys Pro Tyr Pro Lys Ser Arg Tyr Cys Arg Gly Val Pro Asp Pro Lys	
35 40 45	
Ile Arg Ile Tyr Asp Val Gly Met Lys Arg Lys Gly Val Asp Glu Phe	
50 55 60	
Pro Trp Arg Leu Ser Leu Ser Phe Leu Gly	
65 70	

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

Met Gly Arg Arg Pro Ala Arg Cys Tyr Arg Gln Ile Lys Gly Lys Pro	
1 5 10 15	
Tyr Pro Lys Ser Arg Tyr Cys Arg Gly Val Pro Asp Pro Lys Ile Arg	
20 25 30	
Ile Tyr Asp Val Gly Met Lys Arg Lys Gly Val Asp Glu Phe Pro Trp	
35 40 45	
Arg Leu Ser Leu Ser Phe Leu Gly	

50 55  
(2) INFORMATION FOR SEQ ID NO:1161:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1331 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1331  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499765  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:  
attttcttct tcttcttcat ttttctattc acattctctg aaactcatac catatttttca 60  
aagctcttaa cccaaaaaacc ctaagtcttt ttttcttca aattattggt tatattaatg 120  
ttttaagcta tgatggatat gactcctaca ataacaacaa caacaacacc aactcctaaa 180  
tcacccgaac ccgaatccga aactccgacc cggatccaac cggcgaaacc catttccttt 240  
agcaacggca tcatcaaacg ccaccaccac caccaccatc ctctcctctt tacttacaaa 300  
gaatgtctca aaaaccacgc ggcggtctta ggtggtcacg ctctcgacgg ttgcggcgaa 360  
ttcatgccgt ctccgtcgtc aatctcctcc gatccaactt ctctcaaagt tgctgccttg 420  
tggtgccac cgtaatttcc accgccgtga tccagataac aacaacgact cttcccaa 480  
ccctcctctc ccttccactg bcgtagagaa tcaacctcac caccgtcatc atccaccacc 540  
accaccacct cctccaccac cactagatcc taactcagct tctcctccac caatctcttc 600  
ctcttacatg ctcttatctc tctccggtac taataacaac aacaacaact tagcttcttt 660  
ctccgatctt aacttctccg ccggaacaaa ccaccaccac caccaccaac atactcttca 720  
cggatctcgt aaaagattcc gaacaaaatt cagccagttt cagaaagaga agatgcatga 780  
attcgccgaa cgtgttggtt ggaagatgca aaaacgtgac saagacgatg ttcgtgattt 840  
ttgccggcag atcggagttg ataaaagtgt tctcaaagtt tggatgcata acaacaaaaa 900  
cacctttaac cgccgtgata tcgccggaaa cgagatccgg caaatcgata acggcggagg 960  
aaaccacact ccgattctcg ccggcgagat taataaccat aacaatggac accacggtgt 1020  
cggaggagga ggagagcttc accagagtgt tagtagcggc ggtggtggcg gaggatttga 1080  
tagtgatagc ggccggagcta acggtggtta cgttaacgga tcatcgctcg cgtgaagtta 1140  
aagatgagag tgtcaggtta ataagaagct tagagtaagc ttattcgtat tatcatcggt 1200  
aataactttc tattaaatat taattaagat ctttagcttt gtttgttttt gcattattat 1260  
tagttttgat ttaatgttct ttaccacgtc ggtgtctcgc tcgatgagga ataataccat 1320  
aacaatgttc g

(2) INFORMATION FOR SEQ ID NO:1162:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499766  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:  
Met Leu Leu Ser Leu Ser Gly Thr Asn Asn Asn Asn Asn Asn Leu Ala  
1 5 10 15  
Ser Phe Ser Asp Leu Asn Phe Ser Ala Gly Asn Asn His His His His  
20 25 30  
His Gln His Thr Leu His Gly Ser Arg Lys Arg Phe Arg Thr Lys Phe  
35 40 45  
Ser Gln Phe Gln Lys Glu Lys Met His Glu Phe Ala Glu Arg Val Gly  
50 55 60  
Trp Lys Met Gln Lys Arg Asp Xaa Asp Asp Val Arg Asp Phe Cys Arg  
65 70 75 80  
Gln Ile Gly Val Asp Lys Ser Val Leu Lys Val Trp Met His Asn Asn  
85 90 95  
Lys Asn Thr Phe Asn Arg Arg Asp Ile Ala Gly Asn Glu Ile Arg Gln

	100		105		110										
Ile	Asp	Asn	Gly	Gly	Gly	Asn	His	Thr	Pro	Ile	Leu	Ala	Gly	Glu	Ile
	115					120					125				
Asn	Asn	His	Asn	Asn	Gly	His	His	Gly	Val	Gly	Gly	Gly	Gly	Glu	Leu
	130					135					140				
His	Gln	Ser	Val	Ser	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Phe	Asp	Ser	Asp
145						150					155				160
Ser	Gly	Gly	Ala	Asn	Gly	Gly	Asn	Val	Asn	Gly	Ser	Ser	Ser	Ser	
				165				170						175	

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1499767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

Met	His	Glu	Phe		Glu	Arg	Val	Gly	Trp	Lys	Met	Gln	Lys	Arg	Asp
1			5					10						15	
Xaa	Asp	Asp	Val	Arg	Asp	Phe	Cys	Arg	Gln	Ile	Gly	Val	Asp	Lys	Ser
			20					25					30		
Val	Leu	Lys	Val	Trp	Met	His	Asn	Asn	Lys	Asn	Thr	Phe	Asn	Arg	Arg
			35				40					45			
Asp	Ile	Ala	Gly	Asn	Glu	Ile	Arg	Gln	Ile	Asp	Asn	Gly	Gly	Gly	Asn
	50					55					60				
His	Thr	Pro	Ile	Leu	Ala	Gly	Glu	Ile	Asn	Asn	His	Asn	Asn	Gly	His
65				70					75						80
His	Gly	Val	Gly	Gly	Gly	Gly	Glu	Leu	His	Gln	Ser	Val	Ser	Ser	Gly
			85					90					95		
Gly	Gly	Gly	Gly	Gly	Phe	Asp	Ser	Asp	Ser	Gly	Gly	Ala	Asn	Gly	Gly
			100					105					110		
Asn	Val	Asn	Gly	Ser	Ser	Ser	Ser								
	115					120									

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1499768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

Met	Asn	Ser	Pro	Asn	Val	Leu	Val	Gly	Arg	Cys	Lys	Asn	Val	Xaa	Lys
1				5				10						15	
Thr	Met	Phe	Val	Ile	Phe	Ala	Gly	Arg	Ser	Glu	Leu	Ile	Lys	Val	Phe
			20					25					30		
Ser	Lys	Phe	Gly	Cys	Ile	Thr	Thr	Lys	Thr	Pro	Leu	Thr	Ala	Val	Ile
		35				40					45				
Ser	Pro	Glu	Thr	Arg	Ser	Gly	Lys	Ser	Ile	Thr	Ala	Glu	Glu	Thr	Thr
	50					55				60					
Leu	Arg	Phe	Ser	Pro	Ala	Arg	Leu	Ile	Thr	Ile	Thr	Met	Asp	Thr	Thr
65				70					75					80	
Val	Ser	Glu	Glu	Glu	Glu	Ser	Phe	Thr	Arg	Val	Leu	Val	Ala	Ala	Val
			85					90						95	

Val Ala Glu Asp Leu Ile Val Ile Ala Ala Glu Leu Thr Val Val Thr  
100 105 110  
Leu Thr Asp His Arg Arg Arg Glu Val Lys Asp Glu Ser Val Arg Leu  
115 120 125  
Ile Arg Ser Leu Glu  
130

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

aatttgctaa	ggaaaaaaaa	aacgaaaacg	tgtgtctgtc	tcttctcgta	gcgtctctca	60
agctcagatg	aattttgggt	tgccaagtat	atcttggttt	gtagcatca	gcacaaagaa	120
agatgtagct	atgattgatt	ccgtgacacc	aacaacaact	tctctattgg	aacagccaga	180
gcaagagaaa	gcaacaacct	ttcttctcaa	acagccagag	aaagagaaag	gcttatttga	240
tataaagata	tggaattggt	cctccttcag	ttcagttctt	ccttggtctg	caaatgcctc	300
tgatggtaag	cagaaaccca	ctactatcaa	cagaggggta	aaaaggcatg	ctctttctcg	360
gaggtcatca	aggatcaa	ggtgtgaata	ctgtttatcg	gtttagacct	tatggtgtct	420
aaggttccgt	ggcatacagg	gacgarggcg	tttckgtcac	agcttttccc	gagatatgga	480
catttattgt	g					

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

Met	Asn	Phe	Gly	Leu	Pro	Ser	Ile	Ser	Trp	Phe	Gly	Ser	Ile	Ser	Thr
1				5					10					15	
Lys	Lys	Asp	Val	Ala	Met	Ile	Asp	Ser	Val	Thr	Pro	Thr	Thr	Thr	Ser
			20					25					30		
Leu	Leu	Glu	Gln	Pro	Glu	Gln	Glu	Lys	Ala	Thr	Thr	Phe	Leu	Leu	Lys
		35					40					45			
Gln	Pro	Glu	Lys	Glu	Lys	Gly	Leu	Phe	Asp	Ile	Lys	Ile	Trp	Thr	Trp
	50				55				60						
Ser	Ser	Phe	Ser	Ser	Val	Leu	Pro	Trp	Ser	Ala	Asn	Ala	Ser	Asp	Gly
65				70					75					80	
Lys	Gln	Lys	Pro	Thr	Thr	Ile	Asn	Arg	Gly	Leu	Lys	Arg	His	Ala	Leu
			85					90					95		
Ser	Arg	Arg	Ser	Ser	Arg	Ile	Lys	Trp	Cys	Glu	Tyr	Cys	Leu	Ser	Val
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..91  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499771  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:  
Met Ile Asp Ser Val Thr Pro Thr Thr Thr Ser Leu Leu Glu Gln Pro  
1                    5                    10                    15  
Glu Gln Glu Lys Ala Thr Thr Phe Leu Leu Lys Gln Pro Glu Lys Glu  
                    20                    25                    30  
Lys Gly Leu Phe Asp Ile Lys Ile Trp Thr Trp Ser Ser Phe Ser Ser  
                    35                    40                    45  
Val Leu Pro Trp Ser Ala Asn Ala Ser Asp Gly Lys Gln Lys Pro Thr  
                    50                    55                    60  
Thr Ile Asn Arg Gly Leu Lys Arg His Ala Leu Ser Arg Arg Ser Ser  
65                    70                    75                    80  
Arg Ile Lys Trp Cys Glu Tyr Cys Leu Ser Val  
                    85                    90

(2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1277 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1277

(D) OTHER INFORMATION: / Ceres Seq. ID 1499772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

atttcttctt caccgttaga ttttctctcg cttaatttct caataacgct ctcagagaga	60
ccatttgatg aagcttctcg cttctggaat ttgaaaagga ttgataaga cgagttcata	120
gaagattacc gcaagttcat caactttttg aacttggtat ggagataatc tcaactgaacg	180
ttgtgcccc a gtgctctgtg gttacttgga gtagtaaat agcaacgata agattggtcc	240
caaatcggtc aagtttggtta ttctcagggg tcaaaaaatc cagacttggtg attcgaagt	300
gaaattccga tggttatgtt gttggtgaga atgatgactt gggtcgtata gccagaagag	360
gagaatcaac gtcaaagggt ttgattcctg gtttgccctga tgaatcaa at ggtgaaattg	420
ctgctcgaat cagtcattct cactgcgagt ggaagcccaa gcttagagta cattatgaga	480
aagccgggtg tgacaatctc gatgctcctg cggtgttggt tcttctctggc ttggcggtg	540
gttcatttca ctatgagaag cagcttaccg atttggaag ggattatcga gtatgggcta	600
ttgattttct tggacagggt ttatctctcc ctactgaaga tcctactacc atgactgaag	660
aaaccagttc ctcggaagat aaggaaccat tttggggatt tggtgacaaa actgaaccgt	720
gggctgatca acttgatttc tctctggatc tctggaggga tcaagttcag tattttgtag	780
aagaggttat cgggtgagcct gtgtacattg ctgggaactc acttgagggg tatgtagctc	840
tctactttgc agcaacccat cctcacctgg ttaaggggtgt taccttgctt aatgcaacac	900
ctttctgggg tttcttccct aatccagtaa gatccccaaa gctagcacgt ctctttccat	960
ggcccggagc attccctctg ccggaaagag tgaaaaaaaa tcacagaatt ggtgtggcaa	1020
aagataagtg atcctgaaag catagctgag atacttaaac aggtctacac agaccattct	1080
accaatgtgg ataaagtatt ctacagttat gtggagggtca cacagcatcc ggctgctgca	1140
gcacgtttg cttcaattat gcttgctcct ggtggagagc tatctttctc cgaagcttta	1200
tctaggtgta aggaaaacaa tgttcagata tgtctcatgt atggaagaga agatccatgg	1260
gtgagaccgt tatgggg	

(2) INFORMATION FOR SEQ ID NO:1169:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 290 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1499773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

```
Met Glu Ile Ile Ser Leu Asn Val Val Pro Gln Cys Ser Val Val Thr
1      5      10      15
Trp Ser Ser Lys Leu Ala Thr Ile Arg Leu Val Pro Asn Arg Ser Ser
20      25      30
Leu Leu Phe Ser Gly Val Lys Lys Ser Arg Leu Val Ile Arg Ser Gly
35      40      45
Asn Ser Asp Gly Tyr Val Val Gly Glu Asn Asp Asp Leu Gly Arg Ile
50      55      60
Ala Arg Arg Gly Glu Ser Thr Ser Lys Val Leu Ile Pro Gly Leu Pro
65      70      75      80
Asp Glu Ser Asn Gly Glu Ile Ala Ala Arg Ile Ser His Ser His Cys
85      90      95
Glu Trp Lys Pro Lys Leu Arg Val His Tyr Glu Lys Ala Gly Cys Asp
100     105     110
Asn Leu Asp Ala Pro Ala Val Leu Phe Leu Pro Gly Phe Gly Val Gly
115     120     125
Ser Phe His Tyr Glu Lys Gln Leu Thr Asp Leu Gly Arg Asp Tyr Arg
130     135     140
Val Trp Ala Ile Asp Phe Leu Gly Gln Gly Leu Ser Leu Pro Thr Glu
145     150     155     160
Asp Pro Thr Thr Met Thr Glu Glu Thr Ser Ser Ser Glu Asp Lys Glu
165     170     175
Pro Phe Trp Gly Phe Gly Asp Lys Thr Glu Pro Trp Ala Asp Gln Leu
180     185     190
Val Phe Ser Leu Asp Leu Trp Arg Asp Gln Val Gln Tyr Phe Val Glu
195     200     205
Glu Val Ile Gly Glu Pro Val Tyr Ile Ala Gly Asn Ser Leu Gly Gly
210     215     220
Tyr Val Ala Leu Tyr Phe Ala Ala Thr His Pro His Leu Val Lys Gly
225     230     235     240
Val Thr Leu Leu Asn Ala Thr Pro Phe Trp Gly Phe Phe Pro Asn Pro
245     250     255
Val Arg Ser Pro Lys Leu Ala Arg Leu Phe Pro Trp Pro Gly Ala Phe
260     265     270
Pro Leu Pro Glu Arg Val Lys Lys Asn His Arg Ile Gly Val Ala Lys
275     280     285
Asp Lys
290
```

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1843

(D) OTHER INFORMATION: / Ceres Seq. ID 1499777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

```
acacaaccaa agcgtttaga aaaaaaacag cgataaaacc gaaacatcaa gcaaacaataa 60
aaaaagagga gaattttttt tttttgtttt cgttttcaaa aacaaaatct ttgaatttta 120
tggcaaccgg tcttctccga aaaaacttta tccggcgcgc ttaccgttta cccgctttta 180
gcccggtggg tcctcccacc gtgactgctt ccaccgccgt cgtcccggag attctctoct 240
ttggacaaca agcaccggaa ccacctcttc accaccctaa accoactgag caatctcacc 300
atggtctcga tctctccgat caagcccgct ttttctcctc tatcccaacc tctgatctoc 360
tccgttccac cgccgtgttg catgcggcgg cgataggtcc tatggtcgac ctagggacgt 420
gggtcatgag ctctaaactt atggacgctt ccgtgacgcg tggcatgggt ttagggcttg 480
```

tgaaaagtac gttttatgac catttttgcg ccggtgaaga tgccgacgca gccgctgagc 540  
gcgtgagaag cgtttatgaa gctaccggtc ttaaagggat gcttgtctat ggcgctgaac 600  
acgccgatga cgctgtatct tgtgatgata acatgcaaca attcattoga accattgaag 660  
ctgccaaatc tttaccaaca tctcacttta gctcagtggt tgtgaagata actgccatct 720  
gtccaattag tcttctgaaa cgagtgcg atctgcttcg gtgggaatac aaaagtccaa 780  
acttcaaact ctcatggaag ctcaaactgt ttccggtttt ctccgattcg agtcctctct 840  
accacacaaa ctcaagaacc gaaccgttaa ccgcggaaga agaaccggag ctcaagcag 900  
ctcatggaag gattcaagaa atctgttaga aatgccaaag agtccaatgt accattgttg 960  
attgatgcgg aagacacaat cctccaaccc gcgatcgatt acatggctta ttcacggcg 1020  
atcatgttca atgctgacaa agaccgacca atcgtttaca acacgattca ggcgacttg 1080  
agagacgccg gtgagagact gcatttggca gtacaaaatg ctgagaaaga gaatgttctt 1140  
atggggttca agttggtgag aggggcttac atgtctagcg aagctagctt ggcggtattc 1200  
ctgggttgca agtcgccagt ccacgacaca attcaggata ctactcttg ttacaatgat 1260  
tgtatgacat tcctgatgga gaaagcatca aacggttctg gtttcggtgt cgttctcgca 1320  
acacataacg ctgattcggg gagacttgcg tcgaggaaag cgagtgdhct cgggattgat 1380  
aaacagaacg ggaagataga gtttgcacag ctatatggtg tgtcggatgc attgtcttcg 1440  
gtttaaagag agccgggttc aatgtagca agtacatgcc gtttggaccc gtcgaaccg 1500  
ctataccgta tcttctccga cgcgcttatg agaaccggg aatgatggcc accggagctc 1560  
atgaccgtca actcatgagg atggaactta agaggagatt aatcgccggg attgcgtaaa 1620  
gagagagtat ggagccatta aatgaaattg ggaaatgtag atgaataaat ttcttctatg 1680  
tagtttaaga aattgaaaac aaaaaattat aatataagaa atggagtagg taagaacatt 1740  
tcctgtggct aaatattttt catgaggac tatgttttta ctatcaatat atcattcaca 1800  
aatgtatatt cacccttatca ataaaatgt tttttacttt ttt

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..320
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

Thr	Thr	Lys	Ala	Phe	Arg	Lys	Lys	Thr	Ala	Ile	Lys	Pro	Lys	His	Gln
1			5					10						15	
Ala	Asn	Lys	Lys	Lys	Glu	Glu	Asn	Phe	Phe	Phe	Leu	Phe	Ser	Phe	Ser
			20					25					30		
Lys	Thr	Lys	Ser	Leu	Asn	Phe	Met	Ala	Thr	Arg	Leu	Leu	Arg	Thr	Asn
			35				40					45			
Phe	Ile	Arg	Arg	Ser	Tyr	Arg	Leu	Pro	Ala	Phe	Ser	Pro	Val	Gly	Pro
			50			55					60				
Pro	Thr	Val	Thr	Ala	Ser	Thr	Ala	Val	Val	Pro	Glu	Ile	Leu	Ser	Phe
					70					75				80	
Gly	Gln	Gln	Ala	Pro	Glu	Pro	Pro	Leu	His	His	Pro	Lys	Pro	Thr	Glu
				85					90					95	
Gln	Ser	His	Asp	Gly	Leu	Asp	Leu	Ser	Asp	Gln	Ala	Arg	Leu	Phe	Ser
			100					105					110		
Ser	Ile	Pro	Thr	Ser	Asp	Leu	Leu	Arg	Ser	Thr	Ala	Val	Leu	His	Ala
			115				120					125			
Ala	Ala	Ile	Gly	Pro	Met	Val	Asp	Leu	Gly	Thr	Trp	Val	Met	Ser	Ser
			130				135					140			
Lys	Leu	Met	Asp	Ala	Ser	Val	Thr	Arg	Gly	Met	Val	Leu	Gly	Leu	Val
					150					155				160	
Lys	Ser	Thr	Phe	Tyr	Asp	His	Phe	Cys	Ala	Gly	Glu	Asp	Ala	Asp	Ala
				165					170					175	
Ala	Ala	Glu	Arg	Val	Arg	Ser	Val	Tyr	Glu	Ala	Thr	Gly	Leu	Lys	Gly
				180				185					190		
Met	Leu	Val	Tyr	Gly	Val	Glu	His	Ala	Asp	Asp	Ala	Val	Ser	Cys	Asp
				195			200					205			

Asp	Asn	Met	Gln	Gln	Phe	Ile	Arg	Thr	Ile	Glu	Ala	Ala	Lys	Ser	Leu
210						215				220					
Pro	Thr	Ser	His	Phe	Ser	Ser	Val	Val	Val	Lys	Ile	Thr	Ala	Ile	Cys
225					230					235					240
Pro	Ile	Ser	Leu	Leu	Lys	Arg	Val	Ser	Asp	Leu	Leu	Arg	Trp	Glu	Tyr
				245					250					255	
Lys	Ser	Pro	Asn	Phe	Lys	Leu	Ser	Trp	Lys	Leu	Lys	Ser	Phe	Pro	Val
			260					265					270		
Phe	Ser	Asp	Ser	Ser	Pro	Leu	Tyr	His	Thr	Asn	Ser	Glu	Pro	Glu	Pro
			275					280					285		
Leu	Thr	Ala	Glu	Glu	Glu	Arg	Glu	Leu	Glu	Ala	Ala	His	Gly	Arg	Ile
	290					295					300				
Gln	Glu	Ile	Cys	Arg	Lys	Cys	Gln	Arg	Val	Gln	Cys	Thr	Ile	Val	Asp
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1499779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

Met	Ala	Thr	Arg	Leu	Leu	Arg	Thr	Asn	Phe	Ile	Arg	Arg	Ser	Tyr	Arg
1				5						10				15	
Leu	Pro	Ala	Phe	Ser	Pro	Val	Gly	Pro	Pro	Thr	Val	Thr	Ala	Ser	Thr
			20					25					30		
Ala	Val	Val	Pro	Glu	Ile	Leu	Ser	Phe	Gly	Gln	Gln	Ala	Pro	Glu	Pro
		35					40					45			
Pro	Leu	His	His	Pro	Lys	Pro	Thr	Glu	Gln	Ser	His	Asp	Gly	Leu	Asp
	50				55						60				
Leu	Ser	Asp	Gln	Ala	Arg	Leu	Phe	Ser	Ser	Ile	Pro	Thr	Ser	Asp	Leu
65					70					75					80
Leu	Arg	Ser	Thr	Ala	Val	Leu	His	Ala	Ala	Ala	Ile	Gly	Pro	Met	Val
				85					90					95	
Asp	Leu	Gly	Thr	Trp	Val	Met	Ser	Ser	Lys	Leu	Met	Asp	Ala	Ser	Val
			100					105					110		
Thr	Arg	Gly	Met	Val	Leu	Gly	Leu	Val	Lys	Ser	Thr	Phe	Tyr	Asp	His
		115				120						125			
Phe	Cys	Ala	Gly	Glu	Asp	Ala	Asp	Ala	Ala	Ala	Glu	Arg	Val	Arg	Ser
		130				135					140				
Val	Tyr	Glu	Ala	Thr	Gly	Leu	Lys	Gly	Met	Leu	Val	Tyr	Gly	Val	Glu
145					150					155					160
His	Ala	Asp	Asp	Ala	Val	Ser	Cys	Asp	Asp	Asn	Met	Gln	Gln	Phe	Ile
				165					170					175	
Arg	Thr	Ile	Glu	Ala	Ala	Lys	Ser	Leu	Pro	Thr	Ser	His	Phe	Ser	Ser
			180					185					190		
Val	Val	Val	Lys	Ile	Thr	Ala	Ile	Cys	Pro	Ile	Ser	Leu	Leu	Lys	Arg
			195				200					205			
Val	Ser	Asp	Leu	Leu	Arg	Trp	Glu	Tyr	Lys	Ser	Pro	Asn	Phe	Lys	Leu
		210				215					220				
Ser	Trp	Lys	Leu	Lys	Ser	Phe	Pro	Val	Phe	Ser	Asp	Ser	Ser	Pro	Leu
225					230					235					240
Tyr	His	Thr	Asn	Ser	Glu	Pro	Glu	Pro	Leu	Thr	Ala	Glu	Glu	Glu	Arg
				245					250					255	
Glu	Leu	Glu	Ala	Ala	His	Gly	Arg	Ile	Gln	Glu	Ile	Cys	Arg	Lys	Cys



260 265 270  
Gln Arg Val Gln Cys Thr Ile Val Asp  
275 280  
(2) INFORMATION FOR SEQ ID NO:1173:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..187  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499780  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:  
Met Val Asp Leu Gly Thr Trp Val Met Ser Ser Lys Leu Met Asp Ala  
1 5 10 15  
Ser Val Thr Arg Gly Met Val Leu Gly Leu Val Lys Ser Thr Phe Tyr  
20 25 30  
Asp His Phe Cys Ala Gly Glu Asp Ala Asp Ala Ala Glu Arg Val  
35 40 45  
Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly Met Leu Val Tyr Gly  
50 55 60  
Val Glu His Ala Asp Asp Ala Val Ser Cys Asp Asp Asn Met Gln Gln  
65 70 75 80  
Phe Ile Arg Thr Ile Glu Ala Ala Lys Ser Leu Pro Thr Ser His Phe  
85 90 95  
Ser Ser Val Val Lys Ile Thr Ala Ile Cys Pro Ile Ser Leu Leu  
100 105 110  
Lys Arg Val Ser Asp Leu Leu Arg Trp Glu Tyr Lys Ser Pro Asn Phe  
115 120 125  
Lys Leu Ser Trp Lys Leu Lys Ser Phe Pro Val Phe Ser Asp Ser Ser  
130 135 140  
Pro Leu Tyr His Thr Asn Ser Glu Pro Glu Pro Leu Thr Ala Glu Glu  
145 150 155 160  
Glu Arg Glu Leu Glu Ala Ala His Gly Arg Ile Gln Glu Ile Cys Arg  
165 170 175  
Lys Cys Gln Arg Val Gln Cys Thr Ile Val Asp  
180 185

(2) INFORMATION FOR SEQ ID NO:1174:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 553 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..553  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499785  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:  
gacgttggtt cttatatcgt tgccagagag agtttgacgg cggagagata tggcggcggt 60  
gatggagtca gtcgtcggcc gagctctaaa attctcatcg acggcgaatt tcagggtcaat 120  
ccgacgcggc gaaacaccaa cactctgtat caaatcattc tccaccatta tgtcaccacc 180  
gtcaaaagcc atcgtctacg aagaacacgg ctctcccgat tccgtcacca gattggtgaa 240  
tctccgcggc gtggaagtga aagaaaacga cgtttgtgtt aaaatgatcg ccgctccgat 300  
caacccctcc gatatcaatc gaattgaagg tgtgtatccg gtgaggccac cggtaggcgc 360  
ggttggtggt tatgaagggt ttggtgaagt ttatgcagtt ggctccaatg ttaatggttt 420  
ttctcctggt gattgggtca ttccatctcc accttcttca gggacttggc agacttatgt 480  
tgtgaaggaa gagagtgtgt ggcacaaaat cgataaagag tgtccaatgg agtatgcagc 540  
gacgattact gtt

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1499786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Met Ala Ala Leu Met Glu Ser Val Val Gly Arg Ala Leu Lys Phe Ser  
1 5 10 15  
Ser Thr Ala Asn Phe Arg Ser Ile Arg Arg Gly Glu Thr Pro Thr Leu  
20 25 30  
Cys Ile Lys Ser Phe Ser Thr Ile Met Ser Pro Pro Ser Lys Ala Ile  
35 40 45  
Val Tyr Glu Glu His Gly Ser Pro Asp Ser Val Thr Arg Leu Val Asn  
50 55 60  
Leu Pro Pro Val Glu Val Lys Glu Asn Asp Val Cys Val Lys Met Ile  
65 70 75 80  
Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Arg Ile Glu Gly Val Tyr  
85 90 95  
Pro Val Arg Pro Pro Val Pro Ala Val Gly Gly Tyr Glu Gly Val Gly  
100 105 110  
Glu Val Tyr Ala Val Gly Ser Asn Val Asn Gly Phe Ser Pro Gly Asp  
115 120 125  
Trp Val Ile Pro Ser Pro Pro Ser Ser Gly Thr Trp Gln Thr Tyr Val  
130 135 140  
Val Lys Glu Glu Ser Val Trp His Lys Ile Asp Lys Glu Cys Pro Met  
145 150 155 160  
Glu Tyr Ala Ala Thr Ile Thr Val  
165

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1499787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

Met Glu Ser Val Val Gly Arg Ala Leu Lys Phe Ser Ser Thr Ala Asn  
1 5 10 15  
Phe Arg Ser Ile Arg Arg Gly Glu Thr Pro Thr Leu Cys Ile Lys Ser  
20 25 30  
Phe Ser Thr Ile Met Ser Pro Pro Ser Lys Ala Ile Val Tyr Glu Glu  
35 40 45  
His Gly Ser Pro Asp Ser Val Thr Arg Leu Val Asn Leu Pro Pro Val  
50 55 60  
Glu Val Lys Glu Asn Asp Val Cys Val Lys Met Ile Ala Ala Pro Ile  
65 70 75 80  
Asn Pro Ser Asp Ile Asn Arg Ile Glu Gly Val Tyr Pro Val Arg Pro  
85 90 95  
Pro Val Pro Ala Val Gly Gly Tyr Glu Gly Val Gly Glu Val Tyr Ala  
100 105 110  
Val Gly Ser Asn Val Asn Gly Phe Ser Pro Gly Asp Trp Val Ile Pro

115	120	125
Ser Pro Pro Ser Ser Gly Thr Trp Gln Thr Tyr Val Val Lys Glu Glu		
130	135	140
Ser Val Trp His Lys Ile Asp Lys Glu Cys Pro Met Glu Tyr Ala Ala		
145	150	155
Thr Ile Thr Val		160

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1499788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

Met Ser Pro Pro Ser Lys Ala Ile Val Tyr Glu Glu His Gly Ser Pro		
1	5	10
Asp Ser Val Thr Arg Leu Val Asn Leu Pro Pro Val Glu Val Lys Glu		
20	25	30
Asn Asp Val Cys Val Lys Met Ile Ala Ala Pro Ile Asn Pro Ser Asp		
35	40	45
Ile Asn Arg Ile Glu Gly Val Tyr Pro Val Arg Pro Pro Val Pro Ala		
50	55	60
Val Gly Gly Tyr Glu Gly Val Gly Glu Val Tyr Ala Val Gly Ser Asn		
65	70	75
Val Asn Gly Phe Ser Pro Gly Asp Trp Val Ile Pro Ser Pro Pro Ser		
85	90	95
Ser Gly Thr Trp Gln Thr Tyr Val Val Lys Glu Glu Ser Val Trp His		
100	105	110
Lys Ile Asp Lys Glu Cys Pro Met Glu Tyr Ala Ala Thr Ile Thr Val		
115	120	125

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1910

(D) OTHER INFORMATION: / Ceres Seq. ID 1499789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

atttaaaaaa	gaaaaaagaa	gaaaagagag	agagagactc	acaaatcata	atatctcctt	60
cattaactca	taatcacttt	aaagaacatt	ggaatcagat	tcattacata	gggattgata	120
tggaaaagtc	aaaccaacca	gttcatgtaa	ccttgtccga	attgaaggac	ggagataaag	180
aaatcgttga	tgctgaatth	ttggttgatc	ttcttgagag	ctatagattt	ggtaaagata	240
atgttcccg	ccgagaatth	cgatccaagg	cggcagcgac	ggctccggcg	ccggtcaaca	300
ccaccgagat	agagttggaa	gaggataatg	atggatctca	agctcaagg	aacaattctg	360
ttagtgaaag	tacatcatcg	ctattttccg	attcagatcc	aatagtactt	gagagtactg	420
tgagcgaaac	cggttcaaac	gaagaatctg	aaaccgggtc	aaacgaagaa	aatggtaata	480
attggttaga	gtcagagctcc	acaaacttgc	caaagttaga	gaacaaaagg	caacggaatg	540
gagaagattg	tgagatagaa	gaggaagaag	aaaataacga	gagatcatta	tcggattcag	600
aagagaagtc	aaacctagag	aagttgcttg	ggacacaaga	aaactatgag	cttggaatg	660
aggatgaaga	aaagaacgag	agatcatcgt	cagattcaga	agagaagtca	aacctagaga	720

attttcttgc	gacacaagaa	aactacgagc	tttactgtcc	tagctgtagc	acatgtatca	780
ccagaaatgt	ggttctcaag	aaaagaaaac	gagggaaagca	cgtaaattca	tctctggatc	840
tgaaccgccg	tataccggtt	gttgaaccgg	acgaaccaag	cgacattgag	gagatggaat	900
caccagttaa	ggtttatgtc	cctgagactc	ggattgagga	tgatcaagaa	gataaagagg	960
gaactatctt	tacttgcttg	gtttgtgatc	taaagtactt	catccggtta	ggaacaaagt	1020
tctttacaact	tgattatatac	aggggaaaac	cggttgagaa	atcagttgaa	gaatatatag	1080
atgtgaggaa	gagtataaac	accacacaat	caccaccaca	aattcaaccg	gacggagaaa	1140
gattcgccat	tgagttgtta	aagagcaccg	tctacggcgg	tctcactgag	accatcacca	1200
gcctcggcgt	tgtatcatct	gcttctgcct	ctgggttcctc	caccatgaat	atattgsctc	1260
ttgctgtcgc	aaatttggcc	ggtgggctca	tcgtcctcgc	tcaaaacttt	caagatctaa	1320
gaaacagttc	agatcaagag	aaagataggt	acgaggaatt	gttagggaga	cgtactaaat	1380
cccggatata	tatcttagta	gcggtcatgt	cttacatttt	cttcggccta	attcctccgt	1440
tagtttacgc	attttccttc	tacgaaaccg	gaatcaagaa	ctacaagctc	atctcggttt	1500
tcttggttgc	tctggtttgc	gtaattttgc	tcggttcgat	caaggtctat	gtccgaaaac	1560
caaccaattc	atgtggatcg	actaaagctt	atctcaaadc	tcggttcgat	tatacgtcta	1620
ttgttggtgc	ttcttgcgga	atctcatagc	ttgtcggaga	tattatggga	gagtatatcg	1680
agaagctcag	tttggttggt	ttagaccaga	tcagtataac	ttcaccatgt	tatggaatta	1740
aaccggagga	gtgccggttt	acttcctttt	aatatacagt	gggactaaga	accggtctga	1800
ccaacgttgt	ataatttctg	ttctaattac	ttactaaadc	tctgtatctt	ttctagtaaa	1860
aatcaaaac	taatgctttc	atagaataaa	tgtgttttga	ggtttttctc		

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..589

(D) OTHER INFORMATION: / Ceres Seq. ID 1499790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

Leu	Lys	Lys	Lys	Lys	Glu	Glu	Lys	Arg	Glu	Arg	Asp	Ser	Gln	Ile	Ile
1				5					10					15	
Ile	Ser	Pro	Ser	Leu	Thr	His	Asn	His	Phe	Lys	Glu	His	Trp	Asn	Gln
			20					25					30		
Ile	His	Tyr	Ile	Gly	Ile	Asp	Met	Glu	Lys	Ser	Asn	Gln	Pro	Val	His
		35					40					45			
Val	Thr	Leu	Ser	Glu	Leu	Lys	Asp	Gly	Asp	Lys	Glu	Ile	Val	Asp	Ala
		50				55					60				
Glu	Phe	Leu	Val	Asp	Leu	Leu	Glu	Ser	Tyr	Arg	Phe	Gly	Lys	Asp	Asn
65					70					75				80	
Val	Pro	Ala	Arg	Glu	Phe	Arg	Ser	Lys	Ala	Ala	Ala	Thr	Ala	Pro	Ala
			85						90					95	
Pro	Val	Asn	Thr	Thr	Glu	Ile	Glu	Leu	Glu	Glu	Asp	Asn	Asp	Gly	Ser
		100						105					110		
Gln	Ala	Gln	Gly	Asn	Asn	Ser	Val	Ser	Glu	Ser	Thr	Ser	Ser	Leu	Phe
		115					120					125			
Ser	Asp	Ser	Asp	Pro	Ile	Val	Leu	Glu	Ser	Thr	Val	Ser	Glu	Thr	Gly
	130					135					140				
Ser	Asn	Glu	Glu	Ser	Glu	Thr	Gly	Ser	Asn	Glu	Glu	Asn	Gly	Asn	Asn
145					150					155				160	
Trp	Leu	Glu	Ser	Ser	Ser	Thr	Asn	Leu	Pro	Asn	Val	Glu	Asn	Lys	Arg
			165						170					175	
Gln	Arg	Asn	Gly	Glu	Asp	Cys	Glu	Ile	Glu	Glu	Glu	Glu	Glu	Asn	Asn
		180						185					190		
Glu	Arg	Ser	Leu	Ser	Asp	Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Lys	Leu
		195					200					205			
Leu	Gly	Thr	Gln	Glu	Asn	Tyr	Glu	Leu	Gly	Asn	Glu	Asp	Glu	Glu	Lys
	210					215					220				
Asn	Glu	Arg	Ser	Ser	Ser	Asp	Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Asn

225		230		235		240									
Phe	Leu	Ala	Thr	Gln	Asn	Tyr	Glu	Leu	Tyr	Cys	Pro	Ser	Cys	Ser	
				245				250					255		
Thr	Cys	Ile	Thr	Arg	Asn	Val	Val	Leu	Lys	Lys	Arg	Lys	Arg	Gly	Lys
			260					265					270		
His	Val	Asn	Ser	Ser	Leu	Asp	Leu	Lys	Pro	Asp	Ile	Pro	Val	Val	Glu
		275					280					285			
Pro	Asp	Glu	Pro	Ser	Asp	Ile	Glu	Glu	Met	Glu	Ser	Pro	Val	Lys	Val
	290					295					300				
Tyr	Val	Pro	Glu	Thr	Arg	Ile	Glu	Asp	Asp	Gln	Glu	Asp	Lys	Glu	Gly
305					310					315					320
Thr	Ile	Phe	Thr	Cys	Leu	Val	Cys	Asp	Leu	Lys	Tyr	Phe	Ile	Arg	Leu
				325					330					335	
Gly	Thr	Lys	Phe	Leu	Gln	Leu	Asp	Tyr	Ile	Arg	Gly	Lys	Pro	Val	Glu
			340				345						350		
Lys	Ser	Val	Glu	Glu	Tyr	Ile	Asp	Val	Arg	Lys	Ser	Ile	Asn	Thr	Thr
		355					360					365			
Gln	Ser	Pro	Pro	Gln	Ile	Gln	Pro	Asp	Gly	Glu	Arg	Phe	Ala	Ile	Glu
	370					375					380				
Leu	Leu	Lys	Ser	Thr	Val	Tyr	Gly	Gly	Leu	Thr	Glu	Thr	Ile	Thr	Ser
385					390					395					400
Leu	Gly	Val	Val	Ser	Ser	Ala	Ser	Ala	Ser	Gly	Ser	Ser	Thr	Met	Asn
				405					410					415	
Ile	Leu	Xaa	Leu	Ala	Val	Ala	Asn	Leu	Ala	Gly	Gly	Leu	Ile	Val	Leu
			420					425					430		
Ala	Gln	Asn	Phe	Gln	Asp	Leu	Arg	Asn	Ser	Ser	Asp	Gln	Glu	Lys	Asp
		435					440					445			
Arg	Tyr	Glu	Glu	Leu	Leu	Gly	Arg	Arg	Thr	Lys	Ser	Arg	Ile	His	Ile
	450					455					460				
Leu	Val	Ala	Val	Met	Ser	Tyr	Ile	Phe	Phe	Gly	Leu	Ile	Pro	Pro	Leu
465					470					475					480
Val	Tyr	Ala	Phe	Ser	Phe	Tyr	Glu	Thr	Gly	Ile	Lys	Asn	Tyr	Lys	Leu
			485						490					495	
Ile	Ser	Val	Phe	Leu	Gly	Ser	Leu	Val	Cys	Val	Ile	Leu	Leu	Gly	Ser
		500						505					510		
Ile	Lys	Val	Tyr	Val	Arg	Lys	Pro	Thr	Asn	Ser	Cys	Gly	Ser	Thr	Lys
		515					520					525			
Ala	Tyr	Leu	Lys	Ser	Ala	Ala	Tyr	Tyr	Thr	Ser	Ile	Val	Val	Ala	Ser
	530					535					540				
Cys	Gly	Ile	Ser	Tyr	Val	Val	Gly	Asp	Ile	Met	Gly	Glu	Tyr	Ile	Glu
545					550					555					560
Lys	Leu	Ser	Leu	Val	Gly	Leu	Asp	Gln	Ile	Ser	Ile	Thr	Ser	Pro	Cys
			565						570					575	
Tyr	Gly	Ile	Lys	Pro	Glu	Glu	Cys	Arg	Phe	Thr	Ser	Phe			
		580						585							

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..550
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

Met	Glu	Lys	Ser	Asn	Gln	Pro	Val	His	Val	Thr	Leu	Ser	Glu	Leu	Lys
1				5				10					15		
Asp	Gly	Asp	Lys	Glu	Ile	Val	Asp	Ala	Glu	Phe	Leu	Val	Asp	Leu	Leu
			20					25					30		

Glu	Ser	Tyr	Arg	Phe	Gly	Lys	Asp	Asn	Val	Pro	Ala	Arg	Glu	Phe	Arg
		35					40					45			
Ser	Lys	Ala	Ala	Ala	Thr	Ala	Pro	Ala	Pro	Val	Asn	Thr	Thr	Glu	Ile
	50					55					60				
Glu	Leu	Glu	Glu	Asp	Asn	Asp	Gly	Ser	Gln	Ala	Gln	Gly	Asn	Asn	Ser
65					70					75					80
Val	Ser	Glu	Ser	Thr	Ser	Ser	Leu	Phe	Ser	Asp	Ser	Asp	Pro	Ile	Val
				85					90					95	
Leu	Glu	Ser	Thr	Val	Ser	Glu	Thr	Gly	Ser	Asn	Glu	Glu	Ser	Glu	Thr
			100					105					110		
Gly	Ser	Asn	Glu	Glu	Asn	Gly	Asn	Trp	Leu	Glu	Ser	Ser	Ser	Ser	Thr
		115					120					125			
Asn	Leu	Pro	Asn	Val	Glu	Asn	Lys	Arg	Gln	Arg	Asn	Gly	Glu	Asp	Cys
	130					135					140				
Glu	Ile	Glu	Glu	Glu	Glu	Glu	Asn	Asn	Glu	Arg	Ser	Leu	Ser	Asp	Ser
145					150					155					160
Glu	Glu	Lys	Ser	Asn	Leu	Glu	Lys	Leu	Leu	Gly	Thr	Gln	Glu	Asn	Tyr
				165					170					175	
Glu	Leu	Gly	Asn	Glu	Asp	Glu	Glu	Lys	Asn	Glu	Arg	Ser	Ser	Ser	Asp
			180					185					190		
Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Asn	Phe	Leu	Ala	Thr	Gln	Glu	Asn
		195					200					205			
Tyr	Glu	Leu	Tyr	Cys	Pro	Ser	Cys	Ser	Thr	Cys	Ile	Thr	Arg	Asn	Val
	210					215					220				
Val	Leu	Lys	Lys	Arg	Lys	Arg	Gly	Lys	His	Val	Asn	Ser	Ser	Leu	Asp
225					230					235					240
Leu	Lys	Pro	Asp	Ile	Pro	Val	Val	Glu	Pro	Asp	Glu	Pro	Ser	Asp	Ile
				245					250					255	
Glu	Glu	Met	Glu	Ser	Pro	Val	Lys	Val	Tyr	Val	Pro	Glu	Thr	Arg	Ile
			260					265					270		
Glu	Asp	Asp	Gln	Glu	Asp	Lys	Glu	Gly	Thr	Ile	Phe	Thr	Cys	Leu	Val
		275					280					285			
Cys	Asp	Leu	Lys	Tyr	Phe	Ile	Arg	Leu	Gly	Thr	Lys	Phe	Leu	Gln	Leu
	290					295					300				
Asp	Tyr	Ile	Arg	Gly	Lys	Pro	Val	Glu	Lys	Ser	Val	Glu	Glu	Tyr	Ile
305					310					315					320
Asp	Val	Arg	Lys	Ser	Ile	Asn	Thr	Thr	Gln	Ser	Pro	Pro	Gln	Ile	Gln
				325					330					335	
Pro	Asp	Gly	Glu	Arg	Phe	Ala	Ile	Glu	Leu	Leu	Lys	Ser	Thr	Val	Tyr
			340					345					350		
Gly	Gly	Leu	Thr	Glu	Thr	Ile	Thr	Ser	Leu	Gly	Val	Val	Ser	Ser	Ala
		355					360					365			
Ser	Ala	Ser	Gly	Ser	Ser	Thr	Met	Asn	Ile	Leu	Xaa	Leu	Ala	Val	Ala
	370					375					380				
Asn	Leu	Ala	Gly	Gly	Leu	Ile	Val	Leu	Ala	Gln	Asn	Phe	Gln	Asp	Leu
385					390					395					400
Arg	Asn	Ser	Ser	Asp	Gln	Glu	Lys	Asp	Arg	Tyr	Glu	Glu	Leu	Leu	Gly
				405				410						415	
Arg	Arg	Thr	Lys	Ser	Arg	Ile	His	Ile	Leu	Val	Ala	Val	Met	Ser	Tyr
			420					425					430		
Ile	Phe	Phe	Gly	Leu	Ile	Pro	Pro	Leu	Val	Tyr	Ala	Phe	Ser	Phe	Tyr
			435				440					445			
Glu	Thr	Gly	Ile	Lys	Asn	Tyr	Lys	Leu	Ile	Ser	Val	Phe	Leu	Gly	Ser
	450					455					460				
Leu	Val	Cys	Val	Ile	Leu	Leu	Gly	Ser	Ile	Lys	Val	Tyr	Val	Arg	Lys
465					470					475					480
Pro	Thr	Asn	Ser	Cys	Gly	Ser	Thr	Lys	Ala	Tyr	Leu	Lys	Ser	Ala	Ala
				485					490					495	
Tyr	Tyr	Thr	Ser	Ile	Val	Val	Ala	Ser	Cys	Gly	Ile	Ser	Tyr	Val	Val
			500					505					510		
Gly	Asp	Ile	Met	Gly	Glu	Tyr	Ile	Glu	Lys	Leu	Ser	Leu	Val	Gly	Leu

515 520 525  
Asp Gln Ile Ser Ile Thr Ser Pro Cys Tyr Gly Ile Lys Pro Glu Glu  
530 535 540  
Cys Arg Phe Thr Ser Phe  
545 550

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

```
atctcttggt ctctccgccc atctctgctc tcttttattt tcccagaaaag tttttttttt 60
tttcccgaat tccgttaatc tcattggggg ttccattgat agcaatggcg acggcctttcg 120
ctcccactaa gctcactgcc acggttcctc tgcattggatc ccatgagaat cgtctcttgc 180
tcccgatccg attggtcctt ccttcttctt tcctcggtac caccggttcc ctctcccttc 240
gcagactcaa tcactccaac gccaccgctc gatctcccggt cgtctctgtc caggaagttg 300
gtcaaggaga agcaatccac caataatacc agcctgttga taaccaaaga ggaaggattg 360
gagttgtatg aagatatgat actaggtaga tctttcgaag acatgtgtgc tcaaagtgtat 420
taccgaggca agatgttttg ttttggtcac ttgtacaatg gccaaagaggc tgtttctact 480
ggcttttatca agctccttac caagtctgac tctgtcggtt gtacctaccg tgaccatgtc 540
catgccctca gcaaagggtg ctctgctcgt gctgttatga gcgagctctt cggcaagggt 600
actggatgct gcagaggcca aggtggatcc atgcacatgt tctccaaaga acacaacatg 660
cttggtggct ttgcttttat tgggtgaaggc attcctgtcg ccactgggtg tgcccttagc 720
tccaagtaca ggagggaagt cttgaaacag gattgtgatg atgtcactgt cgcctttttc 780
ggagatggaa cttgtaacaa cggacagttc ttcgagtgtc tcaacatggc tgctctctat 840
aaactgccta ttatctttgt tgtcgagaat aacttgtggg ccattgggat gtctcacttg 900
agagccactt ctgacccccg gatttggaa gaaaggtcctg catttgggat gcctgggtgt 960
catgttgacg gtvttgatgt cttgaagggtc agggaagtcg ctaaagaggc tgtcactaga 1020
gctagaagag gagaagggtc aaccttggtt gaatgtgaga cttatagatt tagaggacac 1080
tccttggttg atcccgatga gctccgtgat gctgtctgaga aagccaaata cgcggctaga 1140
gacccaatcg cagcattgaa gaagtatttg atagagaaca agcttgcaaa ggaagcagag 1200
ctaaagtcaa tagagaaaaa gatagacgag ttggtggagg aagcggttga gtttgcagac 1260
gctagtccac agcccgggtc cagtcagttg ctagagaatg tgtttgctga tccaaaagga 1320
tttggaaatt gacctgatgg acggtacaga tgtgaggacc ccaagtttac cgaaggcaca 1380
gctcaagtct gagaagacaa gtttaaccat aagctgtcta ctgtctcttc gatgtttcta 1440
tatatcttat taagttaa at gctacagaga atcagtttga atcatttgca ctttttgctg 1500
```

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

```
Met Asp Pro Met Arg Ile Val Ser Cys Ser Arg Ser Asp Trp Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Asp Pro Pro Val Pro Ser Pro Phe Ala Asp Ser
20 25 30
Ile Thr Pro Thr Pro Pro Val Asp Leu Pro Ser Ser Leu Ser Arg Lys
35 40 45
```

Leu	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	Ile	Thr
50						55					60				
Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	Arg	Ser
65					70					75					80
Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	Phe	Gly
				85						90					95
Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	Phe	Ile
				100					105						110
Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	Ser	Thr	Tyr	Arg	Asp	His
				115				120							125
Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala	Arg	Ala	Val	Met	Ser	Glu
				130											140
Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg	Gly	Gln	Gly	Gly	Ser	Met
145					150					155					160
His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu	Gly	Gly	Phe	Ala	Phe	Ile
				165						170					175
Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala	Ala	Phe	Ser	Ser	Lys	Tyr
				180					185						190
Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp	Asp	Val	Thr	Val	Ala	Phe
				195				200							205
Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln	Phe	Phe	Glu	Cys	Leu	Asn
				210				215							220
Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile	Phe	Val	Val	Glu	Asn	Asn
225					230					235					240
Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg	Ala	Thr	Ser	Asp	Pro	Glu
				245						250					255
Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met	Pro	Gly	Val	His	Val	Asp
				260					265						270
Gly	Xaa	Asp	Val	Leu	Lys	Val	Arg	Glu	Val	Ala	Lys	Glu	Ala	Val	Thr
				275					280						285
Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu	Val	Glu	Cys	Glu	Thr	Tyr
				290				295							300
Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro	Asp	Glu	Leu	Arg	Asp	Ala
305					310					315					320
Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp	Pro	Ile	Ala	Ala	Leu	Lys
				325						330					335
Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys	Glu	Ala	Glu	Leu	Lys	Ser
				340					345						350
Ile	Glu	Lys	Lys	Ile	Asp	Glu	Leu	Val	Glu	Glu	Ala	Val	Glu	Phe	Ala
				355					360						365
Asp	Ala	Ser	Pro	Gln	Pro	Gly	Arg	Ser	Gln	Leu	Leu	Glu	Asn	Val	Phe
				370					375						380
Ala	Asp	Pro	Lys	Gly	Phe	Gly	Ile	Gly	Pro	Asp	Gly	Arg	Tyr	Arg	Cys
385					390					395					400
Glu	Asp	Pro	Lys	Phe	Thr	Glu	Gly	Thr	Ala	Gln	Val				
				405						410					

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

Met	Arg	Ile	Val	Ser	Cys	Ser	Arg	Ser	Asp	Trp	Leu	Leu	Leu	Leu	Leu
1				5					10					15	
Ser	Ser	Asp	Pro	Pro	Val	Pro	Ser	Pro	Phe	Ala	Asp	Ser	Ile	Thr	Pro



	20		25		30	
Thr	Pro	Pro	Val	Asp	Leu	Pro
	35					Ser
Glu	Lys	Gln	Ser	Thr	Asn	Asn
	50				55	Thr
Gly	Leu	Glu	Leu	Tyr	Glu	Asp
65					70	Met
Met	Cys	Ala	Gln	Met	Tyr	Tyr
				85		Arg
Leu	Tyr	Asn	Gly	Gln	Glu	Ala
			100			Val
Thr	Lys	Ser	Asp	Ser	Val	Val
	115					Ser
Leu	Ser	Lys	Gly	Val	Ser	Ala
	130				135	Arg
Lys	Val	Thr	Gly	Cys	Cys	Arg
145					150	Gly
Ser	Lys	Glu	His	Asn	Met	Leu
				165		Gly
Ile	Pro	Val	Ala	Thr	Gly	Ala
						Ala
Val	Leu	Lys	Gln	Asp	Cys	Asp
	195					Asp
Gly	Thr	Cys	Asn	Asn	Gly	Gln
	210				215	Phe
Leu	Tyr	Lys	Leu	Pro	Ile	Ile
225					230	Phe
Ile	Gly	Met	Ser	His	Leu	Arg
				245		Ala
Lys	Gly	Pro	Ala	Phe	Gly	Met
				260		Pro
Val	Leu	Lys	Val	Arg	Glu	Val
	275					Ala
Arg	Gly	Glu	Gly	Pro	Thr	Leu
	290				295	Val
Gly	His	Ser	Leu	Ala	Asp	Pro
305					310	Asp
Ala	Lys	Tyr	Ala	Ala	Arg	Asp
				325		Pro
Ile	Glu	Asn	Lys	Leu	Ala	Lys
				340		Glu
Lys	Ile	Asp	Glu	Leu	Val	Glu
				355		Glu
Pro	Gln	Pro	Gly	Arg	Ser	Gln
	370					Leu
Lys	Gly	Phe	Gly	Ile	Gly	Pro
385					390	Asp
Lys	Phe	Thr	Glu	Gly	Thr	Ala
						Gln
						Val
						405

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

Met	Ile	Leu	Gly	Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr
1				5					10					15	
Arg	Gly	Lys	Met	Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala
			20					25					30		
Val	Ser	Thr	Gly	Phe	Ile	Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val
		35					40					45			
Ser	Thr	Tyr	Arg	Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala
	50					55					60				
Arg	Ala	Val	Met	Ser	Glu	Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg
65					70				75						80
Gly	Gln	Gly	Gly	Ser	Met	His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu
				85					90					95	
Gly	Gly	Phe	Ala	Phe	Ile	Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala
			100					105					110		
Ala	Phe	Ser	Ser	Lys	Tyr	Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp
		115					120					125			
Asp	Val	Thr	Val	Ala	Phe	Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln
	130					135					140				
Phe	Phe	Glu	Cys	Leu	Asn	Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile
145					150				155						160
Phe	Val	Val	Glu	Asn	Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg	
			165					170					175		
Ala	Thr	Ser	Asp	Pro	Glu	Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met
		180						185				190			
Pro	Gly	Val	His	Val	Asp	Gly	Xaa	Asp	Val	Leu	Lys	Val	Arg	Glu	Val
	195						200					205			
Ala	Lys	Glu	Ala	Val	Thr	Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu
	210					215					220				
Val	Glu	Cys	Glu	Thr	Tyr	Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro
225					230				235						240
Asp	Glu	Leu	Arg	Asp	Ala	Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp
			245					250						255	
Pro	Ile	Ala	Ala	Leu	Lys	Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys
		260						265					270		
Glu	Ala	Glu	Leu	Lys	Ser	Ile	Glu	Lys	Lys	Ile	Asp	Glu	Leu	Val	Glu
	275						280				285				
Glu	Ala	Val	Glu	Phe	Ala	Asp	Ala	Ser	Pro	Gln	Pro	Gly	Arg	Ser	Gln
	290					295					300				
Leu	Leu	Glu	Asn	Val	Phe	Ala	Asp	Pro	Lys	Gly	Phe	Gly	Ile	Gly	Pro
305					310				315						320
Asp	Gly	Arg	Tyr	Arg	Cys	Glu	Asp	Pro	Lys	Phe	Thr	Glu	Gly	Thr	Ala
				325				330						335	

Gln Val

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

gggtttgaga gttatcggtt cgaagcttga tcctaattt caacaatgac gataatgtca	60
gatcttccac gggatttggt agcggagatt ctctagtagg ttccggttgac atctctaaga	120
gcagtgcgat tgacttgcaa aaagtgggaac gatttatcca aagatcggag ctttctcaag	180
aagcaaatacg tcgaacaaa gaagaagcaa ttggaatcga aggagattga ggtgatcatg	240
atgaggaatt ttaggggttta tctaacaagc atcgatatcc acaacaatgt tgatctatca	300

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tttacgccta aaggtacact tattagctta agcgatgatg caaaccatca tcaagtcgat 360
aatgtatcta gagtctttca ctgcatgggt ttactattat gcatcaccaa agacctccac 420
tataggcttg tbgggtttgga acccttattt tgggtcaaaca agatggatcc aaccagaaaa 480
ttctttaccac agaaaggaca attacgctct tgggtacgat gagaagaaga accacaaaat 540
cctgagattg aaggatgatt attacgctcc acgggaacgg atttgtgagt ttgaactcta 600
cagttttgag tctaattcat ggaaggttgt acttgatgtc agtcctgact ggtatatacc 660
ttctttataac cgtggcttgt ctctaaaggg gaatacttac tggtagtcaa cagagaagca 720
tgtcaatgtt gatttcttga tttgtttcga tttcacaaca gagaaatttg gaccgcgttt 780
gcctctgcct tttaacgcta ccgagtcctc tacttatgaa gatgttggtta ctctctctag 840
tggttgagaaa gagcagcttg cgggtgttgtt tcagagttag tatacattga tgatggagat 900
ttgggttacg agcaaggttg agtccacaga ggttttgttg aacaaattgt tcttagaggt 960
tgatttgata gcaatcagct ctacttttca gtttctggca gaggctggga gtttcttcac 1020
tgaccagaag aagaatgttg ttgtgtgttt tgataaagat atggatgagg ctaccgatcg 1080
cgacatggct tacgttgttg ggaagaacgg atacttcaaa aaagtggata ttggggaaga 1140
agcatacacg agttgtttcc cacttgatg ttcttatgtt ccaagctcag agcaaatcag 1200
gcagctaacc tgattattac gaactactgt tttctttttc tgatcatctc gattgtataa 1260
atctgaccat tgttatcagt tatctggaat ctacagagaca tggcctctct actatatgc
```

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

```
Met Met Gln Thr Ile Lys Ser Ile Met Tyr Leu Glu Ser Phe Thr
1      5      10      15
Ala Met Val Tyr Tyr Tyr Ala Ser Pro Lys Thr Ser Thr Ile Gly Leu
20      25      30
Xaa Val Trp Asn Pro Tyr Phe Gly Gln Thr Arg Trp Ile Gln Pro Arg
35      40      45
Asn Ser Tyr His Arg Lys Asp Asn Tyr Ala Leu Gly Tyr Asp Glu Lys
50      55      60
Lys Asn His Lys Ile Leu Arg Leu Lys Asp Asp Tyr Tyr Ala Pro Arg
65      70      75      80
Glu Arg Ile Cys Glu Phe Glu Leu Tyr Ser Phe Glu Ser Asn Ser Trp
85      90      95
Lys Val Val Leu Asp Val Ser Pro Asp Trp Tyr Ile Pro Ser Tyr Asn
100     105     110
Arg Gly Leu Ser Leu Lys Gly Asn Thr Tyr Trp Tyr Ala Thr Glu Lys
115     120     125
His Val Asn Val Asp Phe Leu Ile Cys Phe Asp Phe Thr Thr Glu Lys
130     135     140
Phe Gly Pro Arg Leu Pro Leu Pro Phe Asn Ala Thr Glu Ser Pro Thr
145     150     155     160
Tyr Glu Asp Val Val Thr Leu Ser Ser Val Gly Glu Glu Gln Leu Ala
165     170     175
Val Leu Phe Gln Ser Glu Tyr Thr Leu Met Met Glu Ile Trp Val Thr
180     185     190
Ser Lys Val Glu Ser Thr Glu Val Leu Trp Asn Lys Leu Phe Leu Glu
195     200     205
Val Asp Leu Ile Ala Ile Ser Ser His Phe Gln Phe Leu Ala Glu Ala
210     215     220
Gly Ser Phe Phe Ile Asp Gln Lys Lys Asn Val Val Val Val Phe Asp
225     230     235     240
Lys Asp Met Asp Glu Ala Thr Asp Arg Asp Met Ala Tyr Val Val Gly
245     250     255
```

Lys Asn Gly Tyr Phe Lys Lys Val Asp Ile Gly Glu Glu Ala Tyr Thr  
260 265 270  
Ser Cys Phe Pro Leu Val Cys Ser Tyr Val Pro Ser Ser Glu Gln Ile  
275 280 285  
Arg Gln Leu Thr  
290

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1499802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Gln Thr Ile Ile Lys Ser Ile Met Tyr Leu Glu Ser Phe Thr Ala  
1 5 10 15  
Met Val Tyr Tyr Tyr Ala Ser Pro Lys Thr Ser Thr Ile Gly Leu Xaa  
20 25 30  
Val Trp Asn Pro Tyr Phe Gly Gln Thr Arg Trp Ile Gln Pro Arg Asn  
35 40 45  
Ser Tyr His Arg Lys Asp Asn Tyr Ala Leu Gly Tyr Asp Glu Lys Lys  
50 55 60  
Asn His Lys Ile Leu Arg Leu Lys Asp Asp Tyr Tyr Ala Pro Arg Glu  
65 70 75 80  
Arg Ile Cys Glu Phe Glu Leu Tyr Ser Phe Glu Ser Asn Ser Trp Lys  
85 90 95  
Val Val Leu Asp Val Ser Pro Asp Trp Tyr Ile Pro Ser Tyr Asn Arg  
100 105 110  
Gly Leu Ser Leu Lys Gly Asn Thr Tyr Trp Tyr Ala Thr Glu Lys His  
115 120 125  
Val Asn Val Asp Phe Leu Ile Cys Phe Asp Phe Thr Thr Glu Lys Phe  
130 135 140  
Gly Pro Arg Leu Pro Leu Pro Phe Asn Ala Thr Glu Ser Pro Thr Tyr  
145 150 155 160  
Glu Asp Val Val Thr Leu Ser Ser Val Gly Glu Glu Gln Leu Ala Val  
165 170 175  
Leu Phe Gln Ser Glu Tyr Thr Leu Met Met Glu Ile Trp Val Thr Ser  
180 185 190  
Lys Val Glu Ser Thr Glu Val Leu Trp Asn Lys Leu Phe Leu Glu Val  
195 200 205  
Asp Leu Ile Ala Ile Ser Ser His Phe Gln Phe Leu Ala Glu Ala Gly  
210 215 220  
Ser Phe Phe Ile Asp Gln Lys Lys Asn Val Val Val Val Phe Asp Lys  
225 230 235 240  
Asp Met Asp Glu Ala Thr Asp Arg Asp Met Ala Tyr Val Val Gly Lys  
245 250 255  
Asn Gly Tyr Phe Lys Lys Val Asp Ile Gly Glu Glu Ala Tyr Thr Ser  
260 265 270  
Cys Phe Pro Leu Val Cys Ser Tyr Val Pro Ser Ser Glu Gln Ile Arg  
275 280 285  
Gln Leu Thr  
290

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..283  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499803  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:  
Met Tyr Leu Glu Ser Phe Thr Ala Met Val Tyr Tyr Tyr Ala Ser Pro  
1                  5                  10                  15  
Lys Thr Ser Thr Ile Gly Leu Xaa Val Trp Asn Pro Tyr Phe Gly Gln  
                  20                  25                  30  
Thr Arg Trp Ile Gln Pro Arg Asn Ser Tyr His Arg Lys Asp Asn Tyr  
                  35                  40                  45  
Ala Leu Gly Tyr Asp Glu Lys Lys Asn His Lys Ile Leu Arg Leu Lys  
                  50                  55                  60  
Asp Asp Tyr Tyr Ala Pro Arg Glu Arg Ile Cys Glu Phe Glu Leu Tyr  
65                  70                  75                  80  
Ser Phe Glu Ser Asn Ser Trp Lys Val Val Leu Asp Val Ser Pro Asp  
                  85                  90                  95  
Trp Tyr Ile Pro Ser Tyr Asn Arg Gly Leu Ser Leu Lys Gly Asn Thr  
                  100                 105                 110  
Tyr Trp Tyr Ala Thr Glu Lys His Val Asn Val Asp Phe Leu Ile Cys  
                 115                 120                 125  
Phe Asp Phe Thr Thr Glu Lys Phe Gly Pro Arg Leu Pro Leu Pro Phe  
                 130                 135                 140  
Asn Ala Thr Glu Ser Pro Thr Tyr Glu Asp Val Val Thr Leu Ser Ser  
145                 150                 155                 160  
Val Gly Glu Glu Gln Leu Ala Val Leu Phe Gln Ser Glu Tyr Thr Leu  
                 165                 170                 175  
Met Met Glu Ile Trp Val Thr Ser Lys Val Glu Ser Thr Glu Val Leu  
                 180                 185                 190  
Trp Asn Lys Leu Phe Leu Glu Val Asp Leu Ile Ala Ile Ser Ser His  
                 195                 200                 205  
Phe Gln Phe Leu Ala Glu Ala Gly Ser Phe Phe Ile Asp Gln Lys Lys  
                 210                 215                 220  
Asn Val Val Val Val Phe Asp Lys Asp Met Asp Glu Ala Thr Asp Arg  
225                 230                 235                 240  
Asp Met Ala Tyr Val Val Gly Lys Asn Gly Tyr Phe Lys Lys Val Asp  
                 245                 250                 255  
Ile Gly Glu Glu Ala Tyr Thr Ser Cys Phe Pro Leu Val Cys Ser Tyr  
                 260                 265                 270  
Val Pro Ser Ser Glu Gln Ile Arg Gln Leu Thr  
                 275                 280

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 957 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

    (A) NAME/KEY: -  
    (B) LOCATION: 1..957  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

aaatgaaatg	tatagagagg	taaagtggga	attttgacat	tggtgggttt	agggaaaaaa	60
cagagagaaa	gagatggatt	cgtcgtcagt	agggaacacc	aacaggtact	gggtcctccg	120
ccacggcaag	agcattccca	acgagagagg	cctcgtcgtc	tcttccatgg	aaaatgggtg	180
cctccccgag	taccagttag	cccctgatgg	tgctcgtcag	gctcgtctcg	ccggcgaatc	240
gttcctccag	caacttaagg	aaagtaacat	agaactggac	aaggttcggc	atttgctact	300
cccccttctc	cagaaccact	cacaccgcta	gggttggtgc	tgaggtcctc	aatctccctc	360

```
ttgatgctcc tcaatgcaag atgatggaag atctgcgcga acgctatattt ggacctacat 420
ttgaactcaa gtcccatgac aagtaccag agatatgggc tcttgatgaa aaagatcctt 480
ttatgggacc agaaggaggt gaaagtgtg atgatgttgt ttcccgactt gccactgcca 540
tgaaatccat ggaagctgaa tatcaaaggt gtgcaattct ggtggtgagt catggagatc 600
ctctgcagat gttgcagaac gttttccatt cagcaaagca acaggaagga gatggtttgg 660
cagagaagtt tcagttgagc agagttgctt ctgtcttgtc acagcaccgc aagtttgctt 720
tgctcactgg ggaactccga cccctcatct gattggcaat caatgtattc agcttttggg 780
atgtctttcc ttgaactctt ttgttatcaa ttcctatttc tctcccattg gcattcttgc 840
aattgccaaa cttggattag cctgtttatt atcacctctg tttgttagag aaaacatgaa 900
gatttactcc tgtaataaga aatcatgctc atttatgtta tatgtatctt caaatct
```

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1499812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

```
Met Met Glu Asp Leu Arg Glu Tyr Phe Gly Pro Thr Phe Glu Leu
1          5          10          15
Lys Ser His Asp Lys Tyr Pro Glu Ile Trp Ala Leu Asp Glu Lys Asp
          20          25          30
Pro Phe Met Gly Pro Glu Gly Gly Glu Ser Ala Asp Asp Val Val Ser
          35          40          45
Arg Leu Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys
          50          55          60
Ala Ile Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn
65          70          75          80
Val Phe His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys
          85          90          95
Phe Gln Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe
          100          105          110
Ala Leu Leu Thr Gly Glu Leu Arg Pro Leu Ile
          115          120
```

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

```
Met Glu Asp Leu Arg Glu Arg Tyr Phe Gly Pro Thr Phe Glu Leu Lys
1          5          10          15
Ser His Asp Lys Tyr Pro Glu Ile Trp Ala Leu Asp Glu Lys Asp Pro
          20          25          30
Phe Met Gly Pro Glu Gly Gly Glu Ser Ala Asp Asp Val Val Ser Arg
          35          40          45
Leu Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys Ala
          50          55          60
Ile Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn Val
65          70          75          80
Phe His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys Phe
```

85 90 95  
Gln Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe Ala  
100 105 110  
Leu Leu Thr Gly Glu Leu Arg Pro Leu Ile  
115 120

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met Gly Pro Glu Gly Gly Glu Ser Ala Asp Asp Val Val Ser Arg Leu  
1 5 10 15  
Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys Ala Ile  
20 25 30  
Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn Val Phe  
35 40 45  
His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys Phe Gln  
50 55 60  
Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe Ala Leu  
65 70 75 80  
Leu Thr Gly Glu Leu Arg Pro Leu Ile  
85

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

gagttcttcc ttcggtggaa agagcaaatt ttacttttaa gaaatttgaa aacaaagttt 60  
cattaaacag attggtggga ttttaaattt gaattttgat cagtgaatca acgataaacg 120  
attcgtcgtt atggaaggag ttggtgcacg gttaggtagg tcctcgacac ggtacggacc 180  
ggcaacggtt ttcaccggac cggtaggaa gtggaagaag aagtgggtac acgtctctcc 240  
ttcctctaag aaagacaata ataatagctc ctccggttcc gccgctgctc ccgccgctgc 300  
tgcagcttcc gtcgttaacg gtggttcgaa ttctgacggt agtaattgat cgcatttggt 360  
gctgtataag tgggcacccat tgtctcagaa tggtaacggc aatgaagatg gtaaaagtga 420  
gagtaattct ccgagcggag atacggtggc aacggtggca gaagatcctc cacggcggag 480  
attcaaatac gttccgatag cagtacttga ggaacagaag aaggaaatta cagaaattga 540  
ggaagatgat aagattgagc aggatgacaa gattgatgag gataataagg ttgagcagga 600  
agacaagggt gatgaggaca aaactgtaga ggagtcgagc gagaagaaat cggaagtgga 660  
agtggaggaa aagcctgaca tcaatgatgt tccgatggaa gatattcagc aggttgaaga 720  
aaaaatagta caggatgatg aagaaaaagt agtgcgacaa gatttgaacg aaagcactgt 780  
ggatttagga ctgaacttaa atgcaaacga tgctgatgct gatgcagaaa acgacccgaa 840  
agaggacaag ccattagaag aatgataaac tgggtgcatt gttttggttc ctcaccctca 900  
actctcaata tgaattagga agaaagacat tacagaaaga acaaagcagt cattagatat 960  
ggacgcagat ccttgatttg gtctgtaacc ccatggctta ttctttttga tgtaaatgga 1020  
aatgactcat tgattcagac tgatcattca attcatagga gattcttgtc tttttgtctg 1080  
aattttattt tgattcaaca ttcagaacat tt

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 244 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..244  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499824  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

Met	Glu	Gly	Val	Gly	Ala	Arg	Leu	Gly	Arg	Ser	Ser	Thr	Arg	Tyr	Gly
1			5					10						15	
Pro	Ala	Thr	Val	Phe	Thr	Gly	Pro	Val	Arg	Lys	Trp	Lys	Lys	Lys	Trp
			20				25					30			
Val	His	Val	Ser	Pro	Ser	Ser	Lys	Lys	Asp	Asn	Asn	Asn	Ser	Ser	Ser
			35				40					45			
Gly	Ser	Ala	Ala	Ala	Pro	Ala	Ala	Ala	Ala	Ser	Val	Val	Asn	Gly	
			50				55			60					
Gly	Ser	Asn	Ser	Asp	Gly	Ser	Asn	Gly	Ser	His	Leu	Leu	Leu	Tyr	Lys
65					70					75				80	
Trp	Ala	Pro	Leu	Ser	Gln	Asn	Gly	Asn	Gly	Asn	Glu	Asp	Gly	Lys	Ser
			85					90						95	
Glu	Ser	Asn	Ser	Pro	Ser	Glu	Asp	Thr	Val	Ala	Thr	Val	Ala	Glu	Asp
			100					105					110		
Pro	Pro	Arg	Arg	Arg	Phe	Lys	Tyr	Val	Pro	Ile	Ala	Val	Leu	Glu	Glu
			115				120					125			
Gln	Lys	Lys	Glu	Ile	Thr	Glu	Ile	Glu	Glu	Asp	Asp	Lys	Ile	Glu	Gln
			130			135				140					
Asp	Asp	Lys	Ile	Asp	Glu	Asp	Asn	Lys	Val	Glu	Gln	Glu	Asp	Lys	Val
145					150					155				160	
Asp	Glu	Asp	Lys	Thr	Val	Glu	Glu	Ser	Ser	Glu	Lys	Lys	Ser	Glu	Val
			165					170						175	
Glu	Val	Glu	Glu	Lys	Pro	Asp	Ile	Asn	Asp	Val	Pro	Met	Glu	Asp	Ile
			180					185				190			
Gln	Gln	Val	Glu	Glu	Lys	Ile	Val	Gln	Asp	Asp	Glu	Glu	Lys	Val	Val
			195				200					205			
Arg	Gln	Asp	Leu	Asn	Glu	Ser	Thr	Val	Asp	Leu	Gly	Leu	Asn	Leu	Asn
			210				215				220				
Ala	Asn	Asp	Ala	Asp	Ala	Asp	Ala	Glu	Asn	Asp	Pro	Lys	Glu	Asp	Lys
225					230					235				240	
Pro	Leu	Glu	Glu												

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1851 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1851  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499825  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

aaaaaaacat	tcactcggtta	actcttctcc	tccatccaat	ttcactttct	ctcactcatt	60
tttattcgtc	gtcgtcggtct	cctctgattt	gttctttttt	ctctaaattc	gcttcgcttc	120
ttctcagttc	tacgaatctt	cgattctctt	tggttttctc	catccccgta	tacgtttaag	180
aacattgcaa	gaaagtgaag	aaaaaaaatg	caggaaggga	ctgatccgta	tggtgagatt	240
gagataagtt	ttggttatca	atgcaataat	aagaagatag	gaatccctga	agataaaatt	300
gctgatggtc	gtgagggttct	tgggtgggttt	aggctacaaa	agactagcag	tttctcttgt	360



```
ttatcaggag ctgctttaag tggaaacccc actttagcca atactaatat ctgcaatgga 420
gtcattgggt ctgagatatt gccgtctctg gattctccga aatctttcag gaaagttccg 480
tcttcgcctg cgcttttcgaa gcttgatata ctctctcctt ctctccatgg aagtatggtg 540
agtctaagct gcagctcgtc tactagtccg agtcctcctg agcctgaatc ttgttacttg 600
acgtcaatga gttctccttc ttctgttaat gaagggtttc ttctctctgc tatggaagtt 660
caagttgcgg gtggtgctgc aggggaagat agagttcaag ctgtttgctc tgaggagaat 720
ggttggttgt ttgctgctat ctatgatgga ttcaacggaa gagatgctgc tgatttcttg 780
gcatgtactt tatatgagtc cattgtgttt catcttcagt tgcttgatcg tcaaatgaag 840
caaacaaagt ccgatgatga tggcgaaaag ttggaattgt tatcaaataa aagtaatgta 900
gattactctt ccactgattt gttcaggcaa ggagtactag attgcttgaa ccgtgcgctt 960
tttcaggcgg aaaccgattt cctaaggatg gttgagcaag aaatggaaga aagaccggat 1020
ttagtatccg ttggatcttg tgttttggtc actctcctgg ttgggaagga tctatacgtc 1080
cttaatcttg gtgatagcag agctgttcta gcgacctaca atggtaataa gaagctgcaa 1140
cctgttcagc tcacagagga tcatacagtt gataacgaag tcgaagaagc tagactctta 1200
agtgagcatc ttgatgatcc taagatcggt attggtggga aaatcaaagg aaagcttaaa 1260
gttactcgtg ctctcggagt tggttacttg aagaaggaga aactaaatga tgcactcatg 1320
gagatcctcc gcgttcgtaa ctttttgagc ccgccttatg tttcagtgga accatcgatg 1380
agagttcaca agataacgga atcagatcac tttgttatag ttgcaagcga tggtttgttt 1440
gatttcttca gcaacgagga agcgattggg ctctgccatt ccttcgtttc tagtaatcct 1500
tctggtgato cagcaaagtt tctgcttgaa cgtctttagt ctaaagctgc tgctcgtgct 1560
ggctttacct tggagaagatt gacgaatgtt ccggctggta ggagaaggag atatcatgac 1620
gatgtgacta taatggtaat cactctaggt accgatcaac gtacctcaaa agcttctacg 1680
ttcgtgtgat tttgatgatg atggcgacaa atggtggatt ggtaaaattg taattagtct 1740
cactgatctt ctttttagact ttggaactga tcatcagttt ttcaattctt tgggaactggt 1800
ataatattat ttcatgtata gtccgtatat atatatcatt gtagtagtct t
```

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

```
Met Gln Glu Gly Thr Asp Pro Tyr Gly Glu Ile Glu Ile Ser Phe Gly
1          5          10          15
Tyr Gln Cys Asn Asn Lys Lys Ile Gly Ile Pro Glu Asp Lys Ile Ala
20          25          30
Asp Gly Arg Glu Val Leu Gly Gly Phe Arg Leu Gln Lys Thr Ser Ser
35          40          45
Phe Ser Cys Leu Ser Gly Ala Ala Leu Ser Gly Asn Pro Thr Leu Ala
50          55          60
Asn Thr Asn Ile Cys Asn Gly Val Ile Gly Ser Glu Ile Leu Pro Ser
65          70          75          80
Leu Asp Ser Pro Lys Ser Phe Arg Lys Val Pro Ser Ser Pro Ala Leu
85          90          95
Ser Lys Leu Asp Ile Leu Ser Pro Ser Leu His Gly Ser Met Val Ser
100         105         110
Leu Ser Cys Ser Ser Ser Thr Ser Pro Ser Pro Pro Glu Pro Glu Ser
115         120         125
Cys Tyr Leu Thr Ser Met Ser Ser Pro Ser Ser Val Asn Glu Gly Phe
130         135         140
Leu Leu Ser Ala Met Glu Val Gln Val Ala Gly Gly Ala Ala Gly Glu
145         150         155         160
Asp Arg Val Gln Ala Val Cys Ser Glu Glu Asn Gly Trp Leu Phe Cys
165         170         175
Ala Ile Tyr Asp Gly Phe Asn Gly Arg Asp Ala Ala Asp Phe Leu Ala
180         185         190
```

Cys	Thr	Leu	Tyr	Glu	Ser	Ile	Val	Phe	His	Leu	Gln	Leu	Leu	Asp	Arg
		195					200					205			
Gln	Met	Lys	Gln	Thr	Lys	Ser	Asp	Asp	Asp	Gly	Glu	Lys	Leu	Glu	Leu
	210					215					220				
Leu	Ser	Asn	Ile	Ser	Asn	Val	Asp	Tyr	Ser	Ser	Thr	Asp	Leu	Phe	Arg
225					230					235					240
Gln	Gly	Val	Leu	Asp	Cys	Leu	Asn	Arg	Ala	Leu	Phe	Gln	Ala	Glu	Thr
				245					250					255	
Asp	Phe	Leu	Arg	Met	Val	Glu	Gln	Glu	Met	Glu	Glu	Arg	Pro	Asp	Leu
			260					265					270		
Val	Ser	Val	Gly	Ser	Cys	Val	Leu	Val	Thr	Leu	Leu	Val	Gly	Lys	Asp
	275						280					285			
Leu	Tyr	Val	Leu	Asn	Leu	Gly	Asp	Ser	Arg	Ala	Val	Leu	Ala	Thr	Tyr
	290					295					300				
Asn	Gly	Asn	Lys	Lys	Leu	Gln	Ala	Val	Gln	Leu	Thr	Glu	Asp	His	Thr
305					310					315					320
Val	Asp	Asn	Glu	Val	Glu	Glu	Ala	Arg	Leu	Leu	Ser	Glu	His	Leu	Asp
				325					330					335	
Asp	Pro	Lys	Ile	Val	Ile	Gly	Gly	Lys	Ile	Lys	Gly	Lys	Leu	Lys	Val
		340					345						350		
Thr	Arg	Ala	Leu	Gly	Val	Gly	Tyr	Leu	Lys	Lys	Glu	Lys	Leu	Asn	Asp
	355						360					365			
Ala	Leu	Met	Glu	Ile	Leu	Arg	Val	Arg	Asn	Leu	Leu	Ser	Pro	Pro	Tyr
	370					375					380				
Val	Ser	Val	Glu	Pro	Ser	Met	Arg	Val	His	Lys	Ile	Thr	Glu	Ser	Asp
385					390					395					400
His	Phe	Val	Ile	Val	Ala	Ser	Asp	Gly	Leu	Phe	Asp	Phe	Phe	Ser	Asn
			405						410					415	
Glu	Glu	Ala	Ile	Gly	Leu	Val	His	Ser	Phe	Val	Ser	Ser	Asn	Pro	Ser
		420						425					430		
Gly	Asp	Pro	Ala	Lys	Phe	Leu	Leu	Glu	Arg	Leu	Val	Ala	Lys	Ala	Ala
	435					440						445			
Ala	Arg	Ala	Gly	Phe	Thr	Leu	Glu	Glu	Leu	Thr	Asn	Val	Pro	Ala	Gly
	450					455					460				
Arg	Arg	Arg	Arg	Tyr	His	Asp	Asp	Val	Thr	Ile	Met	Val	Ile	Thr	Leu
465					470					475					480
Gly	Thr	Asp	Gln	Arg	Thr	Ser	Lys	Ala	Ser	Thr	Phe	Val			
				485					490						

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

Met	Val	Ser	Leu	Ser	Cys	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	Pro	Glu
1				5					10					15	
Pro	Glu	Ser	Cys	Tyr	Leu	Thr	Ser	Met	Ser	Ser	Pro	Ser	Ser	Val	Asn
		20						25					30		
Glu	Gly	Phe	Leu	Leu	Ser	Ala	Met	Glu	Val	Gln	Val	Ala	Gly	Gly	Ala
	35					40					45				
Ala	Gly	Glu	Asp	Arg	Val	Gln	Ala	Val	Cys	Ser	Glu	Glu	Asn	Gly	Trp
	50					55					60				
Leu	Phe	Cys	Ala	Ile	Tyr	Asp	Gly	Phe	Asn	Gly	Arg	Asp	Ala	Ala	Asp
65				70					75					80	
Phe	Leu	Ala	Cys	Thr	Leu	Tyr	Glu	Ser	Ile	Val	Phe	His	Leu	Gln	Leu

Met	Ser	Ser	Pro	Ser	Ser	Val	Asn	Glu	Gly	Phe	Leu	Leu	Ser	Ala	Met
1				5					10					15	
Glu	Val	Gln	Val	Ala	Gly	Gly	Ala	Ala	Gly	Glu	Asp	Arg	Val	Gln	Ala
			20					25					30		
Val	Cys	Ser	Glu	Glu	Asn	Gly	Trp	Leu	Phe	Cys	Ala	Ile	Tyr	Asp	Gly
		35				40						45			
Phe	Asn	Gly	Arg	Asp	Ala	Ala	Asp	Phe	Leu	Ala	Cys	Thr	Leu	Tyr	Glu
	50					55					60				
Ser	Ile	Val	Phe	His	Leu	Gln	Leu	Leu	Asp	Arg	Gln	Met	Lys	Gln	Thr
65					70					75					80

Lys Ser Asp Asp Asp Gly Glu Lys Leu Glu Leu Leu Ser Asn Ile Ser  
85 90 95  
Asn Val Asp Tyr Ser Ser Thr Asp Leu Phe Arg Gln Gly Val Leu Asp  
100 105 110  
Cys Leu Asn Arg Ala Leu Phe Gln Ala Glu Thr Asp Phe Leu Arg Met  
115 120 125  
Val Glu Gln Glu Met Glu Glu Arg Pro Asp Leu Val Ser Val Gly Ser  
130 135 140  
Cys Val Leu Val Thr Leu Leu Val Gly Lys Asp Leu Tyr Val Leu Asn  
145 150 155 160  
Leu Gly Asp Ser Arg Ala Val Leu Ala Thr Tyr Asn Gly Asn Lys Lys  
165 170 175  
Leu Gln Ala Val Gln Leu Thr Glu Asp His Thr Val Asp Asn Glu Val  
180 185 190  
Glu Glu Ala Arg Leu Leu Ser Glu His Leu Asp Asp Pro Lys Ile Val  
195 200 205  
Ile Gly Gly Lys Ile Lys Gly Lys Leu Lys Val Thr Arg Ala Leu Gly  
210 215 220  
Val Gly Tyr Leu Lys Lys Glu Lys Leu Asn Asp Ala Leu Met Glu Ile  
225 230 235 240  
Leu Arg Val Arg Asn Leu Leu Ser Pro Pro Tyr Val Ser Val Glu Pro  
245 250 255  
Ser Met Arg Val His Lys Ile Thr Glu Ser Asp His Phe Val Ile Val  
260 265 270  
Ala Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn Glu Glu Ala Ile Gly  
275 280 285  
Leu Val His Ser Phe Val Ser Ser Asn Pro Ser Gly Asp Pro Ala Lys  
290 295 300  
Phe Leu Leu Glu Arg Leu Val Ala Lys Ala Ala Arg Ala Gly Phe  
305 310 315 320  
Thr Leu Glu Glu Leu Thr Asn Val Pro Ala Gly Arg Arg Arg Arg Tyr  
325 330 335  
His Asp Asp Val Thr Ile Met Val Ile Thr Leu Gly Thr Asp Gln Arg  
340 345 350  
Thr Ser Lys Ala Ser Thr Phe Val  
355 360

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1810
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

atacctacaa gacgacgagt gttccattt ccttggtcta tttcaagaca tggactcttc	60
tccttctgct ttcggattag aagggttttaa tagcaacgac aataatacta atcaaaagaa	120
acgcccaaga aaagacgacg aaggcggtgg tgggtggcggc ggaggaacag aagttctagg	180
agctgttaat ggtaataata aggctgcttt tggagatata ctgcgcacgc ttttggtgtt	240
agacgaggaa gctaaacagc aacaagaaca gtgggatttt gaatctatta aagagaagtc	300
tttacttgaa gctaatacata agaagaaagt gaaaacaatg gatgggttatt acaatcaaat	360
gcaagatcat tactctgcag ctggtgaaac cgatgggttcg cgttcaaaac gcgcacggaa	420
aaccgcggtt gcggtctgtg tttccgcggt agcttccggg gcggacacaa ccggtttagc	480
tgctccggtt ccgaccgcgg atatcgctag cgggttccggg tcaggaccga gtcataggag	540
gttatgggtt aaagaacgaa ccacggactg gtgggacaga gtaagccggc ctgattttcc	600
agaagacgag tttcggcgag agttccgtat gagcaaactc acgtttaacc taatatgcga	660
ggagctagat acgacggtga cgaagaaaaa cacgatgtta agagacgcga ttccagctcc	720
aaaacgcgta ggcgtttgcg tttggcggtt ggcgacagga gctccgcttc gccacgtgtc	780

ggagcgtttc ggtctgggaa tctcaacttg ccacaaacta gtcatcgaag tctgccgcgc 840  
gatctacgac gttctcatgc ccaagtatct cctctggccg tcggattcag agataaactc 900  
aacgaaagcc aaattcgaat cgggtccaca aataccaaac gtcgtcggat caatctacac 960  
cacacatatt ccgatcatcg ctccgaaagt ccacgtggcg gcgtatttta acaagagaca 1020  
cacggagagg aatcagaaga cgtcgtactc gataacagta caaggagtgg tcaacgccga 1080  
cgggatcttc accgacgttt gtatcggaaa cccaggatct ctcaccgacg atcagatcct 1140  
ggagaaatct tcgctttcac ggcaaagagc ggcgcggtgg atgttacgtg acagctggat 1200  
agttggaaac tctgggtttc cgttgactga ttatcttctt gtaccgtaca cgagacagaa 1260  
tctgacgtgg acgcagcacg cgtttaacga gagtatcgga gagattcagg ggattgcgac 1320  
ggctgcgttt gagaggtca aaggacggtg ggcttggttg cagaaacgga cggaggtgaa 1380  
gcttcaggat ctgccgtacg tgcttgagc ttgttggtg ttgcataaca tttgtgagat 1440  
gaggaaggag gagatgttg cggagttgaa gtttgagggt tttgatgatg tggcggtgcc 1500  
ggagaataat atccgatctg ctagtgcggt taatacgagg gatcatatct ctcacaatct 1560  
cttgcatcgt ggacttgccg ggacaagaac tctataggct ctgtttttca ctttttctta 1620  
ttttgaaact gattttttat tgcaaatctt ttttccaaat taggaataaa aacattttag 1680  
ggattgggtg gatacagaaa gaatagttga attgagagta gaagtggctg atgatattgt 1740  
ttgtgttact tattagcatt gtgtaatctt tagttcatgt attttctata caaattgaat 1800  
ctgaaacctt

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1499830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

Tyr Leu Gln Asp Asp Glu Cys Ser His Phe Leu Gly Leu Phe Gln Asp  
1 5 10 15  
Met Asp Ser Ser Pro Ser Ala Phe Gly Leu Glu Gly Phe Asn Ser Asn  
20 25 30  
Asp Asn Asn Thr Asn Gln Lys Lys Arg Pro Arg Lys Asp Asp Glu Gly  
35 40 45  
Gly Gly Gly Gly Gly Gly Thr Glu Val Leu Gly Ala Val Asn Gly  
50 55 60  
Asn Asn Lys Ala Ala Phe Gly Asp Ile Leu Ala Thr Leu Leu Leu Leu  
65 70 75 80  
Asp Glu Glu Ala Lys Gln Gln Gln Glu Gln Trp Asp Phe Glu Ser Ile  
85 90 95  
Lys Glu Lys Ser Leu Leu Glu Ala Asn His Lys Lys Lys Val Lys Thr  
100 105 110  
Met Asp Gly Tyr Tyr Asn Gln Met Gln Asp His Tyr Ser Ala Ala Gly  
115 120 125  
Glu Thr Asp Gly Ser Arg Ser Lys Arg Ala Arg Lys Thr Ala Val Ala  
130 135 140  
Ala Val Val Ser Ala Val Ala Ser Gly Ala Asp Thr Thr Gly Leu Ala  
145 150 155 160  
Ala Pro Val Pro Thr Ala Asp Ile Ala Ser Gly Ser Gly Ser Gly Pro  
165 170 175  
Ser His Arg Arg Leu Trp Val Lys Glu Arg Thr Thr Asp Trp Trp Asp  
180 185 190  
Arg Val Ser Arg Pro Asp Phe Pro Glu Asp Glu Phe Arg Arg Glu Phe  
195 200 205  
Arg Met Ser Lys Ser Thr Phe Asn Leu Ile Cys Glu Glu Leu Asp Thr  
210 215 220  
Thr Val Thr Lys Lys Asn Thr Met Leu Arg Asp Ala Ile Pro Ala Pro  
225 230 235 240  
Lys Arg Val Gly Val Cys Val Trp Arg Leu Ala Thr Gly Ala Pro Leu

Met	Asp	Ser	Ser	Pro	Ser	Ala	Phe	Gly	Leu	Glu	Gly	Phe	Asn	Ser	Asn
1				5					10					15	
Asp	Asn	Asn	Thr	Asn	Gln	Lys	Lys	Arg	Pro	Arg	Lys	Asp	Asp	Glu	Gly
			20					25					30		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Glu	Val	Leu	Gly	Ala	Val	Asn	Gly
			35				40					45			
Asn	Asn	Lys	Ala	Ala	Phe	Gly	Asp	Ile	Leu	Ala	Thr	Leu	Leu	Leu	Leu
	50					55					60				
Asp	Glu	Glu	Ala	Lys	Gln	Gln	Gln	Glu	Gln	Trp	Asp	Phe	Glu	Ser	Ile
65				70						75				80	
Lys	Glu	Lys	Ser	Leu	Leu	Glu	Ala	Asn	His	Lys	Lys	Lys	Val	Lys	Thr
				85					90					95	

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1499832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

Met	Asp	Gly	Tyr	Tyr	Asn	Gln	Met	Gln	Asp	His	Tyr	Ser	Ala	Ala	Gly
1			5					10					15		
Glu	Thr	Asp	Gly	Ser	Arg	Ser	Lys	Arg	Ala	Arg	Lys	Thr	Ala	Val	Ala
			20				25						30		
Ala	Val	Val	Ser	Ala	Val	Ala	Ser	Gly	Ala	Asp	Thr	Thr	Gly	Leu	Ala
			35				40					45			
Ala	Pro	Val	Pro	Thr	Ala	Asp	Ile	Ala	Ser	Gly	Ser	Gly	Ser	Gly	Pro
	50					55				60					
Ser	His	Arg	Arg	Leu	Trp	Val	Lys	Glu	Arg	Thr	Thr	Asp	Trp	Trp	Asp
65					70				75						80
Arg	Val	Ser	Arg	Pro	Asp	Phe	Pro	Glu	Asp	Glu	Phe	Arg	Arg	Glu	Phe
				85				90						95	
Arg	Met	Ser	Lys	Ser	Thr	Phe	Asn	Leu	Ile	Cys	Glu	Glu	Leu	Asp	Thr
			100					105					110		
Thr	Val	Thr	Lys	Lys	Asn	Thr	Met	Leu	Arg	Asp	Ala	Ile	Pro	Ala	Pro
		115					120					125			
Lys	Arg	Val	Gly	Val	Cys	Val	Trp	Arg	Leu	Ala	Thr	Gly	Ala	Pro	Leu
						135					140				
Arg	His	Val	Ser	Glu	Arg	Phe	Gly	Leu	Gly	Ile	Ser	Thr	Cys	His	Lys
145					150				155						160
Leu	Val	Ile	Glu	Val	Cys	Arg	Ala	Ile	Tyr	Asp	Val	Leu	Met	Pro	Lys
				165				170						175	
Tyr	Leu	Leu	Trp	Pro	Ser	Asp	Ser	Glu	Ile	Asn	Ser	Thr	Lys	Ala	Lys
			180					185					190		
Phe	Glu	Ser	Val	His	Lys	Ile	Pro	Asn	Val	Val	Gly	Ser	Ile	Tyr	Thr
		195					200					205			
Thr	His	Ile	Pro	Ile	Ile	Ala	Pro	Lys	Val	His	Val	Ala	Ala	Tyr	Phe
		210				215					220				
Asn	Lys	Arg	His	Thr	Glu	Arg	Asn	Gln	Lys	Thr	Ser	Tyr	Ser	Ile	Thr
225					230					235					240
Val	Gln	Gly	Val	Val	Asn	Ala	Asp	Gly	Ile	Phe	Thr	Asp	Val	Cys	Ile
				245					250					255	
Gly	Asn	Pro	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Leu	Glu	Lys	Ser	Ser
		260						265					270		
Leu	Ser	Arg	Gln	Arg	Ala	Ala	Arg	Gly	Met	Leu	Arg	Asp	Ser	Trp	Ile
		275					280					285			
Val	Gly	Asn	Ser	Gly	Phe	Pro	Leu	Thr	Asp	Tyr	Leu	Leu	Val	Pro	Tyr
		290				295					300				
Thr	Arg	Gln	Asn	Leu	Thr	Trp	Thr	Gln	His	Ala	Phe	Asn	Glu	Ser	Ile
305					310					315					320
Gly	Glu	Ile	Gln	Gly	Ile	Ala	Thr	Ala	Ala	Phe	Glu	Arg	Leu	Lys	Gly
				325					330					335	
Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr	Glu	Val	Lys	Leu	Gln	Asp	Leu
			340					345					350		
Pro	Tyr	Val	Leu	Gly	Ala	Cys	Cys	Val	Leu	His	Asn	Ile	Cys	Glu	Met
		355					360					365			
Arg	Lys	Glu	Glu	Met	Leu	Pro	Glu	Leu	Lys	Phe	Glu	Val	Phe	Asp	Asp
		370				375					380				
Val	Ala	Val	Pro	Glu	Asn	Asn	Ile	Arg	Ser	Ala	Ser	Ala	Val	Asn	Thr
385					390					395					400
Arg	Asp	His	Ile	Ser	His	Asn	Leu	Leu	His	Arg	Gly	Leu	Ala	Gly	Thr
				405					410					415	
Arg	Thr	Leu													

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1540
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499833
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

```
aaaaaatctg aaattctcag gcgagattcc ggaagcaaaa cattcctaaa tttcgccaag      60
tgatccgccca tgggagaaga gaagtctctg cttcagttcc gtagttttcc ttcactcaag      120
acctctgatt tcgctctcac cgaagaacct tcatggaggc tggagaacaa cgtgtcgtcg      180
aatcgccgga gaggaacaa gagaaagcggg ggcgttttta ccaattttgc gtccctttcc      240
gtagcgatta ggagagatcg gagakaatct acatttaacg gtcgtaatgg cggcggaggc      300
ggagcgttcg cgtcggtttc ggtggtgatt ccgaaggaag aggatgaatt cgcgcctacc      360
tcggcccagc tgttgaaaaa ccccattgct ttactgtcga tagtaccgaa agacgccgca      420
ctattcttcg cgggagcgtt cggcggagcc gccgcaaagt cagtgaacgg accgcttgac      480
cgaataaagc tcctaattgca gacacatggt gttcgagctg ggcaacaaag tgctaagaag      540
gctattggtt tcattgaggc cattactctt atcggaaagg aagaaggat taaaggttat      600
tggaagga atctacctca ggtgataagg attgtacctt atagcgagt ccagttgttt      660
gcatatgaaa catacaagaa actcttcagg gggaaagacg gtcaattgtc agtcctcgga      720
aggctcggtg ctggtgcttg tgctggcatt acgtctactc tgattacata ccctttagat      780
gtgctgagat tgaggtttagc tgttgaacca ggttatcgaa ccatgtccca gggtgccttg      840
aacatgctgc gggaggaagg agttgcatca ttctacaacg gtctagggtc ttcgctttta      900
agtatagctc cttacattgc catcaacttc tgcgtctttg atctggtaaa gaaatctctg      960
ccagagaagt atcaacaaaa gacacaatca tctttgttaa cagcagtagt agctgctgct      1020
attgctaccg gtacttgcta tccattggat accattagaa gacagatgca attgaagggt      1080
actccatata aatcgggtatt agacgcttcc tcaggtatca ttgcgcgtga aggagttggt      1140
ggcttgtacc gtggctttgt ccccaatgca ctcaaaagca tgccaaacag cagattaaag      1200
cttacaacat tcgacatcgt caagaaactc atagcagcga gtgagaagga gatccaaaga      1260
atcgcgatg ataaccgcaa gaaagcaagt cctaacacaa ccgatgaaca aacctgaaga      1320
cgcaattttg gatttccaca aggtcatttt tgcccgttat cttatgacct ttgtttgtgt      1380
gttttgaat ttggaatgta ataagttgta tgttctcctc ataattcaaa atgtgcttga      1440
attgaatcct gaagccagag agggtaataa atggctgttt gtgttacggt tggtcgcgct      1500
ggttttgtat aaaccgaatt taaccgggtt gctacactcg
```

(2) INFORMATION FOR SEQ ID NO:1204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 415 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..415
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499834
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

```
Met Gly Glu Glu Lys Ser Leu Leu Gln Phe Arg Ser Phe Pro Ser Leu
1           5           10           15
Lys Thr Ser Asp Phe Ala Leu Thr Glu Glu Pro Ser Trp Arg Leu Glu
20           25           30
Asn Asn Val Ser Ser Asn Arg Arg Gly Asn Lys Arg Ser Gly Gly
35           40           45
Val Phe Thr Asn Phe Ala Ser Leu Ser Val Ala Ile Arg Arg Asp Arg
50           55           60
Arg Xaa Ser Thr Phe Asn Gly Arg Asn Gly Gly Gly Gly Ala Phe
65           70           75           80
Ala Ser Val Ser Val Val Ile Pro Lys Glu Glu Asp Glu Phe Ala Pro
85           90           95
Thr Ser Ala Gln Leu Leu Lys Asn Pro Ile Ala Leu Leu Ser Ile Val
```

100	105	110
Pro Lys Asp Ala Ala Leu Phe Phe Ala Gly Ala Phe Ala Gly Ala Ala		
115	120	125
Ala Lys Ser Val Thr Ala Pro Leu Asp Arg Ile Lys Leu Leu Met Gln		
130	135	140
Thr His Gly Val Arg Ala Gly Gln Gln Ser Ala Lys Lys Ala Ile Gly		
145	150	155
Phe Ile Glu Ala Ile Thr Leu Ile Gly Lys Glu Glu Gly Ile Lys Gly		
165	170	175
Tyr Trp Lys Gly Asn Leu Pro Gln Val Ile Arg Ile Val Pro Tyr Ser		
180	185	190
Ala Val Gln Leu Phe Ala Tyr Glu Thr Tyr Lys Lys Leu Phe Arg Gly		
195	200	205
Lys Asp Gly Gln Leu Ser Val Leu Gly Arg Leu Gly Ala Gly Ala Cys		
210	215	220
Ala Gly Met Thr Ser Thr Leu Ile Thr Tyr Pro Leu Asp Val Leu Arg		
225	230	235
Leu Arg Leu Ala Val Glu Pro Gly Tyr Arg Thr Met Ser Gln Val Ala		
245	250	255
Leu Asn Met Leu Arg Glu Glu Gly Val Ala Ser Phe Tyr Asn Gly Leu		
260	265	270
Gly Pro Ser Leu Leu Ser Ile Ala Pro Tyr Ile Ala Ile Asn Phe Cys		
275	280	285
Val Phe Asp Leu Val Lys Lys Ser Leu Pro Glu Lys Tyr Gln Gln Lys		
290	295	300
Thr Gln Ser Ser Leu Leu Thr Ala Val Val Ala Ala Ala Ile Ala Thr		
305	310	315
Gly Thr Cys Tyr Pro Leu Asp Thr Ile Arg Arg Gln Met Gln Leu Lys		
325	330	335
Gly Thr Pro Tyr Lys Ser Val Leu Asp Ala Phe Ser Gly Ile Ile Ala		
340	345	350
Arg Glu Gly Val Val Gly Leu Tyr Arg Gly Phe Val Pro Asn Ala Leu		
355	360	365
Lys Ser Met Pro Asn Ser Ser Ile Lys Leu Thr Thr Phe Asp Ile Val		
370	375	380
Lys Lys Leu Ile Ala Ala Ser Glu Lys Glu Ile Gln Arg Ile Ala Asp		
385	390	395
Asp Asn Arg Lys Lys Ala Ser Pro Asn Thr Thr Asp Glu Gln Thr		
405	410	415

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..273
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

Met Gln Thr His Gly Val Arg Ala Gly Gln Gln Ser Ala Lys Lys Ala	
1	15
Ile Gly Phe Ile Glu Ala Ile Thr Leu Ile Gly Lys Glu Glu Gly Ile	
20	30
Lys Gly Tyr Trp Lys Gly Asn Leu Pro Gln Val Ile Arg Ile Val Pro	
35	45
Tyr Ser Ala Val Gln Leu Phe Ala Tyr Glu Thr Tyr Lys Lys Leu Phe	
50	60
Arg Gly Lys Asp Gly Gln Leu Ser Val Leu Gly Arg Leu Gly Ala Gly	
65	80

Ala Cys Ala Gly Met Thr Ser Thr Leu Ile Thr Tyr Pro Leu Asp Val  
85 90 95  
Leu Arg Leu Arg Leu Ala Val Glu Pro Gly Tyr Arg Thr Met Ser Gln  
100 105 110  
Val Ala Leu Asn Met Leu Arg Glu Glu Gly Val Ala Ser Phe Tyr Asn  
115 120 125  
Gly Leu Gly Pro Ser Leu Leu Ser Ile Ala Pro Tyr Ile Ala Ile Asn  
130 135 140  
Phe Cys Val Phe Asp Leu Val Lys Lys Ser Leu Pro Glu Lys Tyr Gln  
145 150 155 160  
Gln Lys Thr Gln Ser Ser Leu Leu Thr Ala Val Val Ala Ala Ala Ile  
165 170 175  
Ala Thr Gly Thr Cys Tyr Pro Leu Asp Thr Ile Arg Arg Gln Met Gln  
180 185 190  
Leu Lys Gly Thr Pro Tyr Lys Ser Val Leu Asp Ala Phe Ser Gly Ile  
195 200 205  
Ile Ala Arg Glu Gly Val Val Gly Leu Tyr Arg Gly Phe Val Pro Asn  
210 215 220  
Ala Leu Lys Ser Met Pro Asn Ser Ser Ile Lys Leu Thr Thr Phe Asp  
225 230 235 240  
Ile Val Lys Lys Leu Ile Ala Ala Ser Glu Lys Glu Ile Gln Arg Ile  
245 250 255  
Ala Asp Asp Asn Arg Lys Lys Ala Ser Pro Asn Thr Thr Asp Glu Gln  
260 265 270  
Thr

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

aaaaaaacca	ataaaattgg	tcgcttcgca	aaaactgaga	tvtagattct	tccttcggtg	60
gaaagagcaa	attttacttt	taagaaat	gaaaacaaag	tttcattaaa	cagattgggtg	120
ggatttttaa	tttgaatttt	gatcagtgaa	tcaacgataa	acgattcgtc	gttatggaag	180
gagttggtgc	acggttaggc	aggtcctcga	cacggtacgg	accggcaacg	gttttcaccg	240
gtccggtgcg	gaagtggaa	aagaagtggg	tacacgtctc	tccatccact	aagaaagaca	300
ataataatag	ctcctccggt	tccgccgctg	ctgcagcttc	cgtcgttaat	ggtggttcga	360
attctgacgg	cagtaatgga	tgcattttgt	tgctgtataa	gtgggcacca	ttgtcccaga	420
acggtaacgg	gaatgaagat	ggtaaaagtg	agagtaattc	tccgagcgag	gacacgggtg	480
cgacggtggc	agaagatcct	ccgcggcgga	gattcaaata	cgttccgata	gcagtacttg	540
aggaacagaa	gaaggaaatt	acagaaattg	aggacgatga	taagattgag	gaggatgaca	600
agattgatga	ggataataag	gtcgcagcag	aagacaaggt	tgatgaggac	aaaactgtag	660
aggagtcgag	cgagaagaaa	gcggaagttg	aagtggaa	ggaggaaaag	cctgatatca	720
atgatgttcc	aatggaagat	attcagcag	atgaagaaaa	aatagtagac	gatgatgaag	780
aaaaagtagt	gcgacaagat	ttgaacgaaa	gcactgtgga	tttaggactg	aacttaaatg	840
caaacgatgc	tgatgctgat	gcagaaaacg	acccgaaa	ggacaagcca	ttagaagaat	900
gataaactgg	gtgcattgtt	ttggttcctc	accctcaact	ctcaatatca	attaggaaga	960
aagacattac	agaaagaaca	aagcagtc	tagatatgga	cgcagatcct	tgatttggtc	1020
tgtaacccca	tggcttattc	cttttgatgt	taatggaaat	gactcattga	ttcagactga	1080
tcattcaatt	cataggcaga	ttcttggtcc				

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..242  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499845  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met	Glu	Gly	Val	Gly	Ala	Arg	Leu	Gly	Arg	Ser	Ser	Thr	Arg	Tyr	Gly
1			5					10						15	
Pro	Ala	Thr	Val	Phe	Thr	Gly	Pro	Val	Arg	Lys	Trp	Lys	Lys	Lys	Trp
			20				25					30			
Val	His	Val	Ser	Pro	Ser	Thr	Lys	Lys	Asp	Asn	Asn	Asn	Ser	Ser	Ser
		35				40				45					
Gly	Ser	Ala	Ala	Ala	Ala	Ala	Ser	Val	Val	Asn	Gly	Gly	Ser	Asn	Ser
	50					55				60					
Asp	Gly	Ser	Asn	Gly	Ser	His	Leu	Leu	Leu	Tyr	Lys	Trp	Ala	Pro	Leu
65					70					75				80	
Ser	Gln	Asn	Gly	Asn	Gly	Asn	Glu	Asp	Gly	Lys	Ser	Glu	Ser	Asn	Ser
			85						90					95	
Pro	Ser	Glu	Asp	Thr	Val	Ala	Thr	Val	Ala	Glu	Asp	Pro	Pro	Arg	Arg
			100					105					110		
Arg	Phe	Lys	Tyr	Val	Pro	Ile	Ala	Val	Leu	Glu	Glu	Gln	Lys	Lys	Glu
			115				120					125			
Ile	Thr	Glu	Ile	Glu	Asp	Asp	Asp	Lys	Ile	Glu	Glu	Asp	Asp	Lys	Ile
	130					135					140				
Asp	Glu	Asp	Asn	Lys	Val	Glu	Gln	Glu	Asp	Lys	Val	Asp	Glu	Asp	Lys
145					150					155				160	
Thr	Val	Glu	Glu	Ser	Glu	Lys	Lys	Ala	Glu	Val	Glu	Val	Glu	Val	
			165					170					175		
Glu	Glu	Lys	Pro	Asp	Ile	Asn	Asp	Val	Pro	Met	Glu	Asp	Ile	Gln	Gln
			180					185					190		
Asp	Glu	Glu	Lys	Ile	Val	Gln	Asp	Asp	Glu	Glu	Lys	Val	Val	Arg	Gln
	195					200					205				
Asp	Leu	Asn	Glu	Ser	Thr	Val	Asp	Leu	Gly	Leu	Asn	Leu	Asn	Ala	Asn
	210					215					220				
Asp	Ala	Asp	Ala	Asp	Ala	Glu	Asn	Asp	Pro	Lys	Glu	Asp	Lys	Pro	Leu
225					230					235					240
Glu	Glu														

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 604 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..604  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

gcactgcttc attctctata accaagtata agcttgagg gggttatttt tctaaaaggg	60
attgagtttt taagatcatg tctatgacag tggagataag agttccaaac ttggattgtg	120
aaggatgtgc ttctaagctt aggaagactc tactcaagct taaaggagtg gaagaagtgg	180
aaagtagaga tggaacccca aaaagtgcag gctcgaggat accgggttaga ggaaaagaag	240
gtattgaaag cggtagcagc tgccggtaag gcagctgaac tgtggccata ccgggttaggt	300
aatagccatt ttgcctcttt ctataaatat ccttcttacg tgaccaacca ctattactct	360
gatgcacacc gtacggatcc caccggtggt gtccacactt tcttccacac tcttgccggtt	420
tactcggttg ctgtggctgg agatgagatc gcggcttcga tgttttagcga tgataatccc	480
catgcttgta ctattatgta gtcttttagt atacaaaaat atgttttcag ttcattctct	540

tcgtccaaat ttgatttgat gtgatttttt ttgtacaact aatgttggaa tgagaaagta 600  
aaat

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met	Ser	Met	Thr	Val	Glu	Ile	Arg	Val	Pro	Asn	Leu	Asp	Cys	Glu	Gly
1				5					10					15	
Cys	Ala	Ser	Lys	Leu	Arg	Lys	Thr	Leu	Leu	Lys	Leu	Lys	Gly	Val	Glu
			20					25					30		
Glu	Val	Glu	Ser	Arg	Asp	Gly	Asn	Pro	Lys	Ser	Asp	Gly	Ser	Arg	Ile
		35				40						45			
Pro	Val	Arg	Gly	Lys	Glu	Gly	Ile	Glu	Ser	Gly	Thr	Thr	Cys	Arg	
	50				55						60				

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

Met	Glu	Thr	Gln	Lys	Val	Thr	Ala	Arg	Gly	Tyr	Arg	Leu	Glu	Glu	Lys
1				5					10					15	
Lys	Val	Leu	Lys	Ala	Val	Arg	Arg	Ala	Gly	Lys	Ala	Ala	Glu	Leu	Trp
			20					25					30		
Pro	Tyr	Arg	Leu	Gly	Asn	Ser	His	Phe	Ala	Ser	Phe	Tyr	Lys	Tyr	Pro
		35				40						45			
Ser	Tyr	Val	Thr	Asn	His	Tyr	Tyr	Ser	Asp	Ala	His	Arg	Thr	Asp	Pro
	50				55					60					
Thr	Gly	Gly	Val	His	Thr	Phe	Phe	His	Thr	Pro	Ala	Val	Tyr	Ser	Val
65				70					75					80	
Ala	Val	Ala	Gly	Asp	Glu	Ile	Ala	Ala	Ser	Met	Phe	Ser	Asp	Asp	Asn
			85					90						95	
Pro	His	Ala	Cys	Thr	Ile	Met									
			100												

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

Met His Thr Val Arg Ile Pro Pro Val Val Ser Thr Leu Ser Ser Thr

Ile  
65

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

Met	Ala	Thr	Glu	Gln	Asp	Ala	Glu	Val	Gly	Thr	Glu	Thr	Pro	Ser	Val
1				5					10					15	
Ser	Gly	Arg	Phe	Leu	Arg	Asn	Arg	Asp	Leu	Tyr	Leu	Phe	Leu	Pro	Phe
			20					25					30		
Leu	Leu	Gly	Phe	Ser	Asp	Gln	Glu	Ser	Ser	Asn	Gly	Asp	Asp	Asp	
			35				40					45			
Val	Ala	Ser	Ser	Arg	Glu	Arg	Ile	Ile	Leu	Val	Asn	Pro	Phe	Thr	Gln
						55					60				
Gly	Met	Ile	Val	Leu	Glu	Gly	Ser	Ser	Gly	Met	Asn	Pro	Leu	Leu	Arg
65					70					75					80
Ser	Leu	Leu	Glu	Ser	Arg	Glu	Glu	Gly	Arg	Pro	Pro	Ala	Ser	Lys	Ala
				85					90					95	
Ser	Ile	Asp	Ala	Met	Pro	Ile	Val	Glu	Ile	Asp	Gly	Cys	Glu	Gly	Glu
			100					105					110		

Cys Val Ile Cys Leu Glu Glu Trp Lys Ser Glu Glu Thr Val Lys Glu  
115 120 125  
Met Pro Cys Lys His Arg Phe His Gly Gly Cys Ile Glu Lys Trp Leu  
130 135 140  
Gly Phe His Gly Ser Cys Pro Val Cys Arg Tyr Glu Met Pro Val Asp  
145 150 155 160  
Gly Asp Glu Ile Gly Lys Lys Arg Asn Asp Gly Asn Glu Ile Trp Val  
165 170 175  
Arg Phe Ser Phe Asn Asp Gly Arg Arg Ile Arg Asp Phe Ser Ala Gln  
180 185 190  
Asp Gly Gly Asn Ser Asp Gly Val Glu Ser Glu Asn  
195 200

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

Met Ile Val Leu Glu Gly Ser Ser Gly Met Asn Pro Leu Leu Arg Ser  
1 5 10 15  
Leu Leu Glu Ser Arg Glu Glu Gly Arg Pro Pro Ala Ser Lys Ala Ser  
20 25 30  
Ile Asp Ala Met Pro Ile Val Glu Ile Asp Gly Cys Glu Gly Glu Cys  
35 40 45  
Val Ile Cys Leu Glu Glu Trp Lys Ser Glu Glu Thr Val Lys Glu Met  
50 55 60  
Pro Cys Lys His Arg Phe His Gly Gly Cys Ile Glu Lys Trp Leu Gly  
65 70 75 80  
Phe His Gly Ser Cys Pro Val Cys Arg Tyr Glu Met Pro Val Asp Gly  
85 90 95  
Asp Glu Ile Gly Lys Lys Arg Asn Asp Gly Asn Glu Ile Trp Val Arg  
100 105 110  
Phe Ser Phe Asn Asp Gly Arg Arg Ile Arg Asp Phe Ser Ala Gln Asp  
115 120 125  
Gly Gly Asn Ser Asp Gly Val Glu Ser Glu Asn  
130 135

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

Met Asn Pro Leu Leu Arg Ser Leu Leu Glu Ser Arg Glu Glu Gly Arg  
1 5 10 15  
Pro Pro Ala Ser Lys Ala Ser Ile Asp Ala Met Pro Ile Val Glu Ile  
20 25 30  
Asp Gly Cys Glu Gly Glu Cys Val Ile Cys Leu Glu Glu Trp Lys Ser  
35 40 45  
Glu Glu Thr Val Lys Glu Met Pro Cys Lys His Arg Phe His Gly Gly

50					55					60					
Cys	Ile	Glu	Lys	Trp	Leu	Gly	Phe	His	Gly	Ser	Cys	Pro	Val	Cys	Arg
65					70					75					80
Tyr	Glu	Met	Pro	Val	Asp	Gly	Asp	Glu	Ile	Gly	Lys	Lys	Arg	Asn	Asp
				85					90					95	
Gly	Asn	Glu	Ile	Trp	Val	Arg	Phe	Ser	Phe	Asn	Asp	Gly	Arg	Arg	Ile
			100					105				110			
Arg	Asp	Phe	Ser	Ala	Gln	Asp	Gly	Gly	Asn	Ser	Asp	Gly	Val	Glu	Ser
		115					120					125			
Glu	Asn														
130															

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1745

(D) OTHER INFORMATION: / Ceres Seq. ID 1499875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

aaacaagaaa	gagattagga	agagagagac	ggcgatggcg	gctacaggat	ctggacgggc	60
tcaattcatt	tccagttccg	gcggtaaccg	aagcttctcc	aattctccac	tcatcgagaa	120
ctctgattct	aatcagatta	ttgtctctga	gaagaagagc	tggagaatt	tctttgctta	180
cttaggccct	ggttttcttg	tttcaatcgc	atatattgat	cctggaaact	ttgagactga	240
tctgcaagct	ggagcacact	acaagtatga	attactttgg	atcatattgg	tggcctcatg	300
tgcggtcttg	gtgattcaat	ctctggctgc	taatcttggg	gttgtcacag	gaaaacattt	360
ggctgagcaa	tgtagagccg	agtactccaa	agttccaaac	tttatgttat	gggtcgttgc	420
tgaattgca	gtagttgctt	gtgacatacc	ggaagttatc	ggaacagctt	ttgctctgaa	480
catgctcttt	agcataccgg	tgtggatcgg	tgttctcttg	acaggcttaa	gtacgctgat	540
tcttctcgca	cttcaaaaat	acggggtgag	aaagctggag	ttcttgatag	cgtttcttgt	600
gttcacaatt	gctatatgct	tctttgttga	gcttcattac	tcaaagccag	acccaggaga	660
agtctacat	gggtctcttg	ttcctcaact	taaaggaaat	ggtgcaactg	gtctcgcaat	720
ctctttgctc	ggagccatgg	ttatgccgca	taatctcttc	ctccactcgg	ccttggttct	780
ctcgaggaaa	atccctcgtt	ccgcttcttg	tatcaaggaa	gcttgccagg	tttacttgat	840
agaaagtgga	ttgggtctaa	tgggtggcctt	tctcataaac	gtctctgtaa	tatcagtaag	900
cggggctggt	tgtaatgccc	ccaacttaag	ccctgaagat	cgagctaatt	gtgaggattt	960
ggacttaaac	aaggcttctg	ttctgctacg	gaacgtttgt	ggaaaatgga	gctcaaagct	1020
atttgcaatc	gcgcttcttg	cttctggtca	gagctcgacg	ataaccggaa	cttatgctgg	1080
acaatatgta	atgcagggct	ttcttgatct	cagactcgag	ccatggctca	gaaacttact	1140
aacaagatgt	ttagctataa	tcccgagtct	aattgtttgt	ctcatcggtg	gttcagctgg	1200
agctggaaaag	ttaatcatca	ttgcctcgat	gatcttatcc	tttgagctcc	cgtttgctgt	1260
gggtcctctt	ctaaaattca	caagttgcaa	aaccaagatg	ggttcacatg	tcaacccaat	1320
ggcgattaca	gctttgactt	gggtcatttg	tgggttaaat	atgggaataa	acataacta	1380
tctagtaagc	agtttcatca	aactgcttat	ccacagtcac	atgaagctta	tcctcgtcgt	1440
cttctgtgga	attcttgggt	tgcgaggeat	tgctctctat	ttagccgcca	tagcttacct	1500
tgtcttccgg	aaaaacagag	tagccacttc	tcttcttatt	tcaagagact	cacaaaatgt	1560
ggagacactt	ccaagacagg	acattgtcaa	catgcagtta	ccatgtagag	tatctacctc	1620
cgatgttggc	tgagtcacat	ttaagcttag	gattccaata	aagttagatc	taaaccaagt	1680
tcataaaaac	ctttcgatag	tgtactagaa	taaaggttat	atgaatcggt	ttgcgtcttt	1740
tcttt						

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: peptide

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1499876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

Asn	Lys	Lys	Glu	Ile	Arg	Lys	Arg	Glu	Thr	Ala	Met	Ala	Ala	Thr	Gly	1	5	10	15
Ser	Gly	Arg	Ser	Gln	Phe	Ile	Ser	Ser	Ser	Gly	Gly	Asn	Arg	Ser	Phe	20	25	30	
Ser	Asn	Ser	Pro	Leu	Ile	Glu	Asn	Ser	Asp	Ser	Asn	Gln	Ile	Ile	Val	35	40	45	
Ser	Glu	Lys	Lys	Ser	Trp	Lys	Asn	Phe	Phe	Ala	Tyr	Leu	Gly	Pro	Gly	50	55	60	
Phe	Leu	Val	Ser	Ile	Ala	Tyr	Ile	Asp	Pro	Gly	Asn	Phe	Glu	Thr	Asp	65	70	75	80
Leu	Gln	Ala	Gly	Ala	His	Tyr	Lys	Tyr	Glu	Leu	Leu	Trp	Ile	Ile	Leu	85	90	95	
Val	Ala	Ser	Cys	Ala	Ala	Leu	Val	Ile	Gln	Ser	Leu	Ala	Ala	Asn	Leu	100	105	110	
Gly	Val	Val	Thr	Gly	Lys	His	Leu	Ala	Glu	Gln	Cys	Arg	Ala	Glu	Tyr	115	120	125	
Ser	Lys	Val	Pro	Asn	Phe	Met	Leu	Trp	Val	Val	Ala	Glu	Ile	Ala	Val	130	135	140	
Val	Ala	Cys	Asp	Ile	Pro	Glu	Val	Ile	Gly	Thr	Ala	Phe	Ala	Leu	Asn	145	150	155	160
Met	Leu	Phe	Ser	Ile	Pro	Val	Trp	Ile	Gly	Val	Leu	Leu	Thr	Gly	Leu	165	170	175	
Ser	Thr	Leu	Ile	Leu	Leu	Ala	Leu	Gln	Lys	Tyr	Gly	Val	Arg	Lys	Leu	180	185	190	
Glu	Phe	Leu	Ile	Ala	Phe	Leu	Val	Phe	Thr	Ile	Ala	Ile	Cys	Phe	Phe	195	200	205	
Val	Glu	Leu	His	Tyr	Ser	Lys	Pro	Asp	Pro	Gly	Glu	Val	Leu	His	Gly	210	215	220	
Leu	Phe	Val	Pro	Gln	Leu	Lys	Gly	Asn	Gly	Ala	Thr	Gly	Leu	Ala	Ile	225	230	235	240
Ser	Leu	Leu	Gly	Ala	Met	Val	Met	Pro	His	Asn	Leu	Phe	Leu	His	Ser	245	250	255	
Ala	Leu	Val	Leu	Ser	Arg	Lys	Ile	Pro	Arg	Ser	Ala	Ser	Gly	Ile	Lys	260	265	270	
Glu	Ala	Cys	Arg	Phe	Tyr	Leu	Ile	Glu	Ser	Gly	Leu	Ala	Leu	Met	Val	275	280	285	
Ala	Phe	Leu	Ile	Asn	Val	Ser	Val	Ile	Ser	Val	Ser	Gly	Ala	Val	Cys	290	295	300	
Asn	Ala	Pro	Asn	Leu	Ser	Pro	Glu	Asp	Arg	Ala	Asn	Cys	Glu	Asp	Leu	305	310	315	320
Asp	Leu	Asn	Lys	Ala	Ser	Phe	Leu	Leu	Arg	Asn	Val	Val	Gly	Lys	Trp	325	330	335	
Ser	Ser	Lys	Leu	Phe	Ala	Ile	Ala	Leu	Leu	Ala	Ser	Gly	Gln	Ser	Ser	340	345	350	
Thr	Ile	Thr	Gly	Thr	Tyr	Ala	Gly	Gln	Tyr	Val	Met	Gln	Gly	Phe	Leu	355	360	365	
Asp	Leu	Arg	Leu	Glu	Pro	Trp	Leu	Arg	Asn	Leu	Leu	Thr	Arg	Cys	Leu	370	375	380	
Ala	Ile	Ile	Pro	Ser	Leu	Ile	Val	Ala	Leu	Ile	Gly	Gly	Ser	Ala	Gly	385	390	395	400
Ala	Gly	Lys	Leu	Ile	Ile	Ala	Ser	Met	Ile	Leu	Ser	Phe	Glu	Leu		405	410	415	
Pro	Phe	Ala	Leu	Val	Pro	Leu	Leu	Lys	Phe	Thr	Ser	Cys	Lys	Thr	Lys	420	425	430	
Met	Gly	Ser	His	Val	Asn	Pro	Met	Ala	Ile	Thr	Ala	Leu	Thr	Trp	Val	435	440	445	
Ile	Gly	Gly	Leu	Ile	Met	Gly	Ile	Asn	Ile	Tyr	Tyr	Leu	Val	Ser	Ser				

(2) INFORMATION FOR SEQ ID NO:1218:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1499877

Met 1	Ala 2	Ala 3	Thr 4	Gly 5	Ser 6	Gly 7	Arg 8	Ser 9	Gln 10	Phe 11	Ile 12	Ser 13	Ser 14	Ser 15	Gly 16
Gly	Asn	Arg	Ser	Phe	Ser	Asn	Ser	Pro	Leu	Ile	Glu	Asn	Ser	Asp	Ser
Asn	Gln	Ile	Ile	Val	Ser	Glu	Lys	Lys	Ser	Trp	Lys	Asn	Phe	Phe	Ala
Tyr	Leu	Gly	Pro	Gly	Phe	Leu	Val	Ser	Ile	Ala	Tyr	Ile	Asp	Pro	Gly
Asn	Phe	Glu	Thr	Asp	Leu	Gln	Ala	Gly	Ala	His	Tyr	Lys	Tyr	Glu	Leu
Leu	Trp	Ile	Ile	Leu	Val	Ala	Ser	Cys	Ala	Ala	Leu	Val	Ile	Gln	Ser
Leu	Ala	Ala	Asn	Leu	Gly	Val	Val	Thr	Gly	Lys	His	Leu	Ala	Glu	Gln
Cys	Arg	Ala	Glu	Tyr	Ser	Lys	Val	Pro	Asn	Phe	Met	Leu	Trp	Val	Val
Ala	Glu	Ile	Ala	Val	Val	Ala	Cys	Asp	Ile	Pro	Glu	Val	Ile	Gly	Thr
Ala	Phe	Ala	Leu	Asn	Met	Leu	Phe	Ser	Ile	Pro	Val	Trp	Ile	Gly	Val
Leu	Leu	Thr	Gly	Leu	Ser	Thr	Leu	Ile	Leu	Leu	Ala	Leu	Gln	Lys	Tyr
Gly	Val	Arg	Lys	Leu	Glu	Phe	Leu	Ile	Ala	Phe	Leu	Val	Phe	Thr	Ile
Ala	Ile	Cys	Phe	Phe	Val	Glu	Leu	His	Tyr	Ser	Lys	Pro	Asp	Pro	Gly
Glu	Val	Leu	His	Gly	Leu	Phe	Val	Pro	Gln	Leu	Lys	Gly	Asn	Gly	Ala
Thr	Gly	Leu	Ala	Ile	Ser	Leu	Leu	Gly	Ala	Met	Val	Met	Pro	His	Asn
Leu	Phe	Leu	His	Ser	Ala	Leu	Val	Leu	Ser	Arg	Lys	Ile	Pro	Arg	Ser
Ala	Ser	Gly	Ile	Lys	Glu	Ala	Cys	Arg	Phe	Tyr	Leu	Ile	Glu	Ser	Gly
Leu	Ala	Leu	Met	Val	Ala	Phe	Leu	Ile	Asn	Val	Ser	Val	Ile	Ser	Val
Ser	Gly	Ala	Val	Cys	Asn	Ala	Pro	Asn	Leu	Ser	Pro	Glu	Asp	Arg	Ala

```

Asn Cys Glu Asp Leu Asp Leu Asn Lys Ala Ser Phe Leu Leu Arg Asn
305          310          315          320
Val Val Gly Lys Trp Ser Ser Lys Leu Phe Ala Ile Ala Leu Leu Ala
          325          330          335
Ser Gly Gln Ser Ser Thr Ile Thr Gly Thr Tyr Ala Gly Gln Tyr Val
          340          345          350
Met Gln Gly Phe Leu Asp Leu Arg Leu Glu Pro Trp Leu Arg Asn Leu
          355          360          365
Leu Thr Arg Cys Leu Ala Ile Ile Pro Ser Leu Ile Val Ala Leu Ile
370          375          380
Gly Gly Ser Ala Gly Ala Gly Lys Leu Ile Ile Ala Ser Met Ile
385          390          395          400
Leu Ser Phe Glu Leu Pro Phe Ala Leu Val Pro Leu Leu Lys Phe Thr
          405          410          415
Ser Cys Lys Thr Lys Met Gly Ser His Val Asn Pro Met Ala Ile Thr
          420          425          430
Ala Leu Thr Trp Val Ile Gly Gly Leu Ile Met Gly Ile Asn Ile Tyr
435          440          445
Tyr Leu Val Ser Ser Phe Ile Lys Leu Leu Ile His Ser His Met Lys
450          455          460
Leu Ile Leu Val Val Phe Cys Gly Ile Leu Gly Phe Ala Gly Ile Ala
465          470          475          480
Leu Tyr Leu Ala Ala Ile Ala Tyr Leu Val Phe Arg Lys Asn Arg Val
          485          490          495
Ala Thr Ser Leu Leu Ile Ser Arg Asp Ser Gln Asn Val Glu Thr Leu
          500          505          510
Pro Arg Gln Asp Ile Val Asn Met Gln Leu Pro Cys Arg Val Ser Thr
          515          520          525
Ser Asp Val Gly
530

```

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

```

Met Leu Trp Val Val Ala Glu Ile Ala Val Val Ala Cys Asp Ile Pro
1          5          10          15
Glu Val Ile Gly Thr Ala Phe Ala Leu Asn Met Leu Phe Ser Ile Pro
          20          25          30
Val Trp Ile Gly Val Leu Leu Thr Gly Leu Ser Thr Leu Ile Leu Leu
          35          40          45
Ala Leu Gln Lys Tyr Gly Val Arg Lys Leu Glu Phe Leu Ile Ala Phe
          50          55          60
Leu Val Phe Thr Ile Ala Ile Cys Phe Phe Val Glu Leu His Tyr Ser
          65          70          75          80
Lys Pro Asp Pro Gly Glu Val Leu His Gly Leu Phe Val Pro Gln Leu
          85          90          95
Lys Gly Asn Gly Ala Thr Gly Leu Ala Ile Ser Leu Leu Gly Ala Met
          100          105          110
Val Met Pro His Asn Leu Phe Leu His Ser Ala Leu Val Leu Ser Arg
          115          120          125
Lys Ile Pro Arg Ser Ala Ser Gly Ile Lys Glu Ala Cys Arg Phe Tyr
          130          135          140
Leu Ile Glu Ser Gly Leu Ala Leu Met Val Ala Phe Leu Ile Asn Val

```

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..142
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

```
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
1      5      10      15
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
20     25     30
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser
35     40     45
Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Ile Leu His Arg Asp Gly
50     55     60
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg
65     70     75     80
Asp Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Lys Val Thr Ser
85     90     95
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys
100    105    110
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr
115    120    125
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala
130    135    140
```

(2) INFORMATION FOR SEQ ID NO:1222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

```
Met Ile Ile Lys Thr Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly
1      5      10      15
Glu Glu Ala Val Ile Leu His Arg Asp Gly Glu Ala Ser Phe Asp Leu
20     25     30
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr
35     40     45
Lys Lys Leu Arg Glu Met Lys Val Thr Ser Met Ile Val Gly Val Thr
50     55     60
Ser Val Ala Asp Gln Glu Glu Glu Arg Lys Ala Phe Met Glu Ala Gly
65     70     75     80
Leu Asn His Cys Leu Glu Lys Pro Leu Thr Lys Ala Lys Ile Phe Pro
85     90     95
Leu Ile Ser His Leu Phe Asp Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1499902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

aaggtgtcgg	atcttgatga	agcttcgaag	attcttgtgc	cggagtctgt	gaaaaagctc	60
cggaactta	tgggttacat	attttacaaa	ccggcggttg	caagactggg	tcctacttgt	120
cttctccatg	atttcatcga	acatgctttg	acaagagata	atatggaaga	gaagagagaa	180
ctgattaaag	ccataccaaa	agacagaata	atctcagaga	ttccaaagct	caaacaacca	240
acattgataa	tatgggggga	gcatgatcaa	gtgttcccat	tggagatggg	caagagactt	300
gagaagcatg	taggagataa	tgggaaactc	gttatcatca	agagaactgg	tcatatcttt	360
aacttcgaga	aacctaataa	gtttatcaaa	cttctcaaat	cttttcttct	agagactagt	420
aaaccacaga	ttcctgtctc	taatgtttga	ttcttagtca	tcgttttgaa	gatacctctca	480
taastaattt	ccaaggatta	ataacatata	tatcattttc			

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1499903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

Lys	Val	Ser	Asp	Leu	Asp	Glu	Ala	Ser	Lys	Ile	Leu	Val	Pro	Glu	Ser	
1				5					10					15		
Val	Lys	Lys	Leu	Arg	Glu	Leu	Met	Gly	Tyr	Ile	Phe	Tyr	Lys	Pro	Ala	
			20					25					30			
Leu	Ala	Arg	Leu	Val	Pro	Thr	Cys	Leu	Leu	His	Asp	Phe	Ile	Glu	His	
			35				40					45				
Ala	Leu	Thr	Arg	Asp	Asn	Met	Glu	Glu	Lys	Arg	Glu	Leu	Ile	Lys	Ala	
	50					55					60					
Ile	Pro	Lys	Asp	Arg	Ile	Ile	Ser	Glu	Ile	Pro	Lys	Leu	Lys	Gln	Pro	
65					70					75				80		
Thr	Leu	Ile	Ile	Trp	Gly	Glu	His	Asp	Gln	Val	Phe	Pro	Leu	Glu	Met	
				85					90					95		
Gly	Lys	Arg	Leu	Glu	Lys	His	Val	Gly	Asp	Asn	Gly	Lys	Leu	Val	Ile	
			100					105					110			
Ile	Lys	Arg	Thr	Gly	His	Ile	Phe	Asn	Phe	Glu	Lys	Pro	Lys	Lys	Phe	
	115					120						125				
Ile	Lys	Leu	Leu	Lys	Ser	Phe	Leu	Leu	Glu	Thr	Ser	Lys	Pro	Gln	Ile	
	130					135						140				
Pro	Val	Ser	Asn	Val												
145																

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1499904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

Met	Gly	Tyr	Ile	Phe	Tyr	Lys	Pro	Ala	Leu	Ala	Arg	Leu	Val	Pro	Thr	
1				5					10					15		
Cys	Leu	Leu	His	Asp	Phe	Ile	Glu	His	Ala	Leu	Thr	Arg	Asp	Asn	Met	
			20					25					30			
Glu	Glu	Lys	Arg	Glu	Leu	Ile	Lys	Ala	Ile	Pro	Lys	Asp	Arg	Ile	Ile	

35 40 45  
Ser Glu Ile Pro Lys Leu Lys Gln Pro Thr Leu Ile Ile Trp Gly Glu  
50 55 60  
His Asp Gln Val Phe Pro Leu Glu Met Gly Lys Arg Leu Glu Lys His  
65 70 75 80  
Val Gly Asp Asn Gly Lys Leu Val Ile Ile Lys Arg Thr Gly His Ile  
85 90 95  
Phe Asn Phe Glu Lys Pro Lys Lys Phe Ile Lys Leu Leu Lys Ser Phe  
100 105 110  
Leu Leu Glu Thr Ser Lys Pro Gln Ile Pro Val Ser Asn Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1499905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

Met Glu Glu Lys Arg Glu Leu Ile Lys Ala Ile Pro Lys Asp Arg Ile  
1 5 10 15  
Ile Ser Glu Ile Pro Lys Leu Lys Gln Pro Thr Leu Ile Ile Trp Gly  
20 25 30  
Glu His Asp Gln Val Phe Pro Leu Glu Met Gly Lys Arg Leu Glu Lys  
35 40 45  
His Val Gly Asp Asn Gly Lys Leu Val Ile Ile Lys Arg Thr Gly His  
50 55 60  
Ile Phe Asn Phe Glu Lys Pro Lys Lys Phe Ile Lys Leu Leu Lys Ser  
65 70 75 80  
Phe Leu Leu Glu Thr Ser Lys Pro Gln Ile Pro Val Ser Asn Val  
85 90 95

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1499906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

agaacacaaa caaaaacaca ttgtaacatt agtttaagca ttaagcttct ttatgtcgaa 60  
taataataat tctccgacca ccgtgaatca agaaacgacg acgtctcgtg aagtctcaat 120  
cacattgcct actgatcaat ctctctcaaac ctcaccagga tcattcttctt ctccttcacc 180  
gagaccttcc ggtggatcac cggcgagaag aacggcgact ggattatccg gcaagcactc 240  
tatttttcagg gggattcgac tacgtaacgg aaaatgggta tcggagatta gagagccacg 300  
taaaacgaca agaatttggc tcgggactta tccggatccg gagatggctg ccgccgctta 360  
cgacgtggct gcgttagctt taaaaggacc aggccgtttt gaattttcct gggtttagct 420  
ttgacttacg tggctccggt ttcaaactct gctgcggata taagagcggc tgctagtaga 480  
gcagcggaga tgaagcaacc ggatcagggt ggggatgaga aggtattgga accggttcaa 540  
cccggcaaaag aggaagaatt agaagaagtg tcgtgtaact cgtgttcgtt ggagtttatg 600  
gatgaggaag cgatgttgaa tatgccgact ttgttgacgg agatggctga agggatgttg 660  
atgagtccac cgagaatgat gatacatccg acgatggaag atgattcgcc ggagaatcat 720  
gaaggagata atctttggag ttataaatga atccattgaa gctgctctct tttttattgt 780  
tttccggtcg aatgagattt tccccctttt tttttctttt tgggtcgctg ttatggaaa 840

tcaaataagggt tattaatatg atctattaat atttttgaaa cataatgagt ttgaatttga 900  
atttttccat ttttatataa atatggttta tatgaggggaa aaatagatac atatcgaaga 960  
tataagaatt gtttttctgc tt

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

Met	Ser	Asn	Asn	Asn	Asn	Ser	Pro	Thr	Thr	Val	Asn	Gln	Glu	Thr	Thr
1				5					10					15	
Thr	Ser	Arg	Glu	Val	Ser	Ile	Thr	Leu	Pro	Thr	Asp	Gln	Ser	Pro	Gln
			20					25					30		
Thr	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Pro	Ser	Pro	Arg	Pro	Ser	Gly	Gly
		35					40					45			
Ser	Pro	Ala	Arg	Arg	Thr	Ala	Thr	Gly	Leu	Ser	Gly	Lys	His	Ser	Ile
		50				55					60				
Phe	Arg	Gly	Ile	Arg	Leu	Arg	Asn	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg
65					70				75					80	
Glu	Pro	Arg	Lys	Thr	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Tyr	Pro	Val	Pro
				85					90					95	
Glu	Met	Ala	Ala	Ala	Tyr	Asp	Val	Ala	Ala	Leu	Ala	Leu	Lys	Gly	
			100				105					110			
Pro	Gly	Arg	Phe	Glu	Phe	Ser	Trp	Val							
			115				120								

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

Met	Lys	Gln	Pro	Asp	Gln	Gly	Gly	Asp	Glu	Lys	Val	Leu	Glu	Pro	Val
1				5					10					15	
Gln	Pro	Gly	Lys	Glu	Glu	Glu	Leu	Glu	Val	Ser	Cys	Asn	Ser	Cys	
			20					25				30			
Ser	Leu	Glu	Phe	Met	Asp	Glu	Glu	Ala	Met	Leu	Asn	Met	Pro	Thr	Leu
		35					40					45			
Leu	Thr	Glu	Met	Ala	Glu	Gly	Met	Leu	Met	Ser	Pro	Pro	Arg	Met	Met
		50				55					60				
Ile	His	Pro	Thr	Met	Glu	Asp	Asp	Ser	Pro	Glu	Asn	His	Glu	Gly	Asp
65					70				75					80	
Asn	Leu	Trp	Ser	Tyr	Lys										
				85											

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..932

(D) OTHER INFORMATION: / Ceres Seq. ID 1499909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

aactgtttga	tttctgagga	gaatccattg	tttccattcg	aagaaaactc	taactttctc	60
gttgaagctt	tgagctctct	acctctttat	ctccggagat	gtataataac	atggggacctc	120
aaccggggat	gccaagacct	ccaggaaacc	ctgagcctgg	tccatttggg	aatccttttca	180
ctggagctgg	ctcgggtttt	atccgtgggt	gtttggggagc	gtatggggag	agaatttttag	240
gatcgartc	tgagtatgtt	cagagcaata	taagccggta	cttctctgat	ccgcaatact	300
atttccaagt	gaatgatcaa	tatgtgagga	ataaactgaa	ggttggtctg	tttccctttcc	360
tacaccgggg	acactggacc	agaatatctg	aaccagttgg	tggtaggctc	tcatacaagc	420
ctccaatata	tgatatcaat	gctcccagac	ttgtacattc	cccttatggc	atttgggtacc	480
tacgtttgtc	ttgctgggtc	ttcattggga	cttaatggaa	agtttacacc	ggaagctttg	540
aattggctgt	ttgtgaaagg	attggttggg	tggtttttgc	aagtaatgct	cctgaaagta	600
acacttctat	cacttggtag	tggagaggca	ccattactag	atattgtggc	atacggagggg	660
tatgcttttg	ctggtctgtg	tcttgcgggc	tttgccaaaa	taatgtgggg	atactcgtag	720
tacgcgttga	tgccatggac	ttgtctatgc	actgggattt	tcttggtgaa	gacgatgaaa	780
cgtgttctgt	ttgctgaagt	aagaagttac	gattcgagca	aacatcacta	ccttcttctg	840
tttttagcct	tggtccagtt	cccacttttg	atatggcttg	gtaacattag	tggttaattgg	900
cttctttgaa	atgaaaaaag	acgtttttgt	gt			

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1499910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

Met	Ile	Ser	Met	Leu	Pro	Asp	Leu	Tyr	Ile	Pro	Phe	Met	Ala	Phe	Gly	
1				5				10						15		
Thr	Tyr	Val	Val	Leu	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Asn	Gly	Lys	Phe	
				20				25					30			
Thr	Pro	Glu	Ala	Leu	Asn	Trp	Leu	Phe	Val	Lys	Gly	Leu	Val	Gly	Trp	
				35			40					45				
Phe	Leu	Gln	Val	Met	Leu	Leu	Lys	Val	Thr	Leu	Leu	Ser	Leu	Gly	Ser	
				50			55					60				
Gly	Glu	Ala	Pro	Leu	Leu	Asp	Ile	Val	Ala	Tyr	Gly	Gly	Tyr	Ala	Phe	
65					70					75				80		
Ala	Gly	Leu	Cys	Leu	Ala	Gly	Phe	Ala	Lys	Ile	Met	Trp	Gly	Tyr	Ser	
				85					90					95		
Tyr	Tyr	Ala	Leu	Met	Pro	Trp	Thr	Cys	Leu	Cys	Thr	Gly	Ile	Phe	Leu	
				100				105					110			
Val	Lys	Thr	Met	Lys	Arg	Val	Leu	Phe	Ala	Glu	Val	Arg	Ser	Tyr	Asp	
				115				120					125			
Ser	Ser	Lys	His	His	Tyr	Leu	Leu	Leu	Phe	Leu	Ala	Leu	Val	Gln	Phe	
				130				135				140				
Pro	Leu	Leu	Ile	Trp	Leu	Gly	Asn	Ile	Ser	Val	Asn	Trp	Leu	Leu		
145					150						155					

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1499911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

```
Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly Thr Tyr Val
1           5           10           15
Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe Thr Pro Glu
          20           25           30
Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp Phe Leu Gln
          35           40           45
Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser Gly Glu Ala
          50           55           60
Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe Ala Gly Leu
65           70           75           80
Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser Tyr Tyr Ala
          85           90           95
Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu Val Lys Thr
          100          105          110
Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp Ser Ser Lys
          115          120          125
His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe Pro Leu Leu
130           135           140
Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu
145           150           155
```

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1499912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

```
Met Ala Phe Gly Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu
1           5           10           15
Asn Gly Lys Phe Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly
          20           25           30
Leu Val Gly Trp Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu
          35           40           45
Ser Leu Gly Ser Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly
          50           55           60
Gly Tyr Ala Phe Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met
65           70           75           80
Trp Gly Tyr Ser Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr
          85           90           95
Gly Ile Phe Leu Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val
          100          105          110
Arg Ser Tyr Asp Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala
          115          120          125
Leu Val Gln Phe Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn
130           135           140
Trp Leu Leu
145
```

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..619
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

atttcg	ggcg	actgtgaatt	atgtggtcgg	cgacgttatac	tttcccttct	tttgtggctt	60					
cttcac	tcttc	tctaccta	aat	tacaggaacc	gtaggtttcc	aaagattaaa	gcttcgctct	120				
ttaatt	accc	tctagc	gagc	aaaatcat	gg	tcagaaat	tt accg	tttct mcaagtgaag	180			
at	tttctaaa	gagagag	ttt	tcagcttt	tg	gagagata	gc	tgaagtgaag	cttatcaaa	240		
atgagg	caat	gcagagat	ca	aaagg	ttatg	cttttatt	ca	attcacgt	tct caagatgatg	300		
cttttct	ttgc	catagag	acc	atggacc	gtc	ggatgtaca	a	tggaaga	atg atttatatag	360		
acattg	cgaa	acccgg	taaa	cgtgatt	tcc	aaggact	acc	gaggact	tct ggtccccctg	420		
agaagt	cgga	tgtgcc	agaa	gaagcc	gcta	atgatg	agg	t	tgctgattgc	tggtattag	480	
tg	tagt	atc	aa	gtc	acca	aactg	ta	act	tgcat	aaatcagatg	tcaaattatg	540
cttct	tatta	ggaatt	tgat	caatg	tgaag	aatgt	tgtt	actgata	aa	aattattgac	600	
acggt	tccag	ttacag	ctc									

(2) INFORMATION FOR SEQ ID NO:1235:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..152
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

Met	Trp	Ser	Ala	Thr	Leu	Ser	Phe	Pro	Ser	Phe	Val	Ala	Ser	Ser	Ser	
1				5				10				15				
Ser	Leu	Pro	Asn	Tyr	Arg	Asn	Arg	Arg	Phe	Pro	Lys	Ile	Lys	Ala	Ser	
			20					25				30				
Leu	Phe	Asn	Tyr	Pro	Leu	Ala	Ser	Lys	Ile	Met	Val	Arg	Asn	Leu	Pro	
		35						40				45				
Phe	Ser	Xaa	Ser	Glu	Asp	Phe	Leu	Lys	Arg	Glu	Phe	Ser	Ala	Phe	Gly	
	50					55				60						
Glu	Ile	Ala	Glu	Val	Lys	Leu	Ile	Lys	Asp	Glu	Ala	Met	Gln	Arg	Ser	
65					70					75				80		
Lys	Gly	Tyr	Ala	Phe	Ile	Gln	Phe	Thr	Ser	Gln	Asp	Asp	Ala	Phe	Leu	
			85					90						95		
Ala	Ile	Glu	Thr	Met	Asp	Arg	Arg	Met	Tyr	Asn	Gly	Arg	Met	Ile	Tyr	
			100					105						110		
Ile	Asp	Ile	Ala	Lys	Pro	Gly	Lys	Arg	Asp	Phe	Gln	Gly	Leu	Pro	Arg	
		115						120					125			
Thr	Ser	Gly	Pro	Pro	Glu	Lys	Ser	Asp	Val	Pro	Glu	Glu	Ala	Ala	Asn	
	130							135					140			
Asp	Glu	Val	Ala	Asp	Cys	Trp	Tyr									
145					150											

(2) INFORMATION FOR SEQ ID NO:1236:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1499926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Met Val Arg Asn Leu Pro Phe Ser Xaa Ser Glu Asp Phe Leu Lys Arg  
1 5 10 15  
Glu Phe Ser Ala Phe Gly Glu Ile Ala Glu Val Lys Leu Ile Lys Asp  
20 25 30  
Glu Ala Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser  
35 40 45  
Gln Asp Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr  
50 55 60  
Asn Gly Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp  
65 70 75 80  
Phe Gln Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val  
85 90 95  
Pro Glu Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1499927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser Gln Asp  
1 5 10 15  
Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr Asn Gly  
20 25 30  
Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp Phe Gln  
35 40 45  
Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val Pro Glu  
50 55 60  
Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..622

(D) OTHER INFORMATION: / Ceres Seq. ID 1499928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

acttcaaattc cataatcgct ctacttctct ctctctcttag attcgaaaaa atggcgaaac 60  
tggtgatggt gttggttctc tgtatcttac cggcgatagc catggcggca aggaggggaa 120  
atattggaaa gaatacaatg gtggttcaag gtagcaccta ctgtgacatt tgcaaattcg 180  
gcttcgagac tcctgaatcc tcctacttca tccccgggtgc aacgggtgaag ctatcatgca 240  
aagacaggaa gacaatggaa gaggtttaca cagacaaagc tgtatcagac aaagaaggaa 300  
agtataagtt cattgtccac gacgatcaga catgctaaca acatgggatt tgagaaagaa 360  
gtgagtgatg tgttctgctc tgctttgttt cagaagtata tgggttgatga agatgaggat 420  
gatattaaaa accatctcta atctctctgt ttaattcttat gatctgctgt tttcttcatt 480  
aatgagtttc gagttatgga agagatatat tctgtatttg tttgattact tatttggtgt 540  
ctttagagat gttgactctg gtgatcggat aactatctgt ttgtgtaagc ttcttatata 600  
ttgatgtgtc atttccttgc tt

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

Phe	Lys	Ser	Ile	Ile	Ala	Leu	Leu	Leu	Ser	Leu	Ser	Arg	Phe	Glu	Lys
1				5				10						15	
Met	Ala	Lys	Leu	Val	Met	Leu	Leu	Val	Leu	Cys	Ile	Leu	Pro	Ala	Ile
			20					25					30		
Ala	Met	Ala	Ala	Arg	Arg	Gly	Asn	Ile	Gly	Lys	Asn	Thr	Met	Val	Val
			35				40				45				
Gln	Gly	Ser	Thr	Tyr	Cys	Asp	Ile	Cys	Lys	Phe	Gly	Phe	Glu	Thr	Pro
	50					55				60					
Glu	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Ala	Thr	Val	Lys	Leu	Ser	Cys	Lys
65					70					75				80	
Asp	Arg	Lys	Thr	Met	Glu	Glu	Val	Tyr	Thr	Asp	Lys	Ala	Val	Ser	Asp
				85					90					95	
Lys	Glu	Gly	Lys	Tyr	Lys	Phe	Ile	Val	His	Asp	Asp	Gln	Thr	Cys	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met	Ala	Lys	Leu	Val	Met	Leu	Leu	Val	Leu	Cys	Ile	Leu	Pro	Ala	Ile
1				5					10					15	
Ala	Met	Ala	Ala	Arg	Arg	Gly	Asn	Ile	Gly	Lys	Asn	Thr	Met	Val	Val
			20					25					30		
Gln	Gly	Ser	Thr	Tyr	Cys	Asp	Ile	Cys	Lys	Phe	Gly	Phe	Glu	Thr	Pro
			35				40					45			
Glu	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Ala	Thr	Val	Lys	Leu	Ser	Cys	Lys
	50					55				60					
Asp	Arg	Lys	Thr	Met	Glu	Glu	Val	Tyr	Thr	Asp	Lys	Ala	Val	Ser	Asp
65					70					75				80	
Lys	Glu	Gly	Lys	Tyr	Lys	Phe	Ile	Val	His	Asp	Asp	Gln	Thr	Cys	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

```
Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
1          5          10          15
Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
          20          25          30
Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
          35          40          45
Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
          50          55          60
Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
65          70          75          80
Lys Phe Ile Val His Asp Asp Gln Thr Cys
          85          90
```

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1010
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

```
acaatcaaag atgacactag ctagacatatt tegttttcat ctccccacga atcaaaagat      60
ggctttttgcc attgcttctg ctctcacttc cacactcaca ttatccacga gcagagtcca      120
aaatcctacc cagagaagac cacatgtagc gtccacatca tccaccggtg gaagattaat      180
gagagagcgc ttggtggtgg ttcgtgcccg caaagaagtt tctagcgtct gtgaaccact      240
tcctccggac cgtcctttat ggttccctgg tagctctcca cctgaatggc tctgatggcag      300
cttacctggt gatttcgggt tcgatcctct cggtttaggg tctggatccg gacaccctca      360
aatggtttgc acaagctgag cttatacata gccggtggggc aatgctggcc gtgaccggta      420
tcataatacc agaatgtmhh cgagcggwta ggtttcattg aaaatttctc atgggtatgac      480
gcagggtctc gtgagtactt bgcggattcc actacgctgt ttgtggctca aatgggttta      540
atgggctggg cagaaggtak aagatgggct gatttgatta aaccgggggtc tgttgacata      600
gaaccaaagt acccgcataa agtaaatcct aaaccggatg ttggttacct tggaggtttg      660
tggttcgatt ttatgatgtg ggggagaggt tctcctgaac cggtaatggt tttgaggact      720
aaagagatta agaacggacg gctcgcgatg cttgctttcc ttgggttctg tttccaagct      780
acctacacta gccaatgatcc aattgagaat ctcattggctc atctggctga tcctgggtcat      840
tgcaacgtct tttcggcatt tacatcacat taatgaggat tagcttgggg cgaatataat      900
attttttata tatttatgga tgttgaactt ttgtatagtg tcactcggcc ttgttacaac      960
ttctgcttac ttaattaaca tgtaaaatat attatatata tatgtagaag
```

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

```
Gln Ser Lys Met Thr Leu Ala Arg His Phe Arg Phe His Leu Pro Thr
1          5          10          15
Asn Gln Lys Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu
          20          25          30
Thr Leu Ser Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His
          35          40          45
Val Ala Ser Thr Ser Ser Thr Gly Gly Arg Leu Met Arg Glu Arg Leu
```

50	55	60
Val Val Val Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Pro Leu		
65	70	75
Pro Pro Asp Arg Pro Leu Trp Phe Pro Gly Ser Ser Pro Pro Glu Trp		80
	85	90
Leu Asp Gly Ser Leu Pro Gly Asp Phe Gly Phe Asp Pro Leu Gly Leu		95
	100	105
Gly Ser Gly Ser Gly His Pro Gln Met Val Cys Thr Ser		110
	115	120
		125

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

Met Thr Leu Ala Arg His Phe Arg Phe His Leu Pro Thr Asn Gln Lys		
1	5	10
Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu Thr Leu Ser		15
	20	25
Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His Val Ala Ser		30
	35	40
Thr Ser Ser Thr Gly Gly Arg Leu Met Arg Glu Arg Leu Val Val Val		45
	50	55
Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Pro Leu Pro Pro Asp		60
	65	70
Arg Pro Leu Trp Phe Pro Gly Ser Ser Pro Pro Glu Trp Leu Asp Gly		75
	85	90
Ser Leu Pro Gly Asp Phe Gly Phe Asp Pro Leu Gly Leu Gly Ser Gly		95
	100	105
Ser Gly His Pro Gln Met Val Cys Thr Ser		110
	115	120

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1499938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Val Leu Met Gly Trp Ala Glu Gly Xaa Arg Trp Ala Asp Leu Ile		
1	5	10
Lys Pro Gly Ser Val Asp Ile Glu Pro Lys Tyr Pro His Lys Val Asn		15
	20	25
Pro Lys Pro Asp Val Gly Tyr Pro Gly Gly Leu Trp Phe Asp Phe Met		30
	35	40
Met Trp Gly Arg Gly Ser Pro Glu Pro Val Met Val Leu Arg Thr Lys		45
	50	55
Glu Ile Lys Asn Gly Arg Leu Ala Met Leu Ala Phe Leu Gly Phe Cys		60
	65	70
Phe Gln Ala Thr Tyr Thr Ser Gln Asp Pro Ile Glu Asn Leu Met Ala		75
	85	90
		95

His Leu Ala Asp Pro Gly His Cys Asn Val Phe Ser Ala Phe Thr Ser  
100 105 110  
His

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

acggatccac	cggagagatc	tggctctgcc	ttccctcgct	ccttcccgtg	aaccacaaac	60
ctaacgcgga	rmggcgcggg	ccggcmrccg	ggcgaggtgc	gcgtagctgc	cgtcgattgt	120
cgccggatcc	atccaccatg	ggcgggtggc	acggccagaa	gtccaagatg	gcccgcgagc	180
gcaacttgg	gaagaacaag	ggggccaagg	ggagccagct	cgagaccaac	aagaaggcca	240
tgagcatcca	gtgcaaagt	tgcatgcaaa	cattcatgtg	taccacgayt	gaagtgaagt	300
gccgggagca	cgccgaggcc	aagcatccca	agacagacgt	gtaccagtgc	ttcccccatc	360
tgaagaagt	aaaggcctga	acttagcaac	cagtgtctgt	ttggctacta	cgatcggggc	420
agggggcggt	ccttgtgttg	aggggtgttc	ttccgtgtta	tcttcccgtc	agtcatgcgt	480
cctgtcctat	gttaacctac	ataagaaaag	gatgtggtgt	ccacttctag	tgaaactact	540
gtctgtgtgt	aaaacctggt	tggtttcg				

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Gly	Ser	Thr	Gly	Glu	Ile	Trp	Ser	Ala	Ile	Pro	Ser	Leu	Leu	Pro	Val	
1				5					10					15		
Asn	His	Lys	Pro	Asn	Ala	Xaa	Xaa	Arg	Gly	Pro	Xaa	Xaa	Gly	Arg	Gly	
			20					25					30			
Ala	Arg	Ser	Cys	Arg	Arg	Leu	Ser	Pro	Asp	Pro	Ser	Thr	Met	Gly	Gly	
			35				40					45				
Gly	Asn	Gly	Gln	Lys	Ser	Lys	Met	Ala	Arg	Glu	Arg	Asn	Leu	Glu	Lys	
	50					55					60					
Asn	Lys	Gly	Ala	Lys	Gly	Ser	Gln	Leu	Glu	Thr	Asn	Lys	Lys	Ala	Met	
	65				70					75					80	
Ser	Ile	Gln	Cys	Lys	Val	Cys	Met	Gln	Thr	Phe	Met	Cys	Thr	Thr	Xaa	
			85					90						95		
Glu	Val	Lys	Cys	Arg	Glu	His	Ala	Glu	Ala	Lys	His	Pro	Lys	Thr	Asp	
			100					105					110			
Val	Tyr	Gln	Cys	Phe	Pro	His	Leu	Lys	Lys							
			115					120								

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

```
Met Gly Gly Gly Asn Gly Gln Lys Ser Lys Met Ala Arg Glu Arg Asn
1          5          10          15
Leu Glu Lys Asn Lys Gly Ala Lys Gly Ser Gln Leu Glu Thr Asn Lys
          20          25          30
Lys Ala Met Ser Ile Gln Cys Lys Val Cys Met Gln Thr Phe Met Cys
          35          40          45
Thr Thr Xaa Glu Val Lys Cys Arg Glu His Ala Glu Ala Lys His Pro
50          55          60
Lys Thr Asp Val Tyr Gln Cys Phe Pro His Leu Lys Lys
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

```
Met Ala Arg Glu Arg Asn Leu Glu Lys Asn Lys Gly Ala Lys Gly Ser
1          5          10          15
Gln Leu Glu Thr Asn Lys Lys Ala Met Ser Ile Gln Cys Lys Val Cys
          20          25          30
Met Gln Thr Phe Met Cys Thr Thr Xaa Glu Val Lys Cys Arg Glu His
          35          40          45
Ala Glu Ala Lys His Pro Lys Thr Asp Val Tyr Gln Cys Phe Pro His
50          55          60
Leu Lys Lys
65
```

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..531
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

```
aacaacattc aaaagctatt agcgattcctt cttctctctg attcaatctt cttcatagtt      60
tctaagctct caaattcttg acgaagcaat ggctcgtacg aagcaaactg caagaaaatc      120
acacggagga aaagctccga ggactctgct cgctaccaag gcggcgagga aatctgcgcc      180
gactactgga ggagtcaaga aacctcaccg ttaccgtccc ggaaccgtcg ctcttcgtga      240
gattcgtaaa taccagaaga gcacagagtt gttgatccgt aaacttcctt ttcaacgtct      300
tgttcgtgaa atcgctcaag attacaagac ggatctgaga ttccagagcc atgcgntggt      360
agctcttcaa gaagctgctg aagcatattt ggctgggttg tttgaagata caaatctgtg      420
tgccattcat gccaaagagg ttacgatcat gcctaaagat gttcaattgg cagaaggatt      480
cgtggagagc gtgcttagat tcgaattaaa atcatcaact attattctat t
```

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499944  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:  
Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser His Gly Gly Lys Ala  
1 5 10 15  
Pro Arg Thr Leu Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Thr  
20 25 30  
Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala  
35 40 45  
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg  
50 55 60  
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Tyr Lys  
65 70 75 80  
Thr Asp Leu Arg Phe Gln Ser His Ala Xaa Leu Ala Leu Gln Glu Ala  
85 90 95  
Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala  
100 105 110  
Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Val Gln Leu Ala  
115 120 125  
Glu Gly Phe Val Glu Ser Val Leu Arg Phe Glu Leu Lys Ser Ser Thr  
130 135 140  
Ile Ile Leu  
145

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1308  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

atatatttc	ataaataaac	ctctcaacct	ccacactttc	tcacccatca	cacaatcctc	60
aaaacagagt	aacccaaaaa	acagagcaat	ctctaaaaaa	tctcaagaaa	cctcactaaa	120
atgggttcaa	cggcggagac	acaattaact	ccggtgcaag	tcaccgacga	cgaagctgcc	180
ctcttcgcca	tgcaactagc	cagtgccttc	gttcttccga	tggttttaa	atccgcctta	240
gagcttgacc	ttcttgagat	tatggccaag	aatggttctc	ccatgtctcc	taccgagatc	300
gcttctaaac	ttccgaccaa	aaaccctgaa	gctccgggtc	tgctcgaccg	tatcctccgt	360
cttcttacgt	cttactccgt	cttaacctgc	tccaaccgta	aactttccgg	tgatggcggt	420
gaacggatth	acgggcttgg	tccggtttgc	aagtatttga	ccaagaacga	agatgggtgt	480
tccattgctg	ctctttgtct	tatgaaccaa	gacaagggtc	tcatggaaag	ctggtaccat	540
ttgaaggatg	caattcttga	tggtgggatt	ccattcaaca	aggcttatgg	aatgagcgcg	600
ttcgagtacc	acgggactga	ccctagattc	aacaagggtc	ttaacaatgg	aatgtctaac	660
cattccacaa	tcaccatgaa	gaagattctt	gagacctata	agggttttga	agggttgact	720
tctttgggtg	atgttggtgg	tggtcattgg	gctacactca	aaatgattgt	ctccaagtac	780
cctaacttta	aaggcatcaa	ctttgatctc	ccacatgtca	ttgaagatgc	tccttctcat	840
cctggatttg	agcatgttgg	aggagatatg	tttgaagtgc	tccctaaagg	tgatgccata	900
ttcatgaagt	ggatatgtca	tgactggagt	gacgaacatt	gcgtgaaatt	cttgaaaaac	960
tgctacgagt	cacttccaga	ggatggaaaa	gtgatattag	cagagtgtat	acttccagag	1020
acaccagact	caagcctctc	aaccaaacaa	gtagtccatg	tcgattgcat	tatgttggct	1080
cacaatcccc	gaggcaaaga	acgaaccgag	aaagagtttg	aggcattagc	caaagcatca	1140
ggcttcaagg	gcatacaagt	tgtctgcgac	gcttttgggtg	ttaaccttat	tgagttactc	1200

aagaagctct aaaaacaaac aatgttccta tgaagatgat ttatatgtaa acattatctc 1260  
atatctcctt ccacggttcc aaaactatgc tgtttaataa tggttttt

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

Met	Gly	Ser	Thr	Ala	Glu	Thr	Gln	Leu	Thr	Pro	Val	Gln	Val	Thr	Asp
1				5				10						15	
Asp	Glu	Ala	Ala	Leu	Phe	Ala	Met	Gln	Leu	Ala	Ser	Ala	Ser	Val	Leu
			20					25					30		
Pro	Met	Ala	Leu	Lys	Ser	Ala	Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met
		35					40					45			
Ala	Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu
	50					55					60				
Pro	Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg
65					70					75				80	
Leu	Leu	Thr	Ser	Tyr	Ser	Val	Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser
				85					90					95	
Gly	Asp	Gly	Val	Glu	Arg	Ile	Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr
			100					105					110		
Leu	Thr	Lys	Asn	Glu	Asp	Gly	Val	Ser	Ile	Ala	Ala	Leu	Cys	Leu	Met
		115					120						125		
Asn	Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala
	130					135					140				
Ile	Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala
145					150					155				160	
Phe	Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn
				165					170					175	
Gly	Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr
			180					185						190	
Tyr	Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly
		195					200					205			
Ile	Gly	Ala	Thr	Leu	Lys	Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys
	210					215						220			
Gly	Ile	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His
225					230					235				240	
Pro	Gly	Ile	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys
				245					250					255	
Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu
		260						265					270		
His	Cys	Val	Lys	Phe	Leu	Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp
		275					280						285		
Gly	Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser
		290					295					300			
Ser	Leu	Ser	Thr	Lys	Gln	Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala
305					310					315				320	
His	Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu
				325					330					335	
Ala	Lys	Ala	Ser	Gly	Phe	Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe
		340						345					350		
Gly	Val	Asn	Leu	Ile	Glu	Leu	Leu	Lys	Lys	Leu					
		355					360								

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 340 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..340  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499962  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

Met	Gln	Leu	Ala	Ser	Ala	Ser	Val	Leu	Pro	Met	Ala	Leu	Lys	Ser	Ala
1															
Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met	Ala	Lys	Asn	Gly	Ser	Pro	Met
Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu	Pro	Thr	Lys	Asn	Pro	Glu	Ala
Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg	Leu	Leu	Thr	Ser	Tyr	Ser	Val
Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser	Gly	Asp	Gly	Val	Glu	Arg	Ile
65															
Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr	Leu	Thr	Lys	Asn	Glu	Asp	Gly
Val	Ser	Ile	Ala	Ala	Leu	Cys	Leu	Met	Asn	Gln	Asp	Lys	Val	Leu	Met
Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala	Ile	Leu	Asp	Gly	Gly	Ile	Pro
Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala	Phe	Glu	Tyr	His	Gly	Thr	Asp
130															
Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn	Gly	Met	Ser	Asn	His	Ser	Thr
145															
Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr	Tyr	Lys	Gly	Phe	Glu	Gly	Leu
Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly	Ile	Gly	Ala	Thr	Leu	Lys	Met
Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys	Gly	Ile	Asn	Phe	Asp	Leu	Pro
His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His	Pro	Gly	Ile	Glu	His	Val	Gly
210															
Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys	Gly	Asp	Ala	Ile	Phe	Met	Lys
225															
Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu	His	Cys	Val	Lys	Phe	Leu	Lys
Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp	Gly	Lys	Val	Ile	Leu	Ala	Glu
Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser	Ser	Leu	Ser	Thr	Lys	Gln	Val
Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala	His	Asn	Pro	Gly	Gly	Lys	Glu
Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu	Ala	Lys	Ala	Ser	Gly	Phe	Lys
305															
Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe	Gly	Val	Asn	Leu	Ile	Glu	Leu
Leu	Lys	Lys	Leu												

(2) INFORMATION FOR SEQ ID NO:1255:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 330 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..330
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499963
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

Met	Ala	Leu	Lys	Ser	Ala	Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met	Ala
1				5					10					15	
Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu	Pro
			20					25					30		
Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg	Leu
		35					40					45			
Leu	Thr	Ser	Tyr	Ser	Val	Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser	Gly
	50					55					60				
Asp	Gly	Val	Glu	Arg	Ile	Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr	Leu
65					70					75					80
Thr	Lys	Asn	Glu	Asp	Gly	Val	Ser	Ile	Ala	Ala	Leu	Cys	Leu	Met	Asn
				85					90					95	
Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala	Ile
			100						105				110		
Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala	Phe
		115					120					125			
Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn	Gly
	130					135						140			
Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr	Tyr
145					150					155					160
Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly	Ile
			165						170					175	
Gly	Ala	Thr	Leu	Lys	Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys	Gly
			180						185				190		
Ile	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His	Pro
		195					200					205			
Gly	Ile	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys	Gly
	210					215						220			
Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu	His
225					230					235					240
Cys	Val	Lys	Phe	Leu	Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp	Gly
			245						250					255	
Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser	Ser
			260					265					270		
Leu	Ser	Thr	Lys	Gln	Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala	His
		275					280					285			
Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu	Ala
	290					295					300				
Lys	Ala	Ser	Gly	Phe	Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe	Gly
305					310					315					320
Val	Asn	Leu	Ile	Glu	Leu	Leu	Lys	Lys	Leu						
			325						330						

(2) INFORMATION FOR SEQ ID NO:1256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 916 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..916
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1499964
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

acgaaagaag agaacaaaga agaaattttg aaaatagtga aaatggtaac cgtaagccaa

```
agtcacacga cgacgtttct cttcttcacc acattttctt tgatattcgg atcaatctca 120
gccgtccgtt tgcttccacg accaaacact acaacaacca acgatctaga tttcatccga 180
acaagctgca acgctactct atatccagac gtctgttca cgtcactctc cggctacgcc 240
tctgccgttc aagacagtcg ggcgaggcta gccaaagctcg caatcggcgt ttcactttaa 300
caagccaaat ccactgcggc ttttctctcc aaactctcac gctctgccgc taaatactcc 360
ggtgatggcc accaaacagc ttccgccgta atccgagact gcgttttcgaa cgtcgaagac 420
gcgngtggac gagatgagag gatctctccg tcaactacgc gacatgaacg gcagaggagg 480
cggcacggca gctcggaggt cggtagaaac gtttaggttc cagatgagta acgtgcagac 540
gtggatgagt gcagcattga cggatgagga cacgtgtacg aatggatttg aagatatgga 600
cgaaggagga ttgattaaga cgaccgtttg tgatcggctc gaggaagtga agaggctaac 660
gagtaatgct cttgcccttg tcaacactta cgccaacaat ggagctccat gaccatgaga 720
ccatgagacc atgaggagtt ttaactttga tttaagtgtc tctttatata atttaataca 780
ttgtgggggt taagttagag ttatgtgtcg atttcatcat gttttacatt tgtttttgta 840
tcatccgagt ttcttatgtt taaagggttc agagagatgt tgtatctttg atttactaat 900
caaactgcac gatgat
```

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

```
Thr Lys Glu Glu Asn Lys Glu Glu Ile Leu Lys Ile Val Lys Met Val
1          5          10          15
Thr Val Ser Gln Ser His Thr Thr Thr Phe Leu Phe Phe Thr Thr Phe
20          25          30
Leu Leu Ile Phe Gly Ser Ile Ser Ala Val Arg Leu Leu Pro Arg Pro
35          40          45
Asn Thr Thr Thr Thr Asn Asp Leu Asp Phe Ile Arg Thr Ser Cys Asn
50          55          60
Ala Thr Leu Tyr Pro Asp Val Cys Phe Thr Ser Leu Ser Gly Tyr Ala
65          70          75          80
Ser Ala Val Gln Asp Ser Pro Ala Arg Leu Ala Lys Leu Ala Ile Gly
85          90          95
Val Ser Leu
```

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

```
Glu Arg Arg Glu Gln Arg Arg Asn Phe Glu Asn Ser Glu Asn Gly Asn
1          5          10          15
Arg Lys Pro Lys Ser His Asp Asp Val Ser Leu Leu His His Ile Ser
20          25          30
Leu Asp Ile Arg Ile Asn Leu Ser Arg Pro Phe Ala Ser Thr Thr Lys
35          40          45
His Tyr Asn Asn Gln Arg Ser Arg Phe His Pro Asn Lys Leu Gln Arg
50          55          60
```

Tyr Ser Ile Ser Arg Arg Leu Leu His Val Thr Leu Arg Leu Arg Leu  
65 70 75 80  
Cys Arg Ser Arg Gln Ser Gly Glu Ala Ser Gln Ala Arg Asn Arg Arg  
85 90 95  
Phe Thr Leu Thr Ser Gln Ile His Cys Gly Phe Ser Leu Gln Thr Leu  
100 105 110  
Thr Leu Cys Arg  
115

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Met Arg Gly Ser Leu Arg Gln Leu Arg Asp Met Asn Gly Arg Gly Gly  
1 5 10 15  
Gly Thr Ala Ala Arg Arg Ser Val Glu Thr Phe Arg Phe Gln Met Ser  
20 25 30  
Asn Val Gln Thr Trp Met Ser Ala Ala Leu Thr Asp Glu Asp Thr Cys  
35 40 45  
Thr Asn Gly Phe Glu Asp Met Asp Glu Gly Gly Leu Ile Lys Thr Thr  
50 55 60  
Val Cys Asp Arg Leu Glu Val Lys Arg Leu Thr Ser Asn Ala Leu  
65 70 75 80  
Ala Leu Val Asn Thr Tyr Ala Asn Asn Gly Ala Pro  
85 90

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

ctattgtgtt tgatcagggt accaaatcca ttgaaggact gcttcctttg ccaaagatcc 60  
ataacccaaa tgaccctcgg agaatcgagt ttaaagagct tgaagctgaa aaggcagtga 120  
tcgatgtgaa agctcacact ttggtgcgag agctttgggc tgggtctcgg tacttgatcc 180  
tacagactgc ggggttcatt aggctaactg tttgggaact ctggtgggac gtgatggagc 240  
caatctgttt ctatgtc

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

Ile Val Phe Asp Gln Val Thr Lys Ser Ile Glu Gly Leu Leu Pro Leu  
1 5 10 15  
Pro Lys Ile His Asn Pro Asn Asp Pro Arg Arg Ile Glu Phe Lys Glu  
20 25 30  
Leu Glu Ala Glu Lys Ala Val Ile Asp Val Lys Ala His Thr Leu Val  
35 40 45  
Arg Glu Leu Trp Ala Gly Leu Gly Tyr Leu Ile Leu Gln Thr Ala Gly  
50 55 60  
Phe Met Arg Leu Thr Phe Trp Glu Leu Ser Trp Asp Val Met Glu Pro  
65 70 75 80  
Ile Cys Phe Tyr Val  
85

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..573
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

ggagaagacg	tcgtgattat	ccgagtagta	gctcagattc	cgaatcagaa	tcggagtcgg	60
aatattctga	ttctgaggag	agtgagagt	aagatgagag	aagaaggaag	aagaggaaga	120
gaaaggagag	ggaagaggaa	gagaaagaga	ggaagagaag	gagaagagag	aaagataaga	180
agaagaggaa	caagtctgat	aaagatggag	ataagaagag	gaaggagaag	agaagaaga	240
agtctgagaa	agtgaagaaa	ggagctgtta	ctgaatcatg	gggcaagtat	ggaatcatca	300
gagaaactga	tatgtggaat	aaacgtccag	agttcacagc	atggttgctt	gaagtaaaga	360
agggttaattt	ggaaagcttg	ccaccttggg	aagagaagaa	aatgtttaaa	gattttatgg	420
aggatcataa	tactggtaca	tttacctcga	aaaaatacta	tgacattgat	ggttactata	480
gacttaagtt	ggaaaaagag	atgaaaaagg	gtttgaagaa	agctgggatt	agtgaacgta	540
ctgtgttcaa	tgatgaggaa	caacgccgac	tg			

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

Arg Arg Arg Arg Asp Tyr Pro Ser Ser Ser Ser Asp Ser Glu Ser Glu  
1 5 10 15  
Ser Glu Ser Glu Tyr Ser Asp Ser Glu Glu Ser Glu Ser Glu Asp Glu  
20 25 30  
Arg Arg Arg Lys Lys Arg Lys Arg Lys Glu Arg Glu Glu Glu Lys  
35 40 45  
Glu Arg Lys Arg Arg Arg Arg Glu Lys Asp Lys Lys Lys Arg Asn Lys  
50 55 60  
Ser Asp Lys Asp Gly Asp Lys Lys Arg Lys Glu Lys Lys Lys Lys Lys  
65 70 75 80  
Ser Glu Lys Val Lys Lys Gly Ala Val Thr Glu Ser Trp Gly Lys Tyr  
85 90 95  
Gly Ile Ile Arg Glu Thr Asp Met Trp Asn Lys Arg Pro Glu Phe Thr  
100 105 110  
Ala Trp Leu Leu Glu Val Lys Lys Val Asn Leu Glu Ser Leu Pro Pro



(2) INFORMATION FOR SEQ ID NO:1264:

(A) LENGTH: 1770 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1770  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499972

(XI) SEQUENCE DESCRIPTION: SEQ ID: 11-15						
atcactagtc	actatacacc	aatcttagat	cgggaagct	aatttctctt	ctccgatcgg	60
tgaatgcagt	tacattgacc	tcggatctaa	ccaagctctt	ctggtttcca	gctctctgga	120
attcaaaaaa	atggaggaga	aatccaagtc	aagaggttgg	tgcggttgg	tcatcgccat	180
tattgtgcta	gcttctgtta	tcctcgccgt	cgtttacact	gttaaattga	gaacgaagaa	240
atccggtgac	gatgacggtg	gctgtcccgt	tcctggacct	cccggcgcca	ttgataagaa	300
atacgccgac	gctcttaagc	tcgctttgca	gttcttcgat	atccagaaat	ctggtaaatt	360
ggagaacaat	aagatacctt	ggagaggaga	ttcaggtctt	aaagatggaa	gtgaagataa	420
tctggatctt	tccaaaggct	tatatgatgc	tggagatcat	ataaaagttg	gttttccaat	480
ggctttcact	gctacagttt	tgctatggtc	gattctttgag	tatcgtgatc	aaatgaatgc	540
agtcaaccaa	ttggatcctg	ctaaagactc	tctccgttgg	ctcgtgact	atcttatcaa	600
agctcatcct	tctgacaatg	tcctctatat	ccaggtggga	gatccaaaag	tagatcatcc	660
atgctgggag	agaccagagg	atatgaaaga	gaagagacca	cttactaaaa	ttgatgtaga	720
tactccaggg	acagaggttg	ctgctgaaac	tgctgcagct	atggcttcag	cgtctttggt	780
gtttaaggat	agtgatccta	catattcagc	aacgcttctg	aaacatgcga	agcagttggt	840
tgattttgca	gatacaaaga	gaggctctta	cagtgttaac	atacctgagg	ttcagaagtt	900
ttacaattcg	actggatatg	gtgatgagct	actatgggca	gctagtgtgt	tgtatcatgc	960
aacagaggat	aaaacttacc	ttgattatgt	gtctaatcat	ggaaaagaat	ttgctagtgt	1020
tgaaaatcct	acttggttta	gttgggacaa	caagcttgca	ggaacacagg	tactattatc	1080
aagattactc	tcttttaaga	aagatttatc	aggaagcaag	ggacttggaa	attacaggaa	1140
cacagctaaa	gctgtcatgt	gtggacttct	accaaagtct	ccaacatcta	cagctagtag	1200
aacaaaacgt	ggtcttatat	gggttagtga	atggaactcg	atgcaacaat	ccgtttcgtc	1260
agcgttttta	gcctcgcttt	tcagtgatta	catgctcact	tcccgtatcc	ataaaatatc	1320
ttgcgacggg	aaaatcttca	aagcaacaga	gcttagagat	ttcgccaaat	cgcaggctga	1380
ttacatgctg	gggaagaatc	cgttgggaac	gagcttcgtg	gtgggttatg	gagacaaata	1440
cccacaattt	gtgcatcata	gaggagcttc	gatcccggca	gatgcaacaa	cgggttgctt	1500
agatggattc	aaatggttta	actcaacgaa	accaaaccga	aacatagcat	atggtgcact	1560
cgtagggtgg	cctttcttca	atgagacgtt	cactgactca	cgagagaacc	caatgcagaa	1620
cgagccaacc	acttacaaca	atgcactcct	cgttggtctc	ttgtctagtc	ttgtcactac	1680
atcttctact	ttacagtcgt	tgaagtgagc	tttgcggtgt	ttagccttct	tattgaaaat	1740
cacattgctt	cattttttatt	tgtaattttc				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..525
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1499973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Lys | Ser | Lys | Ser | Arg | Gly | Trp | Cys | Gly | Trp | Phe | Ile | Ala | 1   | 5   | 10  | 15  |
| Ile | Ile | Val | Leu | Ala | Ser | Val | Ile | Leu | Ala | Val | Val | Tyr | Thr | Val | Lys | 20  | 25  | 30  |     |
| Leu | Arg | Thr | Lys | Lys | Ser | Gly | Asp | Asp | Asp | Gly | Gly | Cys | Pro | Val | Pro | 35  | 40  | 45  |     |
| Gly | Pro | Pro | Gly | Ala | Ile | Asp | Lys | Lys | Tyr | Ala | Asp | Ala | Leu | Lys | Leu | 50  | 55  | 60  |     |
| Ala | Leu | Gln | Phe | Phe | Asp | Ile | Gln | Lys | Ser | Gly | Lys | Leu | Glu | Asn | Asn | 65  | 70  | 75  | 80  |
| Lys | Ile | Pro | Trp | Arg | Gly | Asp | Ser | Gly | Leu | Lys | Asp | Gly | Ser | Glu | Asp | 85  | 90  | 95  |     |
| Asn | Leu | Asp | Leu | Ser | Lys | Gly | Leu | Tyr | Asp | Ala | Gly | Asp | His | Ile | Lys | 100 | 105 | 110 |     |
| Phe | Gly | Phe | Pro | Met | Ala | Phe | Thr | Ala | Thr | Val | Leu | Ser | Trp | Ser | Ile | 115 | 120 | 125 |     |
| Leu | Glu | Tyr | Gly | Asp | Gln | Met | Asn | Ala | Val | Asn | Gln | Leu | Asp | Pro | Ala | 130 | 135 | 140 |     |
| Lys | Asp | Ser | Leu | Arg | Trp | Ile | Thr | Asp | Tyr | Leu | Ile | Lys | Ala | His | Pro | 145 | 150 | 155 | 160 |
| Ser | Asp | Asn | Val | Leu | Tyr | Ile | Gln | Val | Gly | Asp | Pro | Lys | Val | Asp | His | 165 | 170 | 175 |     |
| Pro | Cys | Trp | Glu | Arg | Pro | Glu | Asp | Met | Lys | Glu | Lys | Arg | Pro | Leu | Thr | 180 | 185 | 190 |     |
| Lys | Ile | Asp | Val | Asp | Thr | Pro | Gly | Thr | Glu | Val | Ala | Ala | Glu | Thr | Ala | 195 | 200 | 205 |     |
| Ala | Ala | Met | Ala | Ser | Ala | Ser | Leu | Val | Phe | Lys | Asp | Ser | Asp | Pro | Thr | 210 | 215 | 220 |     |
| Tyr | Ser | Ala | Thr | Leu | Leu | Lys | His | Ala | Lys | Gln | Leu | Phe | Asp | Phe | Ala | 225 | 230 | 235 | 240 |
| Asp | Thr | Lys | Arg | Gly | Ser | Tyr | Ser | Val | Asn | Ile | Pro | Glu | Val | Gln | Lys | 245 | 250 | 255 |     |
| Phe | Tyr | Asn | Ser | Thr | Gly | Tyr | Gly | Asp | Glu | Leu | Leu | Trp | Ala | Ala | Ser | 260 | 265 | 270 |     |
| Trp | Leu | Tyr | His | Ala | Thr | Glu | Asp | Lys | Thr | Tyr | Leu | Asp | Tyr | Val | Ser | 275 | 280 | 285 |     |
| Asn | His | Gly | Lys | Glu | Phe | Ala | Ser | Phe | Gly | Asn | Pro | Thr | Trp | Phe | Ser | 290 | 295 | 300 |     |
| Trp | Asp | Asn | Lys | Leu | Ala | Gly | Thr | Gln | Val | Leu | Leu | Ser | Arg | Leu | Leu | 305 | 310 | 315 | 320 |
| Phe | Phe | Lys | Lys | Asp | Leu | Ser | Gly | Ser | Lys | Gly | Leu | Gly | Asn | Tyr | Arg | 325 | 330 | 335 |     |
| Asn | Thr | Ala | Lys | Ala | Val | Met | Cys | Gly | Leu | Leu | Pro | Lys | Ser | Pro | Thr | 340 | 345 | 350 |     |
| Ser | Thr | Ala | Ser | Arg | Thr | Asn | Gly | Gly | Leu | Ile | Trp | Val | Ser | Glu | Trp | 355 | 360 | 365 |     |
| Asn | Ser | Met | Gln | Gln | Ser | Val | Ser | Ser | Ala | Phe | Leu | Ala | Ser | Leu | Phe | 370 | 375 | 380 |     |
| Ser | Asp | Tyr | Met | Leu | Thr | Ser | Arg | Ile | His | Lys | Ile | Ser | Cys | Asp | Gly | 385 | 390 | 395 | 400 |
| Lys | Ile | Phe | Lys | Ala | Thr | Glu | Leu | Arg | Asp | Phe | Ala | Lys | Ser | Gln | Ala | 405 | 410 | 415 |     |
| Asp | Tyr | Met | Leu | Gly | Lys | Asn | Pro | Leu | Gly | Thr | Ser | Phe | Val | Val | Gly | 420 | 425 | 430 |     |
| Tyr | Gly | Asp | Lys | Tyr | Pro | Gln | Phe | Val | His | His | Arg | Gly | Ala | Ser | Ile | 435 | 440 | 445 |     |
| Pro | Ala | Asp | Ala | Thr | Thr | Gly | Cys | Leu | Asp | Gly | Phe | Lys | Trp | Phe | Asn | 450 | 455 | 460 |     |
| Ser | Thr | Lys | Pro | Asn | Pro | Asn | Ile | Ala | Tyr | Gly | Ala | Leu | Val | Gly | Gly |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1266:

(A) LENGTH: 409 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(IX) FEATURE:  
(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1499974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

| (A1) SEQUENCE DESCRIPTION: 335 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                            | Ala | Phe | Thr | Ala | Thr | Val | Leu | Ser | Trp | Ser | Ile | Leu | Glu | Tyr | Gly |  |
| 1                              |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp                            | Gln | Met | Asn | Ala | Val | Asn | Gln | Leu | Asp | Pro | Ala | Lys | Asp | Ser | Leu |  |
|                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg                            | Trp | Ile | Thr | Asp | Tyr | Leu | Ile | Lys | Ala | His | Pro | Ser | Asp | Asn | Val |  |
|                                |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu                            | Tyr | Ile | Gln | Val | Gly | Asp | Pro | Lys | Val | Asp | His | Pro | Cys | Trp | Glu |  |
|                                | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg                            | Pro | Glu | Asp | Met | Lys | Glu | Lys | Arg | Pro | Leu | Thr | Lys | Ile | Asp | Val |  |
| 65                             |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asp                            | Thr | Pro | Gly | Thr | Glu | Val | Ala | Ala | Glu | Thr | Ala | Ala | Ala | Met | Ala |  |
|                                |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser                            | Ala | Ser | Leu | Val | Phe | Lys | Asp | Ser | Asp | Pro | Thr | Tyr | Ser | Ala | Thr |  |
|                                |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu                            | Leu | Lys | His | Ala | Lys | Gln | Leu | Phe | Asp | Phe | Ala | Asp | Thr | Lys | Arg |  |
|                                |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly                            | Ser | Tyr | Ser | Val | Asn | Ile | Pro | Glu | Val | Gln | Lys | Phe | Tyr | Asn | Ser |  |
|                                | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Thr                            | Gly | Tyr | Gly | Asp | Glu | Leu | Leu | Trp | Ala | Ala | Ser | Trp | Leu | Tyr | His |  |
| 145                            |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala                            | Thr | Glu | Asp | Lys | Thr | Tyr | Leu | Asp | Tyr | Val | Ser | Asn | His | Gly | Lys |  |
|                                |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Glu                            | Phe | Ala | Ser | Phe | Gly | Asn | Pro | Thr | Trp | Phe | Ser | Trp | Asp | Asn | Lys |  |
|                                |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu                            | Ala | Gly | Thr | Gln | Val | Leu | Leu | Ser | Arg | Leu | Leu | Phe | Phe | Lys | Lys |  |
|                                |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Asp                            | Leu | Ser | Gly | Ser | Lys | Gly | Leu | Gly | Asn | Tyr | Arg | Asn | Thr | Ala | Lys |  |
|                                | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ala                            | Val | Met | Cys | Gly | Leu | Leu | Pro | Lys | Ser | Pro | Thr | Ser | Thr | Ala | Ser |  |
| 225                            |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Arg                            | Thr | Asn | Gly | Gly | Leu | Ile | Trp | Val | Ser | Glu | Trp | Asn | Ser | Met | Gln |  |
|                                |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Gln                            | Ser | Val | Ser | Ser | Ala | Phe | Leu | Ala | Ser | Leu | Phe | Ser | Asp | Tyr | Met |  |
|                                |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu                            | Thr | Ser | Arg | Ile | His | Lys | Ile | Ser | Cys | Asp | Gly | Lys | Ile | Phe | Lys |  |
|                                |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ala                            | Thr | Glu | Leu | Arg | Asp | Phe | Ala | Lys | Ser | Gln | Ala | Asp | Tyr | Met | Leu |  |
|                                | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Gly                            | Lys | Asn | Pro | Leu | Gly | Thr | Ser | Phe | Val | Val | Gly | Tyr | Gly | Asp | Lys |  |
| 305                            |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Tyr                            | Pro | Gln | Phe | Val | His | His | Arg | Gly | Ala | Ser | Ile | Pro | Ala | Asp | Ala |  |
|                                |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |

Thr Thr Gly Cys Leu Asp Gly Phe Lys Trp Phe Asn Ser Thr Lys Pro  
340 345 350  
Asn Pro Asn Ile Ala Tyr Gly Ala Leu Val Gly Gly Pro Phe Phe Asn  
355 360 365  
Glu Thr Phe Thr Asp Ser Arg Glu Asn Pro Met Gln Asn Glu Pro Thr  
370 375 380  
Thr Tyr Asn Asn Ala Leu Leu Val Gly Leu Leu Ser Ser Leu Val Thr  
385 390 395 400  
Thr Ser Ser Thr Leu Gln Ser Leu Lys  
405

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1499975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Met Asn Ala Val Asn Gln Leu Asp Pro Ala Lys Asp Ser Leu Arg Trp  
1 5 10 15  
Ile Thr Asp Tyr Leu Ile Lys Ala His Pro Ser Asp Asn Val Leu Tyr  
20 25 30  
Ile Gln Val Gly Asp Pro Lys Val Asp His Pro Cys Trp Glu Arg Pro  
35 40 45  
Glu Asp Met Lys Glu Lys Arg Pro Leu Thr Lys Ile Asp Val Asp Thr  
50 55 60  
Pro Gly Thr Glu Val Ala Ala Glu Thr Ala Ala Ala Met Ala Ser Ala  
65 70 75 80  
Ser Leu Val Phe Lys Asp Ser Asp Pro Thr Tyr Ser Ala Thr Leu Leu  
85 90 95  
Lys His Ala Lys Gln Leu Phe Asp Phe Ala Asp Thr Lys Arg Gly Ser  
100 105 110  
Tyr Ser Val Asn Ile Pro Glu Val Gln Lys Phe Tyr Asn Ser Thr Gly  
115 120 125  
Tyr Gly Asp Glu Leu Leu Trp Ala Ala Ser Trp Leu Tyr His Ala Thr  
130 135 140  
Glu Asp Lys Thr Tyr Leu Asp Tyr Val Ser Asn His Gly Lys Glu Phe  
145 150 155 160  
Ala Ser Phe Gly Asn Pro Thr Trp Phe Ser Trp Asp Asn Lys Leu Ala  
165 170 175  
Gly Thr Gln Val Leu Leu Ser Arg Leu Leu Phe Phe Lys Lys Asp Leu  
180 185 190  
Ser Gly Ser Lys Gly Leu Gly Asn Tyr Arg Asn Thr Ala Lys Ala Val  
195 200 205  
Met Cys Gly Leu Leu Pro Lys Ser Pro Thr Ser Thr Ala Ser Arg Thr  
210 215 220  
Asn Gly Gly Leu Ile Trp Val Ser Glu Trp Asn Ser Met Gln Gln Ser  
225 230 235 240  
Val Ser Ser Ala Phe Leu Ala Ser Leu Phe Ser Asp Tyr Met Leu Thr  
245 250 255  
Ser Arg Ile His Lys Ile Ser Cys Asp Gly Lys Ile Phe Lys Ala Thr  
260 265 270  
Glu Leu Arg Asp Phe Ala Lys Ser Gln Ala Asp Tyr Met Leu Gly Lys  
275 280 285  
Asn Pro Leu Gly Thr Ser Phe Val Val Gly Tyr Gly Asp Lys Tyr Pro  
290 295 300  
Gln Phe Val His His Arg Gly Ala Ser Ile Pro Ala Asp Ala Thr Thr

(2) INFORMATION FOR SEQ ID NO:1268:

(A) LENGTH: 883 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1499976

| (X1) SEQUENCE DESCRIPTION FILE |             |             |             |            |             |  |     |
|--------------------------------|-------------|-------------|-------------|------------|-------------|--|-----|
| aagtgtgtaa                     | ttttctttct  | tcgtaatacta | attttgtttg  | tttactgttg | atthttgtgtc |  | 60  |
| ttttctgttt                     | cgtggaccct  | tttggaatcc  | atcaatttta  | gggtttcatt | cttcttcgtg  |  | 120 |
| tgtgggtttt                     | gattttcttct | tcttctctcg  | agaaaaaaat  | gggtcaagct | ttgggttgta  |  | 180 |
| ttcaagttga                     | tcagtcgaat  | gtagcaatca  | aagagacttt  | tgggaagttt | gacgaattct  |  | 240 |
| tgagccgggt                     | tgctactgtt  | tgccatgggt  | tttgggaagt  | caagtcgctg | gtcacctttc  |  | 300 |
| tttactgtgt                     | caacagctcg  | atgttctcgt  | cgagacaaag  | actaaggata | atgtgtttgt  |  | 360 |
| cacggttgtt                     | gctttccattc | aataccgtgc  | cttagcggag  | agtgtccaag | atgcttttta  |  | 420 |
| caagctcagc                     | aacacaagga  | atcagattca  | agcttatgtc  | tttgatgtga | tccgagcaag  |  | 480 |
| tgtacttaag                     | ctggatctag  | actctacctt  | tgagcaaaag  | aatgacattg | caaaaaccgt  |  | 540 |
| tgagactgag                     | ctcgaaaagg  | ctatgtcgca  | ttacggatat  | gagattgttc | agacactgat  |  | 600 |
| tgtggatatc                     | gagcctgatg  | tgcattgtcaa | gagggaatg   | aatgagatca | atgctgtctc  |  | 660 |
| tagaatgaga                     | gaggcagcga  | gtgagaaaagc | tgagtttagta | atttcaaaca | ggaaagaaac  |  | 720 |
| tcagcaacaa                     | agtgacgtga  | agatgcagaa  | gaagaggatc  | gagaatcatt | ttggtggctt  |  | 780 |
| taaacgtctg                     | aaagtgaaag  | ggctaataaa  | gccgtaacgt  | gacagcttca | agtttcctcc  |  | 840 |
| taactacaat                     | tcttttaaat  | tqcttqatct  | ctaacaatac  | agg        |             |  |     |

(D) OTHER INFORMATION: / Ceres Seq. ID 1499977

| (X1) SEQUENCE DESCRIPTION: 24% IDENTITY WITH PDB ENTRY 1A30 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                                         | Gly | Gln | Ala | Leu | Gly | Cys | Ile | Gln | Val | Asp | Gln | Ser | Asn | Val | Ala |
| 1                                                           |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile                                                         | Lys | Glu | Thr | Phe | Gly | Lys | Phe | Asp | Glu | Phe | Leu | Ser | Arg | Val | Val |
|                                                             |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr                                                         | Val | Cys | His | Gly | Val | Trp | Glu | Val | Lys | Ser | Leu | Val | Thr | Phe | Leu |
|                                                             |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr                                                         | Val | Phe | Asn | Ser | Ser | Met | Phe | Ala | Ala | Arg | Gln | Arg | Leu | Arg | Ile |
|                                                             | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met                                                         | Cys | Leu | Ser | Arg | Leu | Leu | Leu | Pro | Phe | Asn | Thr | Val | Pro |     |     |
| 65                                                          |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 84 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..84  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499978  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:  
Met Ser His Tyr Gly Tyr Glu Ile Val Gln Thr Leu Ile Val Asp Ile  
1                  5                  10                  15  
Glu Pro Asp Val His Val Lys Arg Ala Met Asn Glu Ile Asn Ala Ala  
                  20                  25                  30  
Ser Arg Met Arg Glu Ala Ala Ser Glu Lys Ala Glu Leu Val Ile Ser  
                  35                  40                  45  
Asn Arg Lys Glu Thr Gln Gln Gln Ser Asp Val Lys Met Gln Lys Lys  
                  50                  55                  60  
Arg Ile Glu Asn His Phe Gly Gly Phe Lys Arg Leu Lys Val Lys Gly  
65                  70                  75                  80  
Leu Ile Lys Pro

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..59  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499979  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:  
Met Asn Glu Ile Asn Ala Ala Ser Arg Met Arg Glu Ala Ala Ser Glu  
1                  5                  10                  15  
Lys Ala Glu Leu Val Ile Ser Asn Arg Lys Glu Thr Gln Gln Gln Ser  
                  20                  25                  30  
Asp Val Lys Met Gln Lys Lys Arg Ile Glu Asn His Phe Gly Gly Phe  
                  35                  40                  45  
Lys Arg Leu Lys Val Lys Gly Leu Ile Lys Pro  
50                  55

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1178 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1178  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499984  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:  
ctcaaccttt tgggtgaaaa aaccagaaaa tgggggttgca tccaatttcc gacgccaatg          60  
aacacaatcc cttcggctct ctcaccgccg acgaattcta cgccaaacat tccgttagcc          120  
actcctccgc ttctcatcacc aaccctcgcg gtctcaaact cttcactcaa tgggtggtcac          180  
cactccctcc aactaaacca atcggatatca tcgctgtcgt tcatggcttc accggcgaat          240  
ccagttgggt ccttcagctc acatcaatcc tcttcgctaa atccggtttc ataacctgcg          300  
caattgatca ccaaggccat ggattctccg atggactcat cgctcatatc cctgacatca          360

```
atccccgtcgt cgatgactgt atctcttttct tcgatgactt ccgtagccgt caaacaccgt      420
cagatctgcc gtgtttttctc tactctgaat ccctaggcgg cgcgattgct ctctacatct      480
cgcttcgtca gagagggtgtt tgggatggac ttatcctcaa cggagctatg tgtggaatca      540
gcgataaatt caaacccgccg tggccgttgg agcatttgct attcgtcgtc gcgaatctta      600
tccctacttg gcgcgttatc cccactcgcg gatctattcc cgatgtttcg ttcaaggagc      660
cgtggaagag gaagcttgcc atggctagcc caaggaggac ggtggcgaaa ccacgggccg      720
ctactgctta tgagctgatt cgtgtttgta aggatctgca ggggaggttt gaggaagtgg      780
aggttccgct tctgattgtg cacggcggag gtgatgttgt atgcgacgta gcgtgtgttg      840
aggagcttca tcggagagcg attagtgagg ataagacgat caagatctac cctgagttgt      900
ggcatcagat gattggggaa tcggaggaga aagtcgatct ggtttacggg gatatgctga      960
gctggctcaa gagtcgagct gaaaggaagg cacgcgccgc cgttgatgga ggagcagctt    1020
agagtccttt ttgagtcctt gggtgttgta ttgtagtcca ataggactgt gccatctggc    1080
aagaaactat ttatggtttt actgtttcgt aatcgtagca catggtttac agttaaacca    1140
atacctttgg gtatcatcaa taatataaaa aatcgttg
```

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1499985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

```
Gln Pro Phe Gly Gly Lys Asn Gln Lys Met Gly Leu His Pro Ile Ser
1          5          10          15
Asp Ala Asn Glu His Asn Pro Phe Gly Ser Leu Thr Ala Asp Glu Phe
20          25          30
Tyr Ala Lys His Ser Val Ser His Ser Ser Ala Phe Ile Thr Asn Pro
35          40          45
Arg Gly Leu Lys Leu Phe Thr Gln Trp Trp Ser Pro Leu Pro Pro Thr
50          55          60
Lys Pro Ile Gly Ile Ile Ala Val Val His Gly Phe Thr Gly Glu Ser
65          70          75          80
Ser Trp Phe Leu Gln Leu Thr Ser Ile Leu Phe Ala Lys Ser Gly Phe
85          90          95
Ile Thr Cys Ala Ile Asp His Gln Gly His Gly Phe Ser Asp Gly Leu
100          105          110
Ile Ala His Ile Pro Asp Ile Asn Pro Val Val Asp Asp Cys Ile Ser
115          120          125
Phe Phe Asp Asp Phe Arg Ser Arg Gln Thr Pro Ser Asp Leu Pro Cys
130          135          140
Phe Leu Tyr Ser Glu Ser Leu Gly Gly Ala Ile Ala Leu Tyr Ile Ser
145          150          155          160
Leu Arg Gln Arg Gly Val Trp Asp Gly Leu Ile Leu Asn Gly Ala Met
165          170          175
Cys Gly Ile Ser Asp Lys Phe Lys Pro Pro Trp Pro Leu Glu His Leu
180          185          190
Leu Phe Val Val Ala Asn Leu Ile Pro Thr Trp Arg Val Ile Pro Thr
195          200          205
Arg Gly Ser Ile Pro Asp Val Ser Phe Lys Glu Pro Trp Lys Arg Lys
210          215          220
Leu Ala Met Ala Ser Pro Arg Arg Thr Val Ala Lys Pro Arg Ala Ala
225          230          235          240
Thr Ala Tyr Glu Leu Ile Arg Val Cys Lys Asp Leu Gln Gly Arg Phe
245          250          255
Glu Glu Val Glu Val Pro Leu Leu Ile Val His Gly Gly Gly Asp Val
260          265          270
Val Cys Asp Val Ala Cys Val Glu Glu Leu His Arg Arg Ala Ile Ser
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 275                                                             | 280 | 285 |
| Glu Asp Lys Thr Ile Lys Ile Tyr Pro Glu Leu Trp His Gln Met Ile |     |     |
| 290                                                             | 295 | 300 |
| Gly Glu Ser Glu Glu Lys Val Asp Leu Val Tyr Gly Asp Met Leu Ser |     |     |
| 305                                                             | 310 | 315 |
| Trp Leu Lys Ser Arg Ala Glu Arg Lys Ala Arg Ala Ala Val Asp Gly |     |     |
| 325                                                             | 330 | 335 |
| Gly Ala Ala                                                     |     |     |

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gly Leu His Pro Ile Ser Asp Ala Asn Glu His Asn Pro Phe Gly |     |     |
| 1                                                               | 5   | 10  |
| Ser Leu Thr Ala Asp Glu Phe Tyr Ala Lys His Ser Val Ser His Ser |     |     |
| 20                                                              | 25  | 30  |
| Ser Ala Phe Ile Thr Asn Pro Arg Gly Leu Lys Leu Phe Thr Gln Trp |     |     |
| 35                                                              | 40  | 45  |
| Trp Ser Pro Leu Pro Pro Thr Lys Pro Ile Gly Ile Ile Ala Val Val |     |     |
| 50                                                              | 55  | 60  |
| His Gly Phe Thr Gly Glu Ser Ser Trp Phe Leu Gln Leu Thr Ser Ile |     |     |
| 65                                                              | 70  | 75  |
| Leu Phe Ala Lys Ser Gly Phe Ile Thr Cys Ala Ile Asp His Gln Gly |     |     |
| 85                                                              | 90  | 95  |
| His Gly Phe Ser Asp Gly Leu Ile Ala His Ile Pro Asp Ile Asn Pro |     |     |
| 100                                                             | 105 | 110 |
| Val Val Asp Asp Cys Ile Ser Phe Phe Asp Asp Phe Arg Ser Arg Gln |     |     |
| 115                                                             | 120 | 125 |
| Thr Pro Ser Asp Leu Pro Cys Phe Leu Tyr Ser Glu Ser Leu Gly Gly |     |     |
| 130                                                             | 135 | 140 |
| Ala Ile Ala Leu Tyr Ile Ser Leu Arg Gln Arg Gly Val Trp Asp Gly |     |     |
| 145                                                             | 150 | 155 |
| Leu Ile Leu Asn Gly Ala Met Cys Gly Ile Ser Asp Lys Phe Lys Pro |     |     |
| 165                                                             | 170 | 175 |
| Pro Trp Pro Leu Glu His Leu Leu Phe Val Val Ala Asn Leu Ile Pro |     |     |
| 180                                                             | 185 | 190 |
| Thr Trp Arg Val Ile Pro Thr Arg Gly Ser Ile Pro Asp Val Ser Phe |     |     |
| 195                                                             | 200 | 205 |
| Lys Glu Pro Trp Lys Arg Lys Leu Ala Met Ala Ser Pro Arg Arg Thr |     |     |
| 210                                                             | 215 | 220 |
| Val Ala Lys Pro Arg Ala Ala Thr Ala Tyr Glu Leu Ile Arg Val Cys |     |     |
| 225                                                             | 230 | 235 |
| Lys Asp Leu Gln Gly Arg Phe Glu Glu Val Glu Val Pro Leu Leu Ile |     |     |
| 245                                                             | 250 | 255 |
| Val His Gly Gly Gly Asp Val Val Cys Asp Val Ala Cys Val Glu Glu |     |     |
| 260                                                             | 265 | 270 |
| Leu His Arg Arg Ala Ile Ser Glu Asp Lys Thr Ile Lys Ile Tyr Pro |     |     |
| 275                                                             | 280 | 285 |
| Glu Leu Trp His Gln Met Ile Gly Glu Ser Glu Glu Lys Val Asp Leu |     |     |
| 290                                                             | 295 | 300 |
| Val Tyr Gly Asp Met Leu Ser Trp Leu Lys Ser Arg Ala Glu Arg Lys |     |     |
| 305                                                             | 310 | 315 |
|                                                                 |     | 320 |



Ala Arg Ala Ala Val Asp Gly Gly Ala Ala  
325 330

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

```
ctcttgtctt ttgtctctcc accaattttt tcttgttctt tctctctcca ccacataaaa      60
aaaaaaaaac ctagctttgt cccctcaact cactgattga actgcttgat ttctgattga      120
tcatctgggt ggttttggat cgaagagtat tgttgattta gtggctggtg gctctccaaa      180
agagtaaggc cggagagaga aatcaatggc ctctggcggc ggagaggcgg ataaatcact      240
tgaaatcggg tccgggaccg cggatcccaa aataggcggg actgggagca ggagcgccgg      300
agaagaacga tacttcaggg cagatacact ggatttcagt aaatgggatt tgcataatggg      360
tcaaacctct actagcagcg tccctaccaa ttccgcttcc acgagcgcgc ccgcaccggc      420
gatgcaggaa tgggagattg acctctccaa actcgatatg aagcacgtcc tcgctcacgg      480
tacttacggc actgtctacc gcggtgtcta cgccggccaa gaagtcgcag tgaaagtgtt      540
agattgggga gaagatggtt acgccacacc agctgaaact acaactctcc gtgcttcctt      600
cgagcaagag gtcgccgtct ggcagaagct cgatcatccc aacgttacca agttcatagg      660
agcatccatg ggaacctctg atctgcggat cctcctctgt ggtgatactg gcggacgtgg      720
taacggtgca catcctgcca gggcctgttg tgttggtggt gaatatgttg ccggaggcac      780
gcttaagaag ttctctcatc agaaatatag ggccaaacta cccatcaagg atgtcattca      840
gctcgctttg gatctcgcta gagggcttag ttacctccac tccaaggcga ttgtacatag      900
ggacgtgaag tcagagaaca tgctgttaca gcctaacaag acgctgaaga tcgctgattt      960
cggggtagct agagttgaag ctccagaacc tcaagacatg acgggtggaa ctggaacact     1020
tggatacatg gcaccagagg ttcttgaagg aaagccttac aacaggaaat gcgatgtcta     1080
tagctttggg gtatgcctct gggaaatata ctgctgtgac atgccctatg ctgactgtag     1140
ttttgctgag atctctcacg ccgttggttca taggaatctg agaccagaga ttccgaaatg     1200
ctgcccgcac gcagtggcaa acatcatgaa gagatgctgg gacccgaatc cagacaggcg     1260
tccggagatg gaggagggtg tgaagctgct tgaagccata gacacaagca aaggtggtgg     1320
aatgatagct cgggaccagt ttcaggggtg cctctgtttc ttcaaaccctc gaggcccttg     1380
aatctctctc cctctctttc ctttttgctc cgtgtctgat atattcttga gagctgcgtg     1440
attctttgga ttttgtattt accttgagct atgggagttg gattggtgtg ggttttgtca     1500
taagaatctt tctgcgctct atgtatttat atacttaaca cagtcgtgta taattcgatt     1560
aagctttatt ttattttttg atgttgattc c
```

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

```
Met Ala Ser Gly Gly Gly Glu Ala Asp Lys Ser Leu Glu Ile Gly Ser
1          5          10          15
Gly Thr Ala Asp Pro Lys Ile Gly Gly Thr Gly Ser Arg Ser Ala Gly
20          25          30
Glu Glu Arg Tyr Phe Arg Ala Asp Thr Leu Asp Phe Ser Lys Trp Asp
35          40          45
Leu His Met Gly Gln Thr Ser Thr Ser Ser Val Leu Thr Asn Ser Ala
50          55          60
```

```

Ser Thr Ser Ala Pro Ala Pro Ala Met Gln Glu Trp Glu Ile Asp Leu
65              70              75              80
Ser Lys Leu Asp Met Lys His Val Leu Ala His Gly Thr Tyr Gly Thr
85              90              95
Val Tyr Arg Gly Val Tyr Ala Gly Gln Glu Val Ala Val Lys Val Leu
100            105            110
Asp Trp Gly Glu Asp Gly Tyr Ala Thr Pro Ala Glu Thr Thr Thr Leu
115            120            125
Arg Ala Ser Phe Glu Gln Glu Val Ala Val Trp Gln Lys Leu Asp His
130            135            140
Pro Asn Val Thr Lys Phe Ile Gly Ala Ser Met Gly Thr Ser Asp Leu
145            150            155            160
Arg Ile Pro Pro Ala Gly Asp Thr Gly Gly Arg Gly Asn Gly Ala His
165            170            175
Pro Ala Arg Ala Cys Cys Val Val Val Glu Tyr Val Ala Gly Gly Thr
180            185            190
Leu Lys Lys Phe Leu Ile Lys Lys Tyr Arg Ala Lys Leu Pro Ile Lys
195            200            205
Asp Val Ile Gln Leu Ala Leu Asp Leu Ala Arg Gly Leu Ser Tyr Leu
210            215            220
His Ser Lys Ala Ile Val His Arg Asp Val Lys Ser Glu Asn Met Leu
225            230            235            240
Leu Gln Pro Asn Lys Thr Leu Lys Ile Ala Asp Phe Gly Val Ala Arg
245            250            255
Val Glu Ala Gln Asn Pro Gln Asp Met Thr Gly Gly Thr Gly Thr Leu
260            265            270
Gly Tyr Met Ala Pro Glu Val Leu Glu Gly Lys Pro Tyr Asn Arg Lys
275            280            285
Cys Asp Val Tyr Ser Phe Gly Val Cys Leu Trp Glu Ile Tyr Cys Cys
290            295            300
Asp Met Pro Tyr Ala Asp Cys Ser Phe Ala Glu Ile Ser His Ala Val
305            310            315            320
Val His Arg Asn Leu Arg Pro Glu Ile Pro Lys Cys Cys Pro His Ala
325            330            335
Val Ala Asn Ile Met Lys Arg Cys Trp Asp Pro Asn Pro Asp Arg Arg
340            345            350
Pro Glu Met Glu Glu Val Val Lys Leu Leu Glu Ala Ile Asp Thr Ser
355            360            365
Lys Gly Gly Gly Met Ile Ala Pro Asp Gln Phe Gln Gly Cys Leu Cys
370            375            380
Phe Phe Lys Pro Arg Gly Pro
385            390

```

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

```

Met Gly Gln Thr Thr Ser Ser Val Leu Thr Asn Ser Ala Ser Thr
1              5              10              15
Ser Ala Pro Ala Pro Ala Met Gln Glu Trp Glu Ile Asp Leu Ser Lys
20            25            30
Leu Asp Met Lys His Val Leu Ala His Gly Thr Tyr Gly Thr Val Tyr
35            40            45
Arg Gly Val Tyr Ala Gly Gln Glu Val Ala Val Lys Val Leu Asp Trp

```

(2) INFORMATION FOR SEQ ID NO:1278:

(A) LENGTH: 319 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..319

SEQUENCE DESCRIPTION:

lu Trp Glu Ile Asp Le

Ala His Gly Thr Tyr Gly Thr Val Tyr Arg Gly Val Tyr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | His | Gly | Thr | Tyr | Gly | Thr | Val | Tyr | Arg | Gly | Val | Tyr | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Glu | Val | Ala | Val | Lys | Val | Leu | Asp | Trp | Gly | Glu | Asp | Gly | Tyr | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Pro | Ala | Glu | Thr | Thr | Thr | Leu | Arg | Ala | Ser | Phe | Glu | Gln | Glu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Val | Trp | Gln | Lys | Leu | Asp | His | Pro | Asn | Val | Thr | Lys | Phe | Ile | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Ala | Ser | Met | Gly | Thr | Ser | Asp | Leu | Arg | Ile | Pro | Pro | Ala | Gly | Asp | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

Gly Gly Arg Gly Asn Gly Ala His Pro Ala Arg Ala Cys Cys Val Val  
100 105 110  
Val Glu Tyr Val Ala Gly Gly Thr Leu Lys Lys Phe Leu Ile Lys Lys  
115 120 125  
Tyr Arg Ala Lys Leu Pro Ile Lys Asp Val Ile Gln Leu Ala Leu Asp  
130 135 140  
Leu Ala Arg Gly Leu Ser Tyr Leu His Ser Lys Ala Ile Val His Arg  
145 150 155 160  
Asp Val Lys Ser Glu Asn Met Leu Leu Gln Pro Asn Lys Thr Leu Lys  
165 170 175  
Ile Ala Asp Phe Gly Val Ala Arg Val Glu Ala Gln Asn Pro Gln Asp  
180 185 190  
Met Thr Gly Gly Thr Gly Thr Leu Gly Tyr Met Ala Pro Glu Val Leu  
195 200 205  
Glu Gly Lys Pro Tyr Asn Arg Lys Cys Asp Val Tyr Ser Phe Gly Val  
210 215 220  
Cys Leu Trp Glu Ile Tyr Cys Cys Asp Met Pro Tyr Ala Asp Cys Ser  
225 230 235 240  
Phe Ala Glu Ile Ser His Ala Val Val His Arg Asn Leu Arg Pro Glu  
245 250 255  
Ile Pro Lys Cys Cys Pro His Ala Val Ala Asn Ile Met Lys Arg Cys  
260 265 270  
Trp Asp Pro Asn Pro Asp Arg Arg Pro Glu Met Glu Glu Val Val Lys  
275 280 285  
Leu Leu Glu Ala Ile Asp Thr Ser Lys Gly Gly Gly Met Ile Ala Pro  
290 295 300  
Asp Gln Phe Gln Gly Cys Leu Cys Phe Phe Lys Pro Arg Gly Pro  
305 310 315

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aattaaccgt cacgagctac atgctctgta tcttcagatt tcctaaatac ttacaattcc  | 60  |
| cattccaatt ctgatttggg taatccaaaa caaaaaaaaaa ggaaactttc tttacccta  | 120 |
| aatctataaa aacgaaaccc ttcttcacaa atctttgttc ttcgtaatct ctcttaaaag  | 180 |
| cttttgtttc aatttcaatg gagtggttc gaggagaaac aattgggttc ggaaccttct   | 240 |
| ctactgtcag tacagcgaca aagtctagaa actccggcga ctttcctgca cttatcgctg  | 300 |
| tgaagtcgac gggttcttac ggcgcgcgtt cactctccaa cgagaaatcg gtgttgatt   | 360 |
| cactccgtga ttgtcctgag atcatacggt gttacggcga ggattcaact gtggagaacg  | 420 |
| gagaagagat gcataacttg ttcttagagt acgcttcgag aggaagctta gcgaggtaca  | 480 |
| tgaagaaact tggcgggtgar ggtttacggg agtccaccgt acgtcgctac acaggatcgg | 540 |
| tgcttcgagg gttacgtcat attcacgcta aagggt                            |     |

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499994

(2) INFORMATION FOR SEQ ID NO:1281:

(A) LENGTH: 461 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1499995

| (X1) SEQUENCE DESCRIPTION: SEQ |            |            |            |            |            |     |
|--------------------------------|------------|------------|------------|------------|------------|-----|
| atcatcacta                     | acaaaacaca | catcaaaaac | gattttacaa | gaaaaaaata | tcagaaaaaa | 60  |
| tgtcagagac                     | caacaagaat | gccttccaag | ccggtcaggc | cgctggcaaa | gctgaggaga | 120 |
| agagcaatgt                     | tctgctggac | aaggccaagg | atgctgctgc | tgcagctgga | gcttcgcgc  | 180 |
| aacaggcggg                     | aaagagtata | tcgatgcgg  | cagtgggagg | tgtaacttc  | gtgaaggaca | 240 |
| agaccggcct                     | gaacaagtag | cgatccgagt | caactttggg | agttataatt | tcctctttct | 300 |
| aattaattgt                     | tgggattttt | aaataaaaat | tgggagtcac | aattgattct | cgtactcatc | 360 |
| gtacttgttg                     | tgtgtttttg | tgttgtaaat | ttttaatgtt | tcttctccct | ttagatgtac | 420 |
| tacgtatttg                     | aactttaagt | ttaatcaaca | aaatctagtt | t          |            |     |

(2) INFORMATION FOR SEQ ID NO:1282:

(A) LENGTH: 77 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1499996

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ile                                     | Ile | Thr | Asn | Lys | Thr | His | Ile | Lys | Asn | Asp | Phe | Thr | Arg | Lys | Lys |  |  |
| 1                                       |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Tyr                                     | Gln | Lys | Lys | Cys | Gln | Arg | Pro | Thr | Arg | Met | Pro | Ser | Lys | Pro | Val |  |  |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Arg                                     | Pro | Leu | Ala | Lys | Leu | Arg | Arg | Arg | Ala | Met | Phe | Cys | Trp | Thr | Arg |  |  |
|                                         |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Pro                                     | Arg | Met | Leu | Leu | Leu | Gln | Leu | Glu | Leu | Pro | Arg | Asn | Arg | Arg | Glu |  |  |
|                                         | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Arg                                     | Val | Tyr | Arg | Met | Arg | Gln | Trp | Glu | Val | Leu | Thr | Ser |     |     |     |  |  |
| 65                                      |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..66  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499997  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:  
Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Ala Ala Gly  
1 5 10 15  
Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala  
20 25 30  
Ala Ala Ala Ala Gly Ala Ser Ala Gln Gln Ala Gly Lys Ser Ile Ser  
35 40 45  
Asp Ala Ala Val Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu  
50 55 60  
Asn Lys  
65

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1499998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

Met Pro Ser Lys Pro Val Arg Pro Leu Ala Lys Leu Arg Arg Arg Ala  
1 5 10 15  
Met Phe Cys Trp Thr Arg Pro Arg Met Leu Leu Leu Gln Leu Glu Leu  
20 25 30  
Pro Arg Asn Arg Arg Glu Arg Val Tyr Arg Met Arg Gln Trp Glu Val  
35 40 45  
Leu Thr Ser  
50

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 515 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1499999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acgtttctat | ctagagagaa | cacaacacat | cgaaccatgg | agaaatcaac | aagaacccta | 60  |
| ttcataacca | tcgtgataac | ctccatggtg | ctagggtttg | gaaactctga | tcttgctcag | 120 |
| gacagagagg | agtgtacgaa | ccagctcata | gaactatcca | cgtgtattcc | gtacgttgga | 180 |
| ggagacgcca | aggctccaac | aaaagattgt | tgtgcagggt | ttggccaagt | tataagaaag | 240 |
| agtgagaagt | gtgtttgcat | atttggtctc | tgaccaatat | gcaaacacac | ttctggactc | 300 |
| tttcttcctc | catcatttgt | gctttttttc | ttcttgtggt | ttgtctttta | gacttggtat | 360 |
| atttcttaca | atatgtttgt | tatgttctct | ggtgtgtggt | ttgttttttt | tggtattact | 420 |
| ttcatatttt | tttcgtcgaa | gaggacttgt | attcgacaat | gtcgtttcaa | ttttgttgtt | 480 |
| tccttagaaa | ctaaataaat | attggtttat | attgg      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

```
Thr Phe Leu Ser Arg Glu Asn Thr Thr His Arg Thr Met Glu Lys Ser
1          5          10          15
Thr Arg Thr Leu Phe Ile Thr Ile Val Ile Thr Ser Met Leu Leu Gly
          20          25          30
Phe Gly Asn Ser Asp Leu Ala Gln Asp Arg Glu Glu Cys Thr Asn Gln
          35          40          45
Leu Ile Glu Leu Ser Thr Cys Ile Pro Tyr Val Gly Gly Asp Ala Lys
          50          55          60
Ala Pro Thr Lys Asp Cys Cys Ala Gly Phe Gly Gln Val Ile Arg Lys
65          70          75          80
Ser Glu Lys Cys Val Cys Ile Phe Gly Leu
          85          90
```

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

```
Met Glu Lys Ser Thr Arg Thr Leu Phe Ile Thr Ile Val Ile Thr Ser
1          5          10          15
Met Leu Leu Gly Phe Gly Asn Ser Asp Leu Ala Gln Asp Arg Glu Glu
          20          25          30
Cys Thr Asn Gln Leu Ile Glu Leu Ser Thr Cys Ile Pro Tyr Val Gly
          35          40          45
Gly Asp Ala Lys Ala Pro Thr Lys Asp Cys Cys Ala Gly Phe Gly Gln
          50          55          60
Val Ile Arg Lys Ser Glu Lys Cys Val Cys Ile Phe Gly Leu
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

```
Met Leu Leu Gly Phe Gly Asn Ser Asp Leu Ala Gln Asp Arg Glu Glu
1          5          10          15
Cys Thr Asn Gln Leu Ile Glu Leu Ser Thr Cys Ile Pro Tyr Val Gly
```

20 25 30  
Gly Asp Ala Lys Ala Pro Thr Lys Asp Cys Cys Ala Gly Phe Gly Gln  
35 40 45  
Val Ile Arg Lys Ser Glu Lys Cys Val Cys Ile Phe Gly Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1413
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

```
agttgtttttt ttctttttct ttcttcgac taaagctctc ttcttcttct tcaaacggag      60
ctctcttctt cttcttcaac ctttggtctt cgatctctgt cttttttttt tttatctctt      120
cttcgattgt aagaaaagtt tcagctcaaa gaaatctggg ttaaagtgtg tttgaaattg      180
tggatcgatt catagattct cgataccaat aggatgtggt gatacgtttg taatctcgtg      240
ccatatcttt ggtttgtcaa agagagtgtg ttttaatgtc aatttctggg taaccaagtt      300
tgagcttatt ctttttgatt ctgcccggct ctctgatttt ttaagtgcaa gacgacaagt      360
gatgaaaaga tagagacaaa gaaaggcttc aagtttggtg ataactgctg tctaaagagt      420
tcgttccctt gagagattct cactctgaca taagagttcc cccaaccgga agagaaaattc      480
aaagatcaga aaacggtgaa agatgcgacg acgaccagga attggaggat tacaaaaggc      540
cgcagctgct agggatcagt accggttact aggagaaaat gtagccaagg ttacggactg      600
atatgatgaa rgaacagctc tccacgttcc gttcccagct tgaagagttc gctcgtaaac      660
acaagaatga cattcgtaag aatcctgcct tcagggtctc gttccatgaa atgtgtgcta      720
acattggtgt ggatcctctt gcttctaaca aggttttctg ggctgagctc cttggtattg      780
gtgacttcta ctatgaactt ggagttcaga ttattgaagt ttgcatgctt acaagatcac      840
ataatggagg tttgatcagc ttgcaagagc tctgcaacca tcttcgtcag agaaggaaga      900
aagaccgtga agctgtgact gaagatgatt gtcttcgagc tattagcaag ctaaagggtat      960
tgggtagcgg atttgagggt atcactattg gcaagaaaaa gcttgtccgt tcagtaccca      1020
cagagctgaa caaagaccat aaccagattt tggagttggc tcagggccaa ggctttgtga      1080
ttgtggaaga ggtacaaaga cgccctctcat ggacatctgg tcgcgttata gatgctctcg      1140
aaactttggt agaggagggc cttgccatga tcgacaattg ccataaagac ggaaagtgtc      1200
ggtactggtt tccctgtggt tcttcgggtt actcatccat cgggatctga tacttaaattg      1260
gtacatgctc agttgttttg cttgttttta tacagtatta aatacagtca cactcgttac      1320
atataaatta cgaagaaatc ttttcagtat attactgaaa ttttcttgta catgtatcac      1380
tctgtaaaaa aaatatattat gottggttgt tgt
```

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

```
Met Met Xaa Glu Gln Leu Ser Thr Phe Arg Ser Gln Leu Glu Glu Phe
1 5 10 15
Ala Arg Lys His Lys Asn Asp Ile Arg Lys Asn Pro Ala Phe Arg Ala
20 25 30
Gln Phe His Glu Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser
35 40 45
Asn Lys Gly Phe Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr
50 55 60
```



Glu Leu Gly Val Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His  
65 70 75 80  
Asn Gly Gly Leu Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln  
85 90 95  
Arg Arg Lys Lys Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg  
100 105 110  
Ala Ile Ser Lys Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr  
115 120 125  
Ile Gly Lys Lys Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys  
130 135 140  
Asp His Asn Gln Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile  
145 150 155 160  
Val Glu Glu Val Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile  
165 170 175  
Asp Ala Leu Glu Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn  
180 185 190  
Gly His Lys Asp Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser  
195 200 205  
Val Tyr Ser Ser Ile Gly Ile  
210 215

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1500005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

Met Xaa Glu Gln Leu Ser Thr Phe Arg Ser Gln Leu Glu Glu Phe Ala  
1 5 10 15  
Arg Lys His Lys Asn Asp Ile Arg Lys Asn Pro Ala Phe Arg Ala Gln  
20 25 30  
Phe His Glu Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser Asn  
35 40 45  
Lys Gly Phe Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr Glu  
50 55 60  
Leu Gly Val Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His Asn  
65 70 75 80  
Gly Gly Leu Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln Arg  
85 90 95  
Arg Lys Lys Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg Ala  
100 105 110  
Ile Ser Lys Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr Ile  
115 120 125  
Gly Lys Lys Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys Asp  
130 135 140  
His Asn Gln Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile Val  
145 150 155 160  
Glu Glu Val Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile Asp  
165 170 175  
Ala Leu Glu Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn Gly  
180 185 190  
His Lys Asp Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser Val  
195 200 205  
Tyr Ser Ser Ile Gly Ile  
210

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

```
Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser Asn Lys Gly Phe
1          5          10          15
Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr Glu Leu Gly Val
20          25          30
Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His Asn Gly Gly Leu
35          40          45
Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln Arg Arg Lys Lys
50          55          60
Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg Ala Ile Ser Lys
65          70          75          80
Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr Ile Gly Lys Lys
85          90          95
Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys Asp His Asn Gln
100         105         110
Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile Val Glu Glu Val
115         120         125
Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile Asp Ala Leu Glu
130         135         140
Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn Gly His Lys Asp
145         150         155         160
Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser Val Tyr Ser Ser
165         170         175
Ile Gly Ile
```

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1653
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

```
accataaatag atctaaaaca tggaaaccaa aaccctaatt ttctcaattc tcgtcgttgt      60
tctttctctc atttacttaa ttggaaaact caagcgaaag ccaaattctac ctccgagtcc      120
ggcatggtcg ttaccggtga ttggtcacct cgtcttctc aaaccaccga ttcacgcac      180
attcctctcc ctctctcaat ccctaaacaa tgctccgata ttctccctcc gactcggtaa      240
ccgactcgtt ttcgtgaact cgtcacactc gatcgccgag gaatgtttca ccaaaaacga      300
cgtcgtactg gcgaacagac caaacttcat cctcgctaaa cacgttgctg acgattacac      360
aaccatgatc gcagcttcct acggtgacca ctggcgtaac ctccgccgca tcggctccgt      420
cgagatattc tccaaccacc gtctcaatag ctttctgtct attcgtaas acgagatccg      480
acgacttggtg tttcgtcttt cacgtaactt ttcacaagag tttgtgaagg tggatatgaa      540
atcaatgta tctgacttaa cattcaacaa cattataaga atgggtggccg gaaaacgtta      600
ctacggagac ggtgttgagg atgatccgga ggctaaacgt gtccggcagc ttatagcgga      660
tgtggtggct tgtgtcgtgt ctggaaacgc tgttgattac ttaccggtt tgcggttggt      720
ttcagattac gaaacacggg ttaagaagtt agcgggtagg ctcgacgagt tcttgcaagg      780
attggttgat gagaaacgag acgctaagga gaaaggaaac actatgattg atcacttgct      840
```

```
tactctgcaa gaatcacaaac cggattactt cactgatcgt atcatcaaag gaaacatgct 900
tgctttgata ctagcaggga cgcacacatc agcgggttacg ttagaatggg cattgtcgaa 960
cgtgttgaaac cattcggagg tattgaacaa ggcgagagat gaaatcgata gaaagatcgg 1020
tttagacagg cttatggatg aatcagatat ctcaaacctg ccttatctcc aaaacattgt 1080
gtctgaaacg ttgcgccttt atcctgcggc tcccatgctt cttcctcacg ttgcctcgga 1140
agattgtaaa gttgcaggat atgatatgcc gcgtggcacg atactattga ccaatgtgtg 1200
ggctatacac agagatcctc agctatggga tgatccaatg agcttcaagc cagagagggt 1260
tgagaaggaa ggagaagctc agaagcttat gccgtttggg ttaggaagaa gggcgtgtcc 1320
tggttctgga ctggctcacc ggcttataaa cctgactctt ggatcattga ttcagtgttt 1380
ggaatgggag aagattggag aagaagtggg tatgagttaa ggcaaagggtg ttacaatgcc 1440
taaaagccaag cctttagaag ccatgtgcag agcacgtccc tctgttggtta aaatcttcaa 1500
ctagtccgct tgacgttttag tcttttagta atggctatgt atacactaga taactaatta 1560
tgtttgatg ttttcttttt tttttgggta aaatattatg tttgtatggt atatgagaat 1620
attttaccaa tattcctaga tgatattttg ggc
```

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..494
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

```
Met Glu Thr Lys Thr Leu Ile Phe Ser Ile Leu Val Val Val Leu Ser
1          5          10          15
Leu Ile Tyr Leu Ile Gly Lys Leu Lys Arg Lys Pro Asn Leu Pro Pro
20          25          30
Ser Pro Ala Trp Ser Leu Pro Val Ile Gly His Leu Arg Leu Leu Lys
35          40          45
Pro Pro Ile His Arg Thr Phe Leu Ser Leu Ser Gln Ser Leu Asn Asn
50          55          60
Ala Pro Ile Phe Ser Leu Arg Leu Gly Asn Arg Leu Val Phe Val Asn
65          70          75          80
Ser Ser His Ser Ile Ala Glu Glu Cys Phe Thr Lys Asn Asp Val Val
85          90          95
Leu Ala Asn Arg Pro Asn Phe Ile Leu Ala Lys His Val Ala Tyr Asp
100          105          110
Tyr Thr Thr Met Ile Ala Ala Ser Tyr Gly Asp His Trp Arg Asn Leu
115          120          125
Arg Arg Ile Gly Ser Val Glu Ile Phe Ser Asn His Arg Leu Asn Ser
130          135          140
Phe Leu Ser Ile Arg Lys Xaa Glu Ile Arg Arg Leu Val Phe Arg Leu
145          150          155          160
Ser Arg Asn Phe Ser Gln Glu Phe Val Lys Val Asp Met Lys Ser Met
165          170          175
Leu Ser Asp Leu Thr Phe Asn Asn Ile Ile Arg Met Val Ala Gly Lys
180          185          190
Arg Tyr Tyr Gly Asp Gly Val Glu Asp Asp Pro Glu Ala Lys Arg Val
195          200          205
Arg Gln Leu Ile Ala Asp Val Val Ala Cys Ala Gly Ala Gly Asn Ala
210          215          220
Val Asp Tyr Leu Pro Val Leu Arg Leu Val Ser Asp Tyr Glu Thr Arg
225          230          235          240
Val Lys Lys Leu Ala Gly Arg Leu Asp Glu Phe Leu Gln Gly Leu Val
245          250          255
Asp Glu Lys Arg Asp Ala Lys Glu Lys Gly Asn Thr Met Ile Asp His
260          265          270
Leu Leu Thr Leu Gln Glu Ser Gln Pro Asp Tyr Phe Thr Asp Arg Ile
```

|                         |                                         |     |
|-------------------------|-----------------------------------------|-----|
| 275                     | 280                                     | 285 |
| Ile Lys Gly Asn Met Leu | Ala Leu Ile Leu Ala Gly Thr Asp Thr Ser |     |
| 290                     | 295                                     | 300 |
| Ala Val Thr Leu Glu Trp | Ala Leu Ser Asn Val Leu Asn His Ser Glu |     |
| 305                     | 310                                     | 315 |
| Val Leu Asn Lys Ala Arg | Asp Glu Ile Asp Arg Lys Ile Gly Leu Asp |     |
| 325                     | 330                                     | 335 |
| Arg Leu Met Asp Glu Ser | Asp Ile Ser Asn Leu Pro Tyr Leu Gln Asn |     |
| 340                     | 345                                     | 350 |
| Ile Val Ser Glu Thr Leu | Arg Leu Tyr Pro Ala Ala Pro Met Leu Leu |     |
| 355                     | 360                                     | 365 |
| Pro His Val Ala Ser Glu | Asp Cys Lys Val Ala Gly Tyr Asp Met Pro |     |
| 370                     | 375                                     | 380 |
| Arg Gly Thr Ile Leu Leu | Thr Asn Val Trp Ala Ile His Arg Asp Pro |     |
| 385                     | 390                                     | 395 |
| Gln Leu Trp Asp Asp Pro | Met Ser Phe Lys Pro Glu Arg Phe Glu Lys |     |
| 405                     | 410                                     | 415 |
| Glu Gly Glu Ala Gln Lys | Leu Met Pro Phe Gly Leu Gly Arg Arg Ala |     |
| 420                     | 425                                     | 430 |
| Cys Pro Gly Ser Gly Leu | Ala His Arg Leu Ile Asn Leu Thr Leu Gly |     |
| 435                     | 440                                     | 445 |
| Ser Leu Ile Gln Cys Leu | Glu Trp Glu Lys Ile Gly Glu Glu Val Asp |     |
| 450                     | 455                                     | 460 |
| Met Ser Glu Gly Lys Gly | Val Thr Met Pro Lys Ala Lys Pro Leu Glu |     |
| 465                     | 470                                     | 475 |
| Ala Met Cys Arg Ala Arg | Pro Ser Val Val Lys Ile Phe Asn         |     |
| 485                     | 490                                     |     |

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1500009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ala | Ala | Ser | Tyr | Gly | Asp | His | Trp | Arg | Asn | Leu | Arg | Arg | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Val | Glu | Ile | Phe | Ser | Asn | His | Arg | Leu | Asn | Ser | Phe | Leu | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ile | Arg | Lys | Xaa | Glu | Ile | Arg | Arg | Leu | Val | Phe | Arg | Leu | Ser | Arg | Asn |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Phe | Ser | Gln | Glu | Phe | Val | Lys | Val | Asp | Met | Lys | Ser | Met | Leu | Ser | Asp |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Leu | Thr | Phe | Asn | Asn | Ile | Arg | Met | Val | Ala | Gly | Lys | Arg | Tyr | Tyr |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Asp | Gly | Val | Glu | Asp | Asp | Pro | Glu | Ala | Lys | Arg | Val | Arg | Gln | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Asp | Val | Val | Ala | Cys | Ala | Gly | Ala | Gly | Asn | Ala | Val | Asp | Tyr |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Leu | Pro | Val | Leu | Arg | Leu | Val | Ser | Asp | Tyr | Glu | Thr | Arg | Val | Lys | Lys |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Leu | Ala | Gly | Arg | Leu | Asp | Glu | Phe | Leu | Gln | Gly | Leu | Val | Asp | Glu | Lys |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Arg | Asp | Ala | Lys | Glu | Lys | Gly | Asn | Thr | Met | Ile | Asp | His | Leu | Leu | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Gln | Glu | Ser | Gln | Pro | Asp | Tyr | Phe | Thr | Asp | Arg | Ile | Ile | Lys | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

Asn Met Leu Ala Leu Ile Leu Ala Gly Thr Asp Thr Ser Ala Val Thr  
180 185 190  
Leu Glu Trp Ala Leu Ser Asn Val Leu Asn His Ser Glu Val Leu Asn  
195 200 205  
Lys Ala Arg Asp Glu Ile Asp Arg Lys Ile Gly Leu Asp Arg Leu Met  
210 215 220  
Asp Glu Ser Asp Ile Ser Asn Leu Pro Tyr Leu Gln Asn Ile Val Ser  
225 230 235 240  
Glu Thr Leu Arg Leu Tyr Pro Ala Ala Pro Met Leu Leu Pro His Val  
245 250 255  
Ala Ser Glu Asp Cys Lys Val Ala Gly Tyr Asp Met Pro Arg Gly Thr  
260 265 270  
Ile Leu Leu Thr Asn Val Trp Ala Ile His Arg Asp Pro Gln Leu Trp  
275 280 285  
Asp Asp Pro Met Ser Phe Lys Pro Glu Arg Phe Glu Lys Glu Gly Glu  
290 295 300  
Ala Gln Lys Leu Met Pro Phe Gly Leu Gly Arg Arg Ala Cys Pro Gly  
305 310 315 320  
Ser Gly Leu Ala His Arg Leu Ile Asn Leu Thr Leu Gly Ser Leu Ile  
325 330 335  
Gln Cys Leu Glu Trp Glu Lys Ile Gly Glu Glu Val Asp Met Ser Glu  
340 345 350  
Gly Lys Gly Val Thr Met Pro Lys Ala Lys Pro Leu Glu Ala Met Cys  
355 360 365  
Arg Ala Arg Pro Ser Val Val Lys Ile Phe Asn  
370 375

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1500010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

Met Lys Ser Met Leu Ser Asp Leu Thr Phe Asn Asn Ile Ile Arg Met  
1 5 10 15  
Val Ala Gly Lys Arg Tyr Tyr Gly Asp Gly Val Glu Asp Asp Pro Glu  
20 25 30  
Ala Lys Arg Val Arg Gln Leu Ile Ala Asp Val Val Ala Cys Ala Gly  
35 40 45  
Ala Gly Asn Ala Val Asp Tyr Leu Pro Val Leu Arg Leu Val Ser Asp  
50 55 60  
Tyr Glu Thr Arg Val Lys Lys Leu Ala Gly Arg Leu Asp Glu Phe Leu  
65 70 75 80  
Gln Gly Leu Val Asp Glu Lys Arg Asp Ala Lys Glu Lys Gly Asn Thr  
85 90 95  
Met Ile Asp His Leu Leu Thr Leu Gln Glu Ser Gln Pro Asp Tyr Phe  
100 105 110  
Thr Asp Arg Ile Ile Lys Gly Asn Met Leu Ala Leu Ile Leu Ala Gly  
115 120 125  
Thr Asp Thr Ser Ala Val Thr Leu Glu Trp Ala Leu Ser Asn Val Leu  
130 135 140  
Asn His Ser Glu Val Leu Asn Lys Ala Arg Asp Glu Ile Asp Arg Lys  
145 150 155 160  
Ile Gly Leu Asp Arg Leu Met Asp Glu Ser Asp Ile Ser Asn Leu Pro  
165 170 175  
Tyr Leu Gln Asn Ile Val Ser Glu Thr Leu Arg Leu Tyr Pro Ala Ala

|             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-----|
|             | 180         |             | 185         |             | 190 |
| Pro Met Leu | Pro His Val | Ala Ser Glu | Asp Cys Lys | Val Ala Gly |     |
| 195         | 200         | 205         |             |             |     |
| Tyr Asp Met | Pro Arg Gly | Thr Ile Leu | Leu Thr Asn | Val Trp Ala | Ile |
| 210         | 215         | 220         |             |             |     |
| His Arg Asp | Pro Gln Leu | Trp Asp Asp | Pro Met Ser | Phe Lys Pro | Glu |
| 225         | 230         | 235         |             |             | 240 |
| Arg Phe Glu | Lys Glu Gly | Glu Ala Gln | Lys Leu Met | Pro Phe Gly | Leu |
|             | 245         | 250         |             |             | 255 |
| Gly Arg Arg | Ala Cys Pro | Gly Ser Gly | Leu Ala His | Arg Leu Ile | Asn |
|             | 260         | 265         |             |             | 270 |
| Leu Thr Leu | Gly Ser Leu | Ile Gln Cys | Leu Glu Trp | Glu Lys Ile | Gly |
|             | 275         | 280         |             |             | 285 |
| Glu Glu Val | Asp Met Ser | Glu Gly Lys | Gly Val Thr | Met Pro Lys | Ala |
|             | 290         | 295         |             |             | 300 |
| Lys Pro Leu | Glu Ala Met | Cys Arg Ala | Arg Pro Ser | Val Val Lys | Ile |
| 305         | 310         | 315         |             |             | 320 |
| Phe Asn     |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| gcagtggaga | gagagcatgt | gaataaaaag  | cgtgaagcct | tttgatatct | ctttctcttc | 60   |
| ctcttccttt | ctcctccgat | agatttcgcc  | ggcgtatggc | gtggactcct | tagaaacgga | 120  |
| gattgacacg | gcggtgcgtg | ttgtccacct  | cgcttcttct | ctctgtgtta | aagttcaaga | 180  |
| gaagcttcat | cttcctaacg | gtggtcacgt  | taagtctaaa | gacgatgatt | cccctgtcac | 240  |
| cgtcgctgat | tttggtgtac | aagcaattgt  | gagctggggt | ttagctgaag | tgtttgggtg | 300  |
| tcaaaacctt | tcaattgttg | ctgaagaaga  | cactgagaca | ctctctgagg | ctgattcttt | 360  |
| aggtctttta | ggagctgtgt | cgaatgcggt  | taatgaagca | ttgtccgaag | ctcagaacta | 420  |
| cgggcttccg | aagccagtta | agccattggg  | gtctagttaa | attcttaagg | ctattagtag | 480  |
| atgtaactct | gttggaggac | ctaaaggaag  | gcattggggt | cttgatcctg | ttgatggaac | 540  |
| gttagggttt | gttcgtgggg | atcagtatgc  | tggtgcttta | gctttgatag | agaatggtaa | 600  |
| agttcttttg | ggtgtactag | gatgtcctaa  | ttatccggtt | aagaaagaat | gtttaagtaa | 660  |
| tggttgtaac | caagctatga | agacgaaagc  | tggtgctggt | tcagtatcga | aaggatgtgt | 720  |
| tatgtatgca | aagagaggta | gtgggtcaagc | ttggatgcaa | cctttgatcg | ttggaggaat | 780  |
| accagaatct | gcaacacttc | ttaaggtttc  | ttcagttgat | gatccgggtt | tagctacagt | 840  |
| ttgtgagcca | gtagagagag | caaactcaaa  | ccacttggtc | actgcaggac | ttgccaatag | 900  |
| catgggagtt | agaaagcagc | ctatgcgagt  | gtatagcatg | gtgaaatatg | cagcgattgc | 960  |
| acgtggagac | gctgaagtgt | ttatgaagtt  | tgcacagtca | agttacaaag | agaagatatg | 1020 |
| ggatcacgca | gctggagttg | ttattgtgga  | agaagctggg | ggtgtggtga | ctgatgcggg | 1080 |
| aggggagaac | ttagacttct | cgaaagggtg  | ttacttggaa | ggtcttgacc | gtggaatcat | 1140 |
| cgcagtgtct | ggtcaagttt | tacatgagaa  | gattataggt | gctgtttatg | ctagttggga | 1200 |
| atcttccagt | ctctgaaaaa | gcttatccac  | aatccgtagt | ttggtgcagc | atcatcgagc | 1260 |
| caaagcaaag | gaggaacaag | ggccattacg  | gtttaggatg | agcaagggcc | agtttcaatg | 1320 |
| aatgtgaatg | gcgagagaag | aaatatagtc  | gaggaagcag | cggtaaaagt | aagaatctag | 1380 |
| tttatttacc | tatctaagag | taataaagct  | gctgcatttc | acgaaccctt | atgttctatg | 1440 |
| atctttaatg | gatgatatca | ttttt       |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..373  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Asp | Ser | Leu | Glu | Thr | Glu | Ile | Asp | Thr | Ala | Val | Arg | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | His | Leu | Ala | Ser | Ser | Leu | Cys | Val | Lys | Val | Gln | Glu | Lys | Leu | His |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Pro | Asn | Gly | Gly | His | Val | Lys | Ser | Lys | Asp | Asp | Asp | Ser | Pro | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Thr | Val | Ala | Asp | Phe | Gly | Val | Gln | Ala | Ile | Val | Ser | Trp | Val | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Val | Phe | Gly | Asp | Gln | Asn | Leu | Ser | Ile | Val | Ala | Glu | Glu | Asp | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Thr | Leu | Ser | Glu | Ala | Asp | Ser | Leu | Gly | Leu | Leu | Gly | Ala | Val | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Ala | Val | Asn | Glu | Ala | Leu | Ser | Glu | Ala | Gln | Asn | Tyr | Gly | Leu | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Pro | Val | Lys | Pro | Leu | Gly | Ser | Ser | Glu | Ile | Leu | Lys | Ala | Ile | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Cys | Asn | Ser | Val | Gly | Gly | Pro | Lys | Gly | Arg | His | Trp | Val | Leu | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Pro | Val | Asp | Gly | Thr | Leu | Gly | Phe | Val | Arg | Gly | Asp | Gln | Tyr | Ala | Val |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Leu | Ala | Leu | Ile | Glu | Asn | Gly | Lys | Val | Leu | Leu | Gly | Val | Leu | Gly |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Cys | Pro | Asn | Tyr | Pro | Val | Lys | Lys | Glu | Cys | Leu | Ser | Asn | Gly | Cys | Asn |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Ala | Met | Lys | Thr | Lys | Ala | Val | Ala | Gly | Ser | Val | Ser | Lys | Gly | Cys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Met | Tyr | Ala | Lys | Arg | Gly | Ser | Gly | Gln | Ala | Trp | Met | Gln | Pro | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Val | Gly | Gly | Ile | Pro | Glu | Ser | Ala | Thr | Leu | Leu | Lys | Val | Ser | Ser |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Asp | Asp | Pro | Val | Leu | Ala | Thr | Val | Cys | Glu | Pro | Val | Glu | Arg | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Ser | Asn | His | Leu | Phe | Thr | Ala | Gly | Leu | Ala | Asn | Ser | Met | Gly | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Lys | Gln | Pro | Met | Arg | Val | Tyr | Ser | Met | Val | Lys | Tyr | Ala | Ala | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Arg | Gly | Asp | Ala | Glu | Val | Phe | Met | Lys | Phe | Ala | Gln | Ser | Ser | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Glu | Lys | Ile | Trp | Asp | His | Ala | Ala | Gly | Val | Val | Ile | Val | Glu | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ala | Gly | Gly | Val | Val | Thr | Asp | Ala | Gly | Gly | Arg | Asn | Leu | Asp | Phe | Ser |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Gly | Val | Tyr | Leu | Glu | Gly | Leu | Asp | Arg | Gly | Ile | Ile | Ala | Cys | Ser |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Gly | Gln | Val | Leu | His | Glu | Lys | Ile | Ile | Gly | Ala | Val | Tyr | Ala | Ser | Trp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Ser | Ser | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 370 |

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1472 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1472

(D) OTHER INFORMATION: / Ceres Seq. ID 1500017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

```
aaaaaagtca atcatatcaa atcccaaadc ctcccagatg tttttatcat cttcttcttc 60
ctgaagattt gatttcattt tcctctcttt cagatcccta ttctcatggc ttctggatct 120
tactggtgct atagttgtag ccgattcggt tgggtttccg attcaatctc ttgccctgat 180
tgcgacgggtg gtttcctoga actcatccaa gagcctctcg atttcacacc ttccgattcc 240
ttcaccacca ccaccaccac tcaacatcgc agccccactc gcttccctcc tccttcttct 300
tcttctcca ccccatccgc ttctatgcac gccgataaca gtccactcc taccatcggt 360
actcgtaaac gaagcaatcg atctccta atcagttattg ttctccgtgg atctgctgct 420
gctccttctt ctgatgttgt ttccgaagg tttagatgat ctgcttttca gatgtattac 480
gatgatggta ctgattctgg tcttagacct ttaccaccga gtatgactga gtttttgta 540
ggttctggat ttgatcggtt gttgatcag atctctcaga tcgagcttaa caccaatcgg 600
aatcttcgtt cttgtgaaca tccaccggct tctaaatcgg ccattgaagc tttgcctctg 660
attgaaatcg atccgactca tctcttatcg gattctcaat ctcatcgcg tggttgcaaa 720
gagaatttcg ttttgaaatc atctgctcgc gagatgcctt gtaatcacat ctatcatcct 780
gattgtattc ttcttgggtg tgcgattcgt aactcttgct cggtttgccg tcatgagcta 840
ccggcggagg atctcaccga cggaaaccgg gctgctttga ctgctgttac cgctactgca 900
gaggaagagg aagactcagc tgcgggggta acgatttgga ggttaccagg tggaggattc 960
gctgtaggga gaatccctgg tggttgga gaatgatgcc ggtgggttac 1020
acggagggtg atggtggtag actcgggtg gagagacttc cgagaagagt agcttggggg 1080
tcgagaagag gtggaagaga tggtggaggt agtagagagc agaggtggtg gctttgcggg 1140
tcggatcatg aggttttctg gatgttttag tggatcatct ggatccattg ctgctgctgc 1200
tgctgcatca tccgggtccg ggtccagaat tccgggttact cgtagaacca ggctcgttct 1260
tatgttcagt acggcgtcgt cttcgtcaag gagacgaaat tggctagcgt gattactaga 1320
attaccaagc tctcttctca ggtgaaaact aaacacgaaa gaacacactc ttcttctggt 1380
taaatttttc ctatgttcct tattaagttt ttgtctattt cagtgtaatg attatattca 1440
ttcctaaaat ttgaatctat gcgagtaa at tg
```

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

```
Met Ala Ser Gly Ser Tyr Trp Cys Tyr Ser Cys Ser Arg Phe Val Trp
1          5          10          15
Val Ser Asp Ser Ile Ser Cys Pro Asp Cys Asp Gly Gly Phe Leu Glu
20          25          30
Leu Ile Gln Glu Pro Leu Asp Phe Thr Pro Ser Asp Ser Phe Thr Thr
35          40          45
Thr Thr Thr Thr Gln His Arg Ser Pro Thr Arg Phe Pro Pro Pro Ser
50          55          60
Ser Ser Ser Ser Thr Pro Ser Ala Ser Met His Ala Asp Asn Ser Pro
65          70          75          80
Thr Pro Thr Ile Val Thr Arg Thr Arg Ser Asn Arg Ser Pro Asn Pro
85          90          95
Val Ile Val Leu Arg Gly Ser Ala Ala Ala Pro Ser Ser Asp Val Val
100          105          110
Ser Glu Gly Leu Asp Arg Ser Ala Phe Gln Met Tyr Tyr Asp Asp Gly
115          120          125
Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro Ser Met Thr Glu Phe Leu
130          135          140
```



```

Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp Gln Ile Ser Gln Ile Glu
145          150          155          160
Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys Glu His Pro Pro Ala Ser
          165          170          175
Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile Glu Ile Asp Pro Thr His
          180          185          190
Leu Leu Ser Asp Ser Gln Ser His Cys Ala Val Cys Lys Glu Asn Phe
          195          200          205
Val Leu Lys Ser Ser Ala Arg Glu Met Pro Cys Asn His Ile Tyr His
          210          215          220
Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile Arg Asn Ser Cys Pro Val
225          230          235          240
Cys Arg His Glu Leu Pro Ala Glu Asp Leu Thr Asp Gly Thr Gly Ala
          245          250          255
Ala Leu Thr Ala Val Thr Ala Thr Ala Glu Glu Glu Glu Asp Ser Ala
          260          265          270
Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly Gly Gly Phe Ala Val Gly
          275          280          285
Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp Arg Met Met Pro Val Val
290          295          300
Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly Asp Glu Arg Leu Pro Arg
305          310          315          320
Arg Val Ala Trp Gly Ser Arg Arg Gly Gly Arg Asp Gly Gly Gly Ser
          325          330          335
Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser Asp His Glu Ala Phe Arg
          340          345          350
Met Phe

```

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1500019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

```

Met His Ala Asp Asn Ser Pro Thr Pro Thr Ile Val Thr Arg Thr Arg
1          5          10          15
Ser Asn Arg Ser Pro Asn Pro Val Ile Val Leu Arg Gly Ser Ala Ala
          20          25          30
Ala Pro Ser Ser Asp Val Val Ser Glu Gly Leu Asp Arg Ser Ala Phe
          35          40          45
Gln Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro
          50          55          60
Pro Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu
          65          70          75          80
Asp Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser
          85          90          95
Cys Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu
          100          105          110
Ile Glu Ile Asp Pro Thr His Leu Ser Asp Ser Gln Ser His Cys
          115          120          125
Ala Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met
          130          135          140
Pro Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala
145          150          155          160
Ile Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |
| Leu | Thr | Asp | Gly | Thr | Gly | Ala | Ala | Leu | Thr | Ala | Val | Thr | Ala | Thr | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Glu | Glu | Glu | Asp | Ser | Ala | Ala | Gly | Leu | Thr | Ile | Trp | Arg | Leu | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Gly | Phe | Ala | Val | Gly | Arg | Ile | Pro | Gly | Gly | Trp | Arg | Gly | Gly |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Asp | Arg | Met | Met | Pro | Val | Val | Tyr | Thr | Glu | Val | Asp | Gly | Gly | Arg | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Asp | Glu | Arg | Leu | Pro | Arg | Arg | Val | Ala | Trp | Gly | Ser | Arg | Arg | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Arg | Asp | Gly | Gly | Gly | Ser | Arg | Glu | Gln | Arg | Trp | Trp | Leu | Cys | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Asp | His | Glu | Ala | Phe | Arg | Met | Phe |     |     |     |     |     |     |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1500020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Tyr | Asp | Asp | Gly | Thr | Asp | Ser | Gly | Leu | Arg | Pro | Leu | Pro | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Met | Thr | Glu | Phe | Leu | Leu | Gly | Ser | Gly | Phe | Asp | Arg | Leu | Leu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ile | Ser | Gln | Ile | Glu | Leu | Asn | Thr | Asn | Arg | Asn | Leu | Arg | Ser | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | His | Pro | Pro | Ala | Ser | Lys | Ser | Ala | Ile | Glu | Ala | Leu | Pro | Leu | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ile | Asp | Pro | Thr | His | Leu | Leu | Ser | Asp | Ser | Gln | Ser | His | Cys | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Cys | Lys | Glu | Asn | Phe | Val | Leu | Lys | Ser | Ser | Ala | Arg | Glu | Met | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Asn | His | Ile | Tyr | His | Pro | Asp | Cys | Ile | Leu | Pro | Trp | Leu | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Asn | Ser | Cys | Pro | Val | Cys | Arg | His | Glu | Leu | Pro | Ala | Glu | Asp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asp | Gly | Thr | Gly | Ala | Ala | Leu | Thr | Ala | Val | Thr | Ala | Thr | Ala | Glu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Glu | Glu | Asp | Ser | Ala | Ala | Gly | Leu | Thr | Ile | Trp | Arg | Leu | Pro | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Gly | Phe | Ala | Val | Gly | Arg | Ile | Pro | Gly | Gly | Trp | Arg | Gly | Gly | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Met | Met | Pro | Val | Val | Tyr | Thr | Glu | Val | Asp | Gly | Gly | Arg | Leu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Glu | Arg | Leu | Pro | Arg | Arg | Val | Ala | Trp | Gly | Ser | Arg | Arg | Gly | Gly |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Asp | Gly | Gly | Gly | Ser | Arg | Glu | Gln | Arg | Trp | Trp | Leu | Cys | Gly | Ser |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Asp | His | Glu | Ala | Phe | Arg | Met | Phe |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1467  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

```
attcttcttctt ttctctctct cctctgttct atctctttct aacactcaag cctctcacgg      60
tcacggggtc acggccatgg aagagaactc aagtaaaaaa acgctatcgg aaactatgag      120
cttacaagat acagttctga agtttttcag agtttacata ccaaatacaa ccgcggatga      180
catggtagta cgttgcttaa atctcttaga acagagcatt tccgctctgt ttttgcaaga      240
tcttgtcttt ttccgagttt tgaatgatgt gtattgaaca atcttgaaag ttttagcttt      300
agcagacatt ttttgagttt taggttggtg gtttatgtga tgtgacaaat ccacgggtgg      360
tatgatattg ttttgaaatt atgttagtgt tgttcaaagt aagatgtgtg tttctctatt      420
gttttgtaca gaatctacct ttggtttcag acaagatctc agggaagcct cttcctcggg      480
aggttaactgt taaaagtgtg tctctgggga acatttgagg gatggaaatg aaagcaaacg      540
gtaacacagt gtttctccga gacgggtgga agaaaatcgt caaggacgag aatgtgactg      600
agccaatttt cttggagttt gagttcgatg gttatggtgt gttccacttt tgcgtgtacg      660
agtatggttc aatgtgtaaa aggatgagat ctccaatgga aaaagaagtg attaaagtgg      720
acagtgaaga agatgtgctt gtggggaatg aagagagcac aaaagggctt gaggagtcgc      780
caagaagagg tggtaacaagt agaagacgtg cgaaactgaa gactaatagt cataagattc      840
atgaacatct agacaacaaa ctaaaccgtg cgtttccggt tgatatgact caaaatagaa      900
cggtaaagaa aacgaaatgt gactaaagaa aatttcaaat gactaaatgg tttgtcattc      960
attatgattg gttctgattt tcagcgcata ccgtctttac ttataaagga ctacaacttg     1020
acatttccca acatggttat catgcgtgac aagattggca tattgaagag aagaatcgtg     1080
atttggaaga acagatccgt gtatctaaat ggaatcggta gtatcatccg aaggaatcat     1140
gtgaagccag gtaatgaagt ggtattcgaa cttaagatgg tcaatggtta tcacgggttg     1200
gttcacgaaa tcaaggtcca cattatcaag gcctgatcat attcttacct gttgttctat     1260
cttagagaat gttaattgaa atgtttaagt tatttatctc gttgtgttga tcatgttagt     1320
tttgcatctg tttttcatta tgcatttcct gacactcgat gggttgaaat gggttttttt     1380
ttggcgaact gtctctctat ctctttgtaa tggcatgact ttgccttttc acaaaaaaaa     1440
aaaaawaaaaa aaaaaamngg awtgtcc
```

(2) INFORMATION FOR SEQ ID NO:1304:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 181 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..181  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

```
Met Leu Val Leu Phe Lys Val Arg Cys Val Phe Leu Tyr Cys Phe Val
1          5          10          15
Gln Asn Leu Pro Leu Val Ser Asp Lys Ile Ser Gly Lys Pro Leu Pro
20        25        30
Arg Lys Val Thr Val Lys Ser Val Ser Ser Gly Asn Ile Trp Arg Met
35        40        45
Glu Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp Lys
50        55        60
Lys Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu Phe
65        70        75        80
Glu Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr Gly
85        90        95
Ser Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile Lys
100       105       110
Val Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr Lys
115       120       125
```

Gly Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg Ala  
130 135 140  
Lys Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn Lys  
145 150 155 160  
Leu Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val Lys  
165 170 175  
Lys Thr Lys Cys Asp  
180

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1500027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

Met Glu Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp  
1 5 10 15  
Lys Lys Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu  
20 25 30  
Phe Glu Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr  
35 40 45  
Gly Ser Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile  
50 55 60  
Lys Val Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr  
65 70 75 80  
Lys Gly Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg  
85 90 95  
Ala Lys Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn  
100 105 110  
Lys Leu Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val  
115 120 125  
Lys Lys Thr Lys Cys Asp  
130

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1500028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp Lys Lys  
1 5 10 15  
Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu Phe Glu  
20 25 30  
Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr Gly Ser  
35 40 45  
Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile Lys Val  
50 55 60  
Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr Lys Gly  
65 70 75 80  
Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg Ala Lys

85 90 95  
Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn Lys Leu  
100 105 110  
Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val Lys Lys  
115 120 125  
Thr Lys Cys Asp  
130

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2031
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| ttttaacgaa | cattttgttg  | gtaagaacga | agaagacgtg | gagaagtaga  | agaatgatga | 60   |
| tgcagaaatt | gagaagatcg  | ggggagttca | taagatttgg | atgcaaatct  | ctaattagta | 120  |
| gccgaccaa  | caaggactca  | gtgtcacgtt | ctgtgtcagg | ctttgtgaat  | cactacaaat | 180  |
| caaaaggcaa | gctttttgag  | ctaagtgatg | ggaactataa | gacagagctt  | catcatccat | 240  |
| gtattagtag | aaatgtgggg  | atgcttcttc | agcagtataa | gtgttttgga  | tcatacgcag | 300  |
| cttctttaat | tcagagaaac  | cctttgtttt | cgctcgttga | ttcgaaagat  | gttagctact | 360  |
| ttaaggagat | attaggtgaa  | aaaaacgtgg | ttgaagataa | agaaaggctt  | gagactgcta | 420  |
| atacagattg | gatgcataag  | tacaaaggat | ctagtaagct | gatgctcttg  | cccaagaata | 480  |
| gacaagaggt | gtctcagata  | cttgagyact | gtgattcgag | gcgttttagca | ggttgttcct | 540  |
| caaggaggaa | acactggctt  | tgttgggtga | agtgtgcctg | tctttgatga  | ggtgatcgtc | 600  |
| aatgttggtc | tgatgaacaa  | aatcttatct | tttgatgagg | ttagtggcgt  | cttggtgtgt | 660  |
| gaagcaggat | gcatattaga  | aaatctggca | actttccttg | acacaaaagg  | ttttattatg | 720  |
| cctctagact | taggtgcaaa  | aggaagctgt | catatcggtg | gaaatgtttc  | aactaatgct | 780  |
| ggtggtttgc | gtctaataccg | ttatggctca | cttcatggaa | ctgtattggg  | tctagaagct | 840  |
| gtcacagcaa | atggcaacgt  | gcttgacatg | cttggaaact | tacgcaaaga  | caatactggg | 900  |
| tacgacttaa | aacatttggt  | tattggtagt | gaaggatcac | ttggtattgt  | aactaaagtt | 960  |
| tctattctca | cacaaccaa   | attgtcttct | gtaaaattag | ccttcattgc  | ttgcaaagat | 1020 |
| tatctcagct | gccagaaact  | tcttggtgaa | gcaaagagaa | atcttgagaa  | gatactctcg | 1080 |
| gctttcgagt | ttcttgataa  | caattccatg | gatttggtag | tgaaccacct  | agacggtgta | 1140 |
| cgtaatccag | tttctctctc  | ggagaacttt | tatattctga | tcgagacaac  | agggagtgat | 1200 |
| gaaactaatg | acagggagaa  | gcttgaagct | ttcctgttga | agtcactgga  | aaaaggttta | 1260 |
| gtttctgatg | gtgtaatcgc  | tcaagacatt | aaccaggcat | cctcattttg  | gcgcatacga | 1320 |
| gagggtataa | cagaggcggt  | acagaaagca | ggagctgttt | acaagtatga  | cttatcctta | 1380 |
| ccggttgaag | aaattttaca  | tattgttaac | gatcttcgag | ggagattagg  | tgacttagca | 1440 |
| aatgttatgg | gatatgggtc  | ccttgagagc | ggaaatctac | atttaaacad  | ctcagccgcg | 1500 |
| gaatataacg | ataagctttt  | aggtttgata | gagccttatg | tctatgagtg  | gacatcaaag | 1560 |
| caccgtggaa | gcatacagtc  | ggaacatgga | ttaggtgtaa | tgaaagctaa  | tgaaatcttc | 1620 |
| tacagcaaat | caccgcgaac  | tggtgcatta | atggcttcca | ttaaaaagtt  | gctggacca  | 1680 |
| aagggaattc | tcaaccctta  | caaagttctt | cctcactctc | tcttctccaa  | ctaagggtgg | 1740 |
| tgatgagatg | attcttcaaa  | caggaatttg | gaacatgagc | agccaagttt  | gagcgatatg | 1800 |
| attgatgcaa | aggaacaaaa  | atacaagtgc | tgattaaaaa | gtcttttaac  | tcaaaagtgt | 1860 |
| atatgttcgc | ttcttcttct  | ttgttggtgt | tggtgttacc | ttgttttaat  | atctttttag | 1920 |
| taaaggataa | gaaagaatct  | aaacctattg | atcttacgtg | tatttaaagt  | taaaatttgc | 1980 |
| agtgtatgta | gaccaaact   | cgaaaagata | atctataata | atagtatttc  | c          |      |

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..373

(D) OTHER INFORMATION: / Ceres Seq. ID 1500037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Ile | Leu | Ser | Phe | Asp | Glu | Val | Ser | Gly | Val | Leu | Val | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Ala | Gly | Cys | Ile | Leu | Glu | Asn | Leu | Ala | Thr | Phe | Leu | Asp | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Phe | Ile | Met | Pro | Leu | Asp | Leu | Gly | Ala | Lys | Gly | Ser | Cys | His | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Gly | Asn | Val | Ser | Thr | Asn | Ala | Gly | Gly | Leu | Arg | Leu | Ile | Arg | Tyr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Gly | Ser | Leu | His | Gly | Thr | Val | Leu | Gly | Leu | Glu | Ala | Val | Thr | Ala | Asn |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Asn | Val | Leu | Asp | Met | Leu | Gly | Thr | Leu | Arg | Lys | Asp | Asn | Thr | Gly |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |
| Tyr | Asp | Leu | Lys | His | Leu | Phe | Ile | Gly | Ser | Glu | Gly | Ser | Leu | Gly | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Val | Thr | Lys | Val | Ser | Ile | Leu | Thr | Gln | Pro | Lys | Leu | Ser | Ser | Val | Asn |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Leu | Ala | Phe | Ile | Ala | Cys | Lys | Asp | Tyr | Leu | Ser | Cys | Gln | Lys | Leu | Leu |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Val | Glu | Ala | Lys | Arg | Asn | Leu | Gly | Glu | Ile | Leu | Ser | Ala | Phe | Glu | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Asp | Asn | Asn | Ser | Met | Asp | Leu | Val | Leu | Asn | His | Leu | Asp | Gly | Val |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Arg | Asn | Pro | Val | Ser | Ser | Ser | Glu | Asn | Phe | Tyr | Ile | Leu | Ile | Glu | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Thr | Gly | Ser | Asp | Glu | Thr | Asn | Asp | Arg | Glu | Lys | Leu | Glu | Ala | Phe | Leu |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Leu | Lys | Ser | Leu | Glu | Lys | Gly | Leu | Val | Ser | Asp | Gly | Val | Ile | Ala | Gln |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |
| Asp | Ile | Asn | Gln | Ala | Ser | Ser | Phe | Trp | Arg | Ile | Arg | Glu | Gly | Ile | Thr |
| 225 |     |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ala | Leu | Gln | Lys | Ala | Gly | Ala | Val | Tyr | Lys | Tyr | Asp | Leu | Ser | Leu |
|     |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Pro | Val | Glu | Glu | Ile | Tyr | Asn | Ile | Val | Asn | Asp | Leu | Arg | Gly | Arg | Leu |
|     |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     | 270 |     |
| Gly | Asp | Leu | Ala | Asn | Val | Met | Gly | Tyr | Gly | His | Leu | Gly | Asp | Gly | Asn |
|     |     |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | His | Leu | Asn | Ile | Ser | Ala | Ala | Glu | Tyr | Asn | Asp | Lys | Leu | Leu | Gly |
|     |     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Leu | Ile | Glu | Pro | Tyr | Val | Tyr | Glu | Trp | Thr | Ser | Lys | His | Arg | Gly | Ser |
| 305 |     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Ile | Ser | Ala | Glu | His | Gly | Leu | Gly | Val | Met | Lys | Ala | Asn | Glu | Ile | Phe |
|     |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |
| Tyr | Ser | Lys | Ser | Pro | Glu | Thr | Val | Ala | Leu | Met | Ala | Ser | Ile | Lys | Lys |
|     |     |     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |
| Leu | Leu | Asp | Pro | Lys | Gly | Ile | Leu | Asn | Pro | Tyr | Lys | Val | Leu | Pro | His |
|     |     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |
| Ser | Leu | Phe | Ser | Asn |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 370 |

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1500038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

```
Met Pro Leu Asp Leu Gly Ala Lys Gly Ser Cys His Ile Gly Gly Asn
1      5      10      15
Val Ser Thr Asn Ala Gly Gly Leu Arg Leu Ile Arg Tyr Gly Ser Leu
      20      25      30
His Gly Thr Val Leu Gly Leu Glu Ala Val Thr Ala Asn Gly Asn Val
      35      40      45
Leu Asp Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly Tyr Asp Leu
      50      55      60
Lys His Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile Val Thr Lys
      65      70      75      80
Val Ser Ile Leu Thr Gln Pro Lys Leu Ser Ser Val Asn Leu Ala Phe
      85      90      95
Ile Ala Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Leu Val Glu Ala
      100     105     110
Lys Arg Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe Leu Asp Asn
      115     120     125
Asn Ser Met Asp Leu Val Leu Asn His Leu Asp Gly Val Arg Asn Pro
      130     135     140
Val Ser Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr Thr Gly Ser
      145     150     155     160
Asp Glu Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu Leu Lys Ser
      165     170     175
Leu Glu Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln Asp Ile Asn
      180     185     190
Gln Ala Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr Glu Ala Leu
      195     200     205
Gln Lys Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu Pro Val Glu
      210     215     220
Glu Ile Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu Gly Asp Leu
      225     230     235     240
Ala Asn Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn Leu His Leu
      245     250     255
Asn Ile Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly Leu Ile Glu
      260     265     270
Pro Tyr Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser Ile Ser Ala
      275     280     285
Glu His Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe Tyr Ser Lys
      290     295     300
Ser Pro Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys Leu Leu Asp
      305     310     315     320
Pro Lys Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His Ser Leu Phe
      325     330     335
Ser Asn
```

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1500039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

```
Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly Tyr Asp Leu Lys His
1      5      10      15
```

```

Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile Val Thr Lys Val Ser
      20      25      30
Ile Leu Thr Gln Pro Lys Leu Ser Val Asn Leu Ala Phe Ile Ala
      35      40      45
Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Leu Val Glu Ala Lys Arg
      50      55      60
Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe Leu Asp Asn Asn Ser
      65      70      75      80
Met Asp Leu Val Leu Asn His Leu Asp Gly Val Arg Asn Pro Val Ser
      85      90      95
Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr Thr Gly Ser Asp Glu
      100      105      110
Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu Leu Lys Ser Leu Glu
      115      120      125
Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln Asp Ile Asn Gln Ala
      130      135      140
Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr Glu Ala Leu Gln Lys
      145      150      155      160
Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu Pro Val Glu Glu Ile
      165      170      175
Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu Gly Asp Leu Ala Asn
      180      185      190
Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn Leu His Leu Asn Ile
      195      200      205
Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly Leu Ile Glu Pro Tyr
      210      215      220
Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser Ile Ser Ala Glu His
      225      230      235      240
Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe Tyr Ser Lys Ser Pro
      245      250      255
Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys Leu Leu Asp Pro Lys
      260      265      270
Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His Ser Leu Phe Ser Asn
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

```

aacaacatct ttcacacaac aattcacaca atttctcggt tttttttggt tatcatcaaa      60
agttttaatc taaattacgt atcaaattcc gagcaagatg actattcttg ttgaacattt      120
tgttcctgat tcaagagtgg atgaaaagaa agtgatagag gagagggata atgaattggt      180
gttgatgga ggttttggtg ttccaaaatc aaaggaaact gatgcattcg atgctcctga      240
tatgaatttc ytgggccatt ccttcaggga ttatgagaat gatgaaagcg agagacaaca      300
aggtgttgag gaattttaca ggatgcaaca cattcaccag acctatgact ttgtgaagaa      360
gatgaggaaa gagtatggaa aacttaacaa gatggaaatg agtatatggg aatggtgtga      420
gttattgaac aatgttggtg atgaaagcga tccggatctt gatgagcctc aaattcaaca      480
ccttctccaa accgctgaag ccattcgaag ggactatccc gacgaagatt ggctccatct      540
cactgcccta atccatgatc ttggcaagggt tctccttctg ccagaattcg gtggtcttcc      600
ccagtgggct gtcgttggtg atacatttcc agttggatgt accttcgact cagccaatat      660
tcaccacaag tatttcaaag gaaaccatga tatcaacaac ccaaagtaca acacaaaaaa      720
tggagtttac actgaaggat gtggttttaga caatgtttctc atgtcatggg gtcatgacga      780

```



```
ctacatgtat ttggtggcta agaagaatgg caccaccctt cctcagctg gtctcttcat      840
tattcgatat cattcctttt atccattgca caaggcagga gcctacacac acttgatgaa      900
cgatgaggac agagatgata tcaagtggct ccatgtcttc aataaatatg acctatacag      960
taagagcaaa gttctggtag atgtcgaaca agtgaagcct tactacattt cactcatcaa    1020
caagtatttt cgggcgaaac taaaatggtg agataaagct acgagtcaat taattaacta    1080
tcttttatga ggagaacgag atcgaagggt aacgagtttt ctattgtata caacggaaga    1140
taaattctatc taataaaaaa gttggtgtgt tcatttgtaa ttttttcccc catcagttta    1200
aaagttatgt tgt
```

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1500041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

```
Met Thr Ile Leu Val Glu His Phe Val Pro Asp Ser Arg Val Asp Glu
1      5      10      15
Lys Lys Val Ile Glu Glu Arg Asp Asn Glu Leu Val Leu Asp Gly Gly
20     25     30
Phe Val Val Pro Lys Ser Lys Glu Thr Asp Ala Phe Asp Ala Pro Asp
35     40     45
Met Asn Phe Xaa Gly His Ser Phe Arg Asp Tyr Glu Asn Asp Glu Ser
50     55     60
Glu Arg Gln Gln Gly Val Glu Glu Phe Tyr Arg Met Gln His Ile His
65     70     75     80
Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys Glu Tyr Gly Lys Leu
85     90     95
Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys Glu Leu Leu Asn Asn
100    105    110
Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu Pro Gln Ile Gln His
115    120    125
Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp Tyr Pro Asp Glu Asp
130    135    140
Trp Leu His Leu Thr Ala Leu Ile His Asp Leu Gly Lys Val Leu Leu
145    150    155    160
Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala Val Val Gly Asp Thr
165    170    175
Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn Ile His His Lys Tyr
180    185    190
Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys Tyr Asn Thr Lys Asn
195    200    205
Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn Val Leu Met Ser Trp
210    215    220
Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys Lys Asn Gly Thr Thr
225    230    235    240
Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr His Ser Phe Tyr Pro
245    250    255
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg
260    265    270
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser
275    280    285
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile
290    295    300
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp
305    310    315
```

(2) INFORMATION FOR SEQ ID NO:1313:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 269 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..269  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500042  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

Met Asn Phe Xaa Gly His Ser Phe Arg Asp Tyr Glu Asn Asp Glu Ser  
1                  5                  10                  15  
Glu Arg Gln Gln Gly Val Glu Glu Phe Tyr Arg Met Gln His Ile His  
                  20                  25                  30  
Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys Glu Tyr Gly Lys Leu  
                  35                  40                  45  
Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys Glu Leu Leu Asn Asn  
                  50                  55                  60  
Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu Pro Gln Ile Gln His  
65                  70                  75                  80  
Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp Tyr Pro Asp Glu Asp  
                  85                  90                  95  
Trp Leu His Leu Thr Ala Leu Ile His Asp Leu Gly Lys Val Leu Leu  
                  100                  105                  110  
Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala Val Val Gly Asp Thr  
                  115                  120                  125  
Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn Ile His His Lys Tyr  
130                  135                  140  
Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys Tyr Asn Thr Lys Asn  
145                  150                  155                  160  
Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn Val Leu Met Ser Trp  
                  165                  170                  175  
Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys Lys Asn Gly Thr Thr  
                  180                  185                  190  
Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr His Ser Phe Tyr Pro  
195                  200                  205  
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg  
210                  215                  220  
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser  
225                  230                  235                  240  
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile  
                  245                  250                  255  
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp  
                  260                  265

(2) INFORMATION FOR SEQ ID NO:1314:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 242 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..242  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500043  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

Met Gln His Ile His Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys  
1                  5                  10                  15  
Glu Tyr Gly Lys Leu Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys  
                  20                  25                  30

Glu Leu Leu Asn Asn Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu  
35 40 45  
Pro Gln Ile Gln His Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp  
50 55 60  
Tyr Pro Asp Glu Asp Trp Leu His Leu Thr Ala Leu Ile His Asp Leu  
65 70 75 80  
Gly Lys Val Leu Leu Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala  
85 90 95  
Val Val Gly Asp Thr Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn  
100 105 110  
Ile His His Lys Tyr Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys  
115 120 125  
Tyr Asn Thr Lys Asn Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn  
130 135 140  
Val Leu Met Ser Trp Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys  
145 150 155 160  
Lys Asn Gly Thr Thr Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr  
165 170 175  
His Ser Phe Tyr Pro Leu His Lys Ala Gly Ala Tyr Thr His Leu Met  
180 185 190  
Asn Asp Glu Asp Arg Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys  
195 200 205  
Tyr Asp Leu Tyr Ser Lys Ser Lys Val Leu Val Asp Val Glu Gln Val  
210 215 220  
Lys Pro Tyr Tyr Ile Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu  
225 230 235 240  
Lys Trp

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1579
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| agctctgttg | tggaacatcg  | gaaatcagaa | ctgaaacaga | aacagaaacc | atggagaaga | 60   |
| gagaagacga | acaacaaaag  | cgcgacgatt | ctagattcaa | tcaaacactc | aagaacgtcc | 120  |
| aagggtttct | taaaggtaga  | agtattcctg | gtaaggtatt | gttgactagg | agatcagatc | 180  |
| ctcctccata | cccaatctct  | ccaacatata | aacggagctt | atctgagaat | gacgccggaa | 240  |
| gaaatgagct | attcgaaaag  | cctgttgagg | tggaggatca | caattcaagc | aagaaacatg | 300  |
| ataatacata | tgctggttaag | ctacgatcaa | actctagtgc | tgaaaggagt | gtgaaagaag | 360  |
| ttcaaaactt | gaagataggt  | gttcgatcaa | gtgactctgc | tagagttatg | aagttcaaca | 420  |
| aagtgccttc | agaaacaact  | gtcatattag | agaaactgcg | cgagctagca | tggaatggtg | 480  |
| taccacacta | tatgcggcct  | gatgtctggc | ggcttctctt | gggatatgca | ccacctaat  | 540  |
| cagatagaag | ggaggtgtt   | ctgagaagaa | aacgtcttga | atatctggaa | tctgttgccc | 600  |
| aattttatga | ccttccagat  | tccgaacgtt | ctgatgatga | gatcaatatg | cttcgccaga | 660  |
| ttgctgttga | ctgtccgagg  | actgtaccag | atgtcagttt | ctttcagcaa | gaacaggtgc | 720  |
| agaaatcact | ggagcgatt   | ctttacacgt | gggccattag | acatccagca | agcggatatg | 780  |
| ttcagggaat | aaatgacctg  | gtcacgccct | tcctagtgtg | tttcttgtaa | gaatatctag | 840  |
| atggcggtgt | agacagttgg  | tcaatggatg | atctatctgc | tgaaaaagtc | tcagatgtag | 900  |
| aagcggattg | ctactggtgc  | ttaacaaaag | tccttgacgg | tatgcaagat | cattacacgt | 960  |
| ttgctcaacc | tggaatccag  | agacttgtgt | ttaagctgaa | ggaactggtc | aggcgtatcg | 1020 |
| atgaacctgt | ttcaagacac  | atggaagagc | atgggctaga | gtttcttcaa | tttgctttcc | 1080 |
| ggtggtataa | ttgtcttctg  | attcgtgaga | tccatttcaa | tctcatcaat | cgactatggg | 1140 |
| acacttatct | tgctgaagga  | gatgcgttgc | cagacttcct | ggtgtatata | tgctagcttt | 1200 |
| ctcttgacgt | ggtctgatga  | gctgaagaag | ctagattttc | aagaaatggt | aatgttcctg | 1260 |

```
caacaccttc cgacacataa ctggtcagac caagagctcg aaatggtttt gtcaagagct 1320
tacatgtggc atagtatgtt caataattcc ccaaaccatt tggctagctg aaatgacttt 1380
tcctccatgg tgcttgctgc tgtttttccc ttgtttatat tatcttcttc ttcttggtgt 1440
ctaaatcagc tttcgttttg ttttgggtta tggtaaatgc taacattctt gtcttggttaa 1500
ttgttattag tttatgtatg gtttcacttg ttgaatctgt caccagtttg tgtgtttgta 1560
atattttagt ctttcactg
```

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..275

(D) OTHER INFORMATION: / Ceres Seq. ID 1500051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

```
Leu Cys Cys Gly Thr Ser Glu Ile Arg Thr Glu Thr Glu Thr Glu Thr
1      5      10      15
Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe
20      25      30
Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile
35      40      45
Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Pro Tyr Pro
50      55      60
Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg
65      70      75      80
Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser
85      90      95
Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser
100     105     110
Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg
115     120     125
Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu
130     135     140
Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val
145     150     155     160
Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Leu Gly Tyr Ala
165     170     175
Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu
180     185     190
Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu
195     200     205
Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys
210     215     220
Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Gln Val Gln
225     230     235     240
Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala
245     250     255
Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val
260     265     270
Ile Phe Leu
275
```

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1500052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Arg | Glu | Asp | Glu | Gln | Gln | Lys | Arg | Asp | Asp | Ser | Arg | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Gln | Thr | Leu | Lys | Asn | Val | Gln | Gly | Phe | Leu | Lys | Gly | Arg | Ser | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Gly | Lys | Val | Leu | Leu | Thr | Arg | Arg | Ser | Asp | Pro | Pro | Pro | Tyr | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Pro | Thr | Tyr | Gln | Arg | Ser | Leu | Ser | Glu | Asn | Asp | Ala | Gly | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Glu | Leu | Phe | Glu | Ser | Pro | Val | Glu | Val | Glu | Asp | His | Asn | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Lys | His | Asp | Asn | Thr | Tyr | Ala | Gly | Lys | Leu | Arg | Ser | Asn | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Glu | Arg | Ser | Val | Lys | Glu | Val | Gln | Asn | Leu | Lys | Ile | Gly | Val | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Asp | Ser | Ala | Arg | Val | Met | Lys | Phe | Asn | Lys | Val | Leu | Ser | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Thr | Val | Ile | Leu | Glu | Lys | Leu | Arg | Glu | Leu | Ala | Trp | Asn | Gly | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | His | Tyr | Met | Arg | Pro | Asp | Val | Trp | Arg | Leu | Leu | Leu | Gly | Tyr | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Pro | Asn | Ser | Asp | Arg | Arg | Glu | Ala | Val | Leu | Arg | Arg | Lys | Arg | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Tyr | Leu | Glu | Ser | Val | Gly | Gln | Phe | Tyr | Asp | Leu | Pro | Asp | Ser | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Asp | Asp | Glu | Ile | Asn | Met | Leu | Arg | Gln | Ile | Ala | Val | Asp | Cys |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Pro | Arg | Thr | Val | Pro | Asp | Val | Ser | Phe | Phe | Gln | Gln | Glu | Gln | Val | Gln |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Lys | Ser | Leu | Glu | Arg | Ile | Leu | Tyr | Thr | Trp | Ala | Ile | Arg | His | Pro | Ala |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Gly | Tyr | Val | Gln | Gly | Ile | Asn | Asp | Leu | Val | Thr | Pro | Phe | Leu | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ile | Phe | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Asn | Lys | Val | Leu | Ser | Glu | Thr | Thr | Val | Ile | Leu | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Glu | Leu | Ala | Trp | Asn | Gly | Val | Pro | His | Tyr | Met | Arg | Pro | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Trp | Arg | Leu | Leu | Leu | Gly | Tyr | Ala | Pro | Pro | Asn | Ser | Asp | Arg | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Val | Leu | Arg | Arg | Lys | Arg | Leu | Glu | Tyr | Leu | Glu | Ser | Val | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Phe | Tyr | Asp | Leu | Pro | Asp | Ser | Glu | Arg | Ser | Asp | Asp | Glu | Ile | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

Met Leu Arg Gln Ile Ala Val Asp Cys Pro Arg Thr Val Pro Asp Val  
85 90 95  
Ser Phe Phe Gln Gln Gln Val Gln Lys Ser Leu Glu Arg Ile Leu  
100 105 110  
Tyr Thr Trp Ala Ile Arg His Pro Ala Ser Gly Tyr Val Gln Gly Ile  
115 120 125  
Asn Asp Leu Val Thr Pro Phe Leu Val Ile Phe Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

acaattcaga ttccaatttt ctcaaactct aaaatcaatc tctcaaactc ctcaaccgtg 60  
atcaaggtag atttctgagt tcttattgta tttcttcgat ttgtttcgtt cgatcgcaat 120  
ttaggtctctg ttctttgatt ttgatctcgt taatctctga tcggaggcaa attacatagt 180  
ttcatcgta gatctcttct tatttctcga ttaggttcg tatttttcgc agatctgttt 240  
attttcttgt tgtttccttg tatttgatcc gatttggtga aagaatttgt gtgttctcga 300  
ttatttatgc ttgatctgt gatttttatc tagatttggt gttagtttct tgtttgtgcg 360  
atogaatttg tcgattaatc tcggttttct tgattaacag atgcagatct tcgttaagac 420  
tctcaccgga aagactatca ccctcgaggt ggaaagctct gacaccatcg acaacgtaaa 480  
ggccaagatc caggataagg aaggtattcc tccggatcag cagaggctta tcttcgccgg 540  
aaagcagttg gaggatggcc gcacgttggc ggattacaat atccagaagg aatccaccct 600  
ccacttggtt ctcaaggctcc gtggtggtat gcagattttc gttaaaaccc taacgggaaa 660  
gacgattact cttgaggttg agagctctga caccattgac aacgtcaagg ccaagatcca 720  
agataaggag ggtattcctc cggaccagca gaggttgatc ttcgccgga agcaacttga 780  
ggacggcaga actttggcgg attacaacat ccagaaggag tctacgcttc atttggctct 840  
tgcgtctgcg tggaggtatg cagatcttcg taaagacttt gaccggaaag accatcactc 900  
ttgaagttga gagctccgac accattgata acgtgaaggc taagatccag gacaaggaa 960  
gcattcctcc ggaccagcag cgtctcatct tcgctggaaa gcagcttgag gatggacgta 1020  
ctttggccga ctacaacatc cagaaggagt ctactcttca cttggctcctc cgtctccgtg 1080  
gtggtttcta aaccttgtct ctctctctta tggttactga accaagttca tgtatcgttt 1140  
catctagtac ttgtgtggtt tatgttttgg ggccatgtac agcctctgat aaataattga 1200  
tcgactatgt ttccgtttct ttcatctctc ttttctttc

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60